they slam into high-altitude gas molecules.

But there's one catch: To judge from the range of gamma-ray energies recorded in orbit, the electrons would need energies of over 1 million electron volts. Accelerating electrons to those energies, at least by Wilson's mechanism, would take lightning 30 times more powerful than the typical bolt.

Such "superbolts"—enormous, cloud-to-cloud bolts extending tens of kilometers or even 100 kilometers horizontally—have been sighted, notes Lyons, and he suspects they might trigger optical flashes as well. The storms that consistently produce flashes, he has found, are the very biggest ones, spanning a few hundred kilometers and known as mesoscale convective systems (*Science*, 30 August 1985, p. 848). Storms on that scale, he says, are the most likely to unleash superbolts. Superbolts might also explain why the flashes tend to be concentrated not over the heart of these storms, where ordinary lightning activity peaks, but over the less active margins, which might be anchor points for the long-range lightning.

Space physicist Gennady Milikh of the University of Maryland and his colleagues have independently done calculations that support Lyons' speculation that big, horizontal lightning bolts would be particularly effective triggers for high-altitude optical flashes. But testing that and other ideas will take intensive observations, and researchers will be flocking to the High Plains this summer to make them. Cross your fingers for more dark and stormy nights.

–Richard A. Kerr

Additional Reading

W. A. Lyons, "Characteristics of Luminous Structures in the Stratosphere Above Thunderstorms as Imaged by Low-Light Video," *Geophysical Research Letters* **21**, 875 (1994).

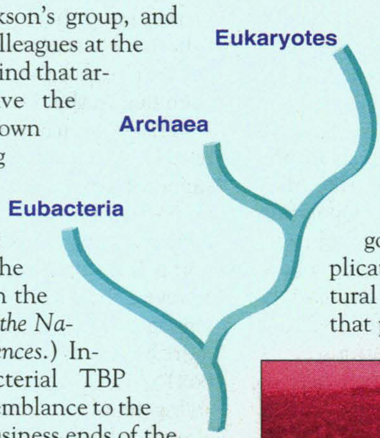
MOLECULAR EVOLUTION

Archaea and Eukaryotes Grow Closer

Once upon a time, biologists drew the tree of life with two main branches. The prokaryotic kingdom, containing single-celled organisms, such as bacteria, that lack nuclei, occupied one limb; the other limb housed the eukaryotic kingdom, comprising all the rest of life, from single-celled paramecia to *Homo sapiens*. But that simple picture changed in 1977 when evolutionist Carl Woese of the University of Illinois discovered that a group of strange organisms he originally called archaebacteria, which were then classified as prokaryotes, appear to differ as much from other bacteria as they do from eukaryotes. That placed the archaebacteria, which generally live in extreme environments such as super-hot ocean hydrothermal vents, in their own kingdom—the Archaea—a separate branch on the tree of life.

But Woese's finding left unanswered the question of *where* that branch belongs on the tree. Did it split off the main trunk before the eukaryotes diverged from the other bacteria (known as eubacteria)? Or did it branch off later, and if so, from which limb? Evidence that appears to answer that question is emerging in the form of similarities in the molecular machineries that Archaea and the eukaryotes use in the first step of gene expression, the transcription of genes into RNA. The latest advance comes from Stephen Jackson and his co-workers at Cambridge University in England, who report on p. 1326 that they have cloned an archaebacterial gene that closely resembles the gene for a key eukaryotic transcription factor, and that the factor seems to function much the same in the Archaea as in humans. "The finding in effect cements what was considered probable before," says Woese, namely that archaebacteria and eukaryotes are each other's closest cousins.

The evidence for this association has been building for the past 5 years. Researchers found that several archaebacterial proteins involved in gene transcription resemble those of eukaryotes more than those of eubacteria. And in 1990, Wolfram Zillig's group at the Max Planck Institute for Biochemistry in Martinsreid, Germany, as well as that of Michael Thomm at the University of Regensburg, Germany, found gene control sequences in archaebacterial DNA that resemble the TATA box, a regulatory sequence found in eukaryotic, but not eubacterial, genes. Now, Jackson's group, and Gary Olsen and his colleagues at the University of Illinois, find that archaebacteria also have the transcription factor, known as the TATA binding protein (TBP), that acts through the TATA box to activate gene expression. (The Olsen results appear in the 10 May *Proceedings of the National Academy of Sciences.*) Indeed, the archaebacterial TBP bears a remarkable resemblance to the human protein; the business ends of the proteins are 40% identical.

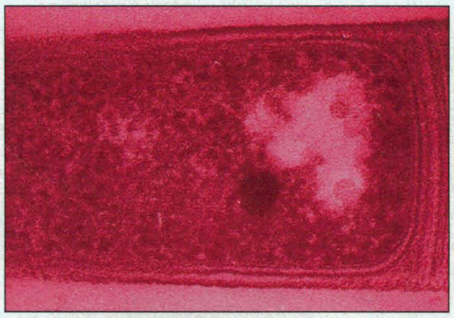


Such similarity implies a common function for the proteins in archaebacteria and eukaryotes, and further work by the Jackson group suggests that is the case. The researchers showed that archaebacterial TBP binds the TATA-like sequence from archaebacteria, just as the eukaryotic counterparts do. Moreover, the binding is enhanced by the involvement of the archaeal form of a transcription factor called TFIIB, recently found to be shared by archaebacteria and eukaryotes, but not prokaryotes. This implies the archaebacterial proteins work together to promote transcription, as their homologs do in eukaryotes. Jackson's group also found that archaebacterial TBP even binds to two human proteins that regulate gene transcription by linking up with TBP. "Even though it diverged from the eukaryotic line of descent over 3 billion years ago, it can still interact with eukaryotic factors," says Jackson.

The implication, Woese says, is that the Archaea and eukaryotes descended from a common lineage that had already split off from the eubacterial lineage. "Here is an essential component of the transcriptional apparatus that must have arisen in the common archaeal and eukaryotic lineage, that did not occur in bacteria," he notes. Moreover, the Olsen group performed a quantitative analysis of nucleotide changes that suggests the Archaea have diverged less from the common ancestor they share with the eukaryotes than the eukaryotes have. If so, says Woese, the Archaea may act as a key to that long-lost ancestor, providing "a fine reading on the origins of the eukaryotic cell."

The impact of the finding goes beyond its evolutionary implications, says Yale University structural biologist Paul Sigler. He notes that proteins from extreme heat-loving organisms often form very stable crystals, which may aid efforts by his group and others to crystallize TBP-containing protein complexes from heat-loving archaebacteria and thus to learn more about the protein-protein interactions central to archaeal gene transcription. And because these complexes resemble those of eukaryotes, our strange new neighbors on the evolutionary tree may help us to better understand ourselves.

–Marcia Barinaga



T. J. BEVERIDGE/VISUALS UNLIMITED

New relations. Archaea like this one, *Methanospirillum hungatei,* may share an ancestral lineage with eukaryotes.