

Scientists find transcription by committee

Anyone curious about how embryos develop, how cancers arise, or even how cells function from day to day must wonder about the transcription of genes. Organisms store the construction plans for proteins in genes. Enzymes called RNA polymerases then retrieve those plans by creating an RNA molecule that matches a particular gene's DNA. The transcribed RNA relays the specifics of the plans to ribosomes, giant cellular complexes that make proteins.

But RNA polymerases do not act alone. Instead, they function as part of a labyrinthine molecular bureaucracy whose organization chart scientists have sought to fathom for decades, says Richard A. Young, a geneticist at the Whitehead Institute for Biomedical Research in Cambridge, Mass.

Earlier, Young's group discovered a group of behind-the-scenes players called SRB proteins. Now, he and Whitehead colleague Anthony J. Koleske have evidence that, in yeast, several SRB proteins chair a committee — called a holoenzyme — that includes RNA polymerase and several other substances important for reading the genetic code. "They come together as a single processing unit," says Young. "It is as large as a ribosome and as complex."

Scientists knew that transcription was

a group activity. Many thought that participating molecules joined one at a time, gathering at the site on DNA close to where transcription begins.

But only after the cell convenes this holoenzyme does RNA polymerase proceed to the specific transcription site, Young and Koleske report in the March 31 NATURE.

Young's group investigated transcription by introducing specific genetic defects that cause the cell to make mutant RNA polymerase or defective SRB proteins. They found that some defects bogged down transcription, while others sped up the reading of the genetic code. They also assessed the status of SRB proteins in the transcription hierarchy by testing the RNA polymerase's ability to read DNA in the presence of different substances.

"The discovery of a holoenzyme clearly has major implications in understanding the mechanism of transcription," says Michael H. Sayre, a biochemist at Johns Hopkins University in Baltimore. "It's a significant development."

The new results suggest that SRB proteins perform three functions, says Young. First, they help unite RNA polymerase with general transcription factors, molecules that make possible the reading of any piece of DNA. Second, they

enable this complex to interact with other factors that activate transcription of specific genes. Third, the SRB proteins seem to control the rate at which transcription occurs, not just whether it occurs, Young says.

But not all data indicate that SRB proteins run this molecular committee — or are even necessary for it to do its work, Sayre told SCIENCE NEWS. Unpublished work by Roger D. Kornberg and his colleagues at Stanford University School of Medicine suggests that other proteins link with RNA polymerase and form a different sort of holoenzyme that then starts transcribing DNA.

"The composition of the holoenzyme is still up in the air as far as I am concerned," says Sayre. "There's still a lot of ambiguity as to what proteins are doing what and which ones are simply going along for the ride."

These lab experiments show only that this holoenzyme protein can exist. But if holoenzymes prove essential in yeast, transcription in other eukaryotic organisms, including mammals, should work similarly, says Ronald C. Conaway, a biochemist at the Oklahoma Medical Research Foundation in Oklahoma City.

"The finding simplifies models for eukaryotic genetic activation and indicates key regulatory checkpoints in the process," says Michael Carey, a biochemist at the University of California, Los Angeles, School of Medicine. — E. Pennisi

Electron pairs in superconducting rings

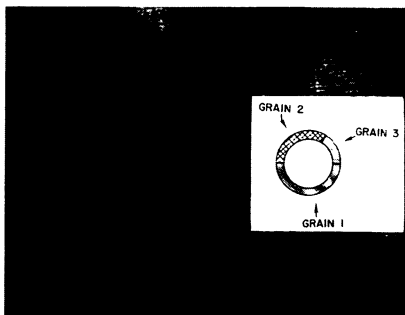
When a material becomes a superconductor, current-carrying electrons behave as if they were paired, even though electrons at close quarters repel each other. In conventional superconductors, this pairing results from the coordinated interaction between electrons and vibrations of the crystal lattice through which the electrons move.

However, such interactions are too weak to account for superconductivity in high-temperature copper-oxide superconductors. Although theorists are certain that pairing occurs, they have so far been unable to agree on what mechanism leads to the formation of electron pairs in these materials.

Now, researchers have obtained new experimental evidence that may help establish how high-temperature superconductivity works. John R. Kirtley, Chang C. Tsuei, and their coworkers at the IBM Thomas J. Watson Research Center in Yorktown Heights, N.Y., have found that a superconducting ring can exhibit magnetization half the size of the magnetic flux quantum.

Kirtley described the findings at an American Physical Society meeting held last week in Pittsburgh.

Kirtley and his colleagues worked



Scanning SQUID microscope image of four superconducting rings, each one 68 micrometers wide. The center ring has three junctions (see inset).

with a set of four microscopic rings made from thin films of the high-temperature superconductor yttrium barium copper oxide (see image). Each ring contained a different number of grain boundaries, where superconducting films with different lattice orientations meet to create junctions.

When the rings are chilled to 4.2 kelvins, a tiny electrical current begins to circulate spontaneously within each one. This supercurrent generates a magnetic field. Using a scanning SQUID (superconducting quantum interfer-

ence device) microscope, the researchers can detect and measure the resulting magnetization at each ring.

Kirtley and his team discovered that a three-junction ring — unlike those having no junction or two junctions — reveals magnetization in "packages" half the size of the magnetic flux quantum.

"If [yttrium barium copper oxide] were an ordinary superconductor, you would never see the effect they claim to see," says Frederick C. Wellstood of the University of Maryland in College Park, who has been working on a similar kind of experiment.

The IBM results may shed light on the particular type of pairing that occurs between two electrons in a high-temperature superconductor. Theorists have debated heatedly whether electron pairing is characterized by so-called s-wave or d-wave symmetry. The new findings — if they hold up — suggest the existence of d-wave pairing.

Such evidence doesn't settle the argument concerning the mechanism by which pairing occurs in high-temperature superconductors, but it may rule out certain possibilities. At the same time, the experimental results need to be checked. For example, magnetic impurities at the junctions may have affected the measurements. — I. Peterson