

Flying observatory seeks intergalactic gas

Cosmologists have sought for decades to detect the intergalactic medium — the tenuous material lying between galaxies — and to characterize its composition. Hydrogen and helium, forged in the aftermath of the Big Bang and spread throughout the universe, presumably provided the tiny building blocks from which the first galaxies formed.

These intergalactic gases should also constitute a tiny, but key fraction of the unseen matter, or dark matter, that astronomers believe the universe harbors. Galaxies alone can't account for the density of ordinary particles, or baryons, predicted by the Big Bang, and intergalactic hydrogen and helium would contribute to the small fraction of dark matter thought to consist of baryons.

Researchers proposed in 1965 that ultraviolet light from a distant quasar could betray the presence of intergalactic hydrogen, because the gas would absorb specific wavelengths of the radiation passing through it. But observers never found evidence of atomic hydrogen or helium in the intergalactic medium, suggesting that the bulk of such gases, if present, must be ionized.

With its launch early this month aboard the space shuttle, the Astro 2 observatory will pursue a 16-day mission to view the universe with ultraviolet

eyes. The observatory carries a trio of telescopes that will take images, spectra, and polarization measurements of nearby stars and distant galaxies. And it will search for the fingerprints of material that had until recently eluded detection: the tenuous mix of hydrogen and helium thought to reside outside of galaxies.

The Hopkins Ultraviolet Telescope (HUT) on Astro 2 should provide a highly accurate probe of the stuff between galaxies, report Wei Zheng and HUT team leader Arthur F. Davidsen of Johns Hopkins University in Baltimore in the Feb. 20 *ASTROPHYSICAL JOURNAL LETTERS*.

Last year, researchers reported that the Hubble Space Telescope had detected a gap, characteristic of ionized helium, in the spectrum of ultraviolet light from a quasar (SN: 7/9/94, p.21). But because of its low spectral resolution, Hubble's faint-object camera can't tell whether the absorption stems from diffuse helium in the space between galaxies or from a series of intergalactic clouds containing the ionized gas.

In their report, Zheng and Davidsen note another caveat. They say that singly ionized helium gas close to a quasar may be further ionized by the quasar light passing through it. As a result, intergalactic helium might carve a gentler absorption feature than the



Astro 1 orbiting Earth in December 1990.

sharply defined gap recorded by Hubble.

HUT has several advantages over Hubble, says Kenneth M. Lanzetta of the State University of New York at Stony Brook. Because HUT detects radiation at shorter wavelengths, it can search for helium in the spectra of quasars with lower redshift. Because they would lie closer to Earth, such quasars are likely to be brighter and their light less likely to pass through hydrogen clouds. These clouds can confound results by giving a spectrum that mimics the absorption of helium at a greater distance. In addition, HUT's higher spectral resolution should distinguish intergalactic helium from helium clouds. — R. Cowen

Ruminations on how enzymes evolved

It's not quite Jurassic Park, but researchers are getting closer to recreating extinct life — or at least extinct molecules. Working backwards from the molecular structures of digestive enzymes in cattle and their modern relatives, a Swiss research team claims to have synthesized ancestral forms of these enzymes from millions of years ago.

In the process, they have found biochemical clues to the evolution of the molecules.

The team, led by Steven A. Benner of the Swiss Federal Institute of Technology (ETH) in Zurich, is among the first to recreate possibly ancient molecules in the laboratory and to compare the results with fossil evidence.

"It's kind of like using a DNA synthesizer [a machine that can assemble genes] as a time machine," says Clyde A. Hutchison III of the University of North Carolina

at Chapel Hill. "It's just one molecule, but this is really exciting."

Benner and his colleagues studied a protein, a form of the enzyme ribonuclease, that breaks down bacterial RNA in the digestive systems of cows, sheep, deer, giraffes, and other ruminants.

The fossil record shows that these creatures' common ancestor, a small, deerlike animal, branched off from non-ruminants 40 million years ago by developing the rumen, a stomach chamber that holds cellulose-chomping bacteria. With these bacteria, and with enzymes such as ribonuclease to digest the bacteria, ruminants can thrive on fibrous plants such as grass.

The 124 amino acids that make up this ribonuclease vary slightly among modern ruminants. By correlating these variations with the evolutionary tree, Benner's group deduced the likely amino acid sequence of ancestral enzymes at 13 points in the animals' evolution. They then put suitably mutated forms of the genes for the modern enzymes into bacteria to make them crank out old-style enzymes.

Finally, as they report in the March 2 *NATURE*, the researchers showed that

their reconstructed enzymes can work on RNA in a test tube.

Their most striking finding was the change of a single amino acid in ribonuclease at the point when the ruminants' ancestor emerged. This tiny alteration helped the enzyme resist heat, thus enabling it to prosper in the digestive system, but also made it one-fifth as efficient at processing double-stranded RNA. This ability is of little importance for digesting bacteria, but it hints at a different function of the more primitive enzyme, the group suggests.

The idea of recreating ancient molecules from modern organisms originated with Linus Pauling and Emile Zuckerkandl in 1963, long before anyone had the techniques to do it, notes Caro-Beth Stewart of the State University of New York in Albany in a comment accompanying the work.

"It was a very visionary idea," Stewart says. "I think we're at the very preliminary stages of what this can be used for." By combining the sequences of molecules from many more species, she notes, "we should be able to reconstruct ancestral molecules going further back in time, perhaps — in the future — to the very root of the 'tree of life'." — J. Kaiser

