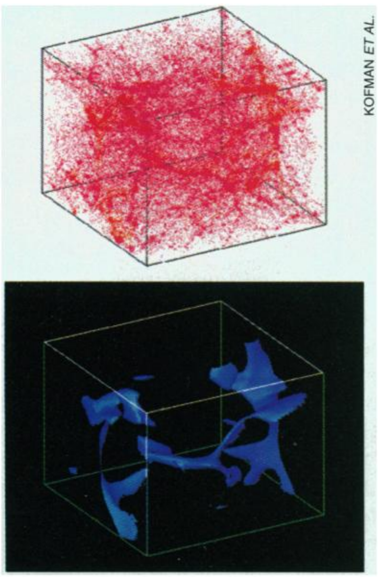
MEETING BRIEFS

Astronomers Paint the Big Picture and Fill in the Blanks

PITTSBURGH—Most everything in astronomy is big. But the truly outsized features of the universe—vast filaments of galaxies and its great dark voids—were highlighted when 772 researchers gathered here on 11–15 June for the 186th meeting of the American Astronomical Society. Talks included a new explanation for the large-scale "tapestry" of the universe and a new glimpse of what may fill its voids.

Cosmic Cobweb

Massachusetts Institute of Technology researcher Edmund Bertschinger calls it the "tapestry of galaxies"—the filamentary structure consisting of thousands of galaxies strung over millions of light-years that shows up so prominently in large-scale telescopic surveys of the universe. How that tapestry was woven from the nearly uniform matter of the newborn universe is one of the most pressing questions in cosmology. Now Bertschinger thinks he may have heard an answer, in a talk by Lev Kofman of the Institute for Astronomy at the University of Hawaii.



KOFMAN ET AL.

Pleasing likeness. A new mathematical scheme predicts the growth of a vast "cobweb" of galaxies *(above)* much like what is seen in computer simulations *(top)*.

Cosmologists already had a partial answer from computer simulations of the motions of millions of particles, each representing a chunk of mass in the early universe. When primed with matter of the right types and densities and a reasonable configuration of initial density fluctuations, these simulations laboriously generate tapestries similar to these observed, purely by gravity. But the match-up begs the question of why these particular structures take shape from an almost uniform sea of particles, says Bertschinger. "Cosmologists want more than numerical results," he says. "They want understanding."

Kofman and his colleagues—Richard Bond and Dmitri Pogosyan of the Canadian Institute for Theoretical Astrophysics in Toronto, Anatoly Klypin of New Mexico State University, and Steven Myers of Caltech—try to provide that understanding. By modifying some classic Russian mathematical techniques, they have come up with a set of equations that directly predicts the present structure of the universe. Looking understandably rumpled after a 15-hour flight from Hawaii, an excited Kofman showed how the equations describe the evolution of tiny density fluctuations in the early universe into what he calls a "cosmic cobweb" of filaments much like the ones seen in galaxy maps and computer simulations (see illustration). "Kofman may really have found the correct answer," says Bertschinger.

In its original form, the mathematics of the cobweb goes back to the 1970s, when it was developed in Moscow by physicist Yakov Zel'dovich. The equations treat large-scale density fluctuations like "ripples on a swimming pool," says David Weinberg of Ohio State University. Just as the ripples focus light into narrow ribbons on the bottom of the pool, the density ripples—acting by gravity rather than refraction—would "focus" matter into vast, pancakelike structures. The pancakes would then evolve to produce filaments, galaxy clusters, and individual galaxies.

But this "top-down" theory had trouble dealing with finer scale density fluctuations, which must also have riddled the early universe. What's more, the pancakes don't seem to appear in surveys of the cosmos or in simulations. Many theorists thought that theory "would decline along with the [old] Soviet Union," in Kofman's words.

Theorists in the West instead favored so-called hierarchical clustering, a "bottom-up" scenario in which structure formation in the early universe begins on small scales, spawning small clumps that later merge to form larger ones. This scenario is adept at explaining galaxy and cluster formation but has a hard time predicting the large-scale tapestry.

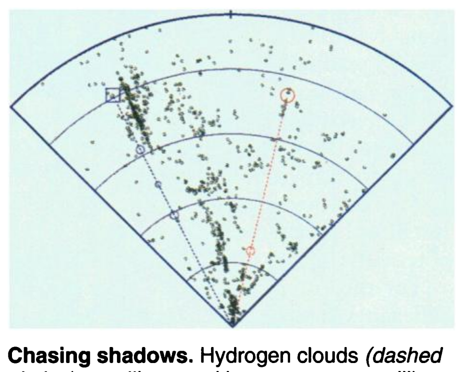
The new theory merges the top-down and bottom-up pictures by allowing hierarchical clustering to take place at small scales, while a Zel'dovich-like scenario dominates larger scales. When Kofman and his colleagues visualized the equations on a computer, they seemed to match observations, predicting a pancake stage so short as to be nearly unobservable and yielding clumps and filaments closely resembling those observed.

Although the match with observations is intriguing, not everyone is convinced. "I'm a little worried that you may be able to choose parameters in slightly different ways and get different answers," says Weinberg, who wants to read the group's paper before deciding. But if the result holds up, he says, it could go a long way toward helping cosmologists understand why the universe spins the tapestries we observe in the sky.

Clouds in the Voids

Drive westward through Kansas at night, and the stretches of blackness between farm lights get longer and longer. The absence of light "doesn't mean there's nothing there," says astronomer Michael Shull of the University of Colorado, Boulder. That much may be obvious on the Great Plains, but it has been less clear in the great voids between galaxies and clusters of galaxies. Ground-based observations of the nearby universe can't reveal the most likely inhabitants of the voids, dark clouds of gas. Such clouds leave "shadows" in the light of distant quasars—but only in the ultraviolet region of the spectrum, which is blocked by Earth's atmosphere.

But by making a similar observation from space, a team led by Shull and his Colorado colleague John Stocke has shown that the cosmic voids, far from being empty, have their own shadowy geography. Using the Hubble Space Telescope (HST), the team detected two clouds of hydrogen floating in nearby, well-mapped voids, hinting that these previously invisible objects could make up a large fraction of the universe. They "could contain as much mass as there is in galaxies that we see," says Shull. Now he and his colleagues hope to learn whether the clouds consist of



STOCKE, SHULL, AND PENTON

Chasing shadows. Hydrogen clouds *(dashed circles)* are silhouetted by two quasars, millions of light-years away; at least two of the clouds lie in voids, far from known galaxies *(dots)*.

pristine gas left over from the big bang, or whether they are the halos of small, dim galaxies lost in the voids—the leftover building blocks, perhaps, of the assembly process that may have formed larger galaxies.

Such Lyman-α clouds, as they are called, aren't new to astronomers, but observers have only been able to see them in more distant regions of the universe, where it's difficult to tell whether they lie in voids. In the distant universe, cosmic expansion shifts the dark absorption lines—the Lyman-α lines—created by the clouds' neutral hydrogen into the visible region of the spectrum, making them observable from the ground.

Now the Hubble team, which also includes Steven Penton at Colorado, Megan Donahue at the Space Telescope Science Institute in Baltimore, and Chris Carilli at the Harvard-Smithsonian Center for Astrophysics, has found Lyman-α lines from nearby clouds in the light from four bright quasars. Nine clouds turned up in mapped regions of the universe, and two of the nine fell within great voids, far from any known galaxy.

For many theorists, the presence of the clouds is no great surprise. "People had thought all along that [the clouds] were widely distributed in the universe," says Jeremiah Ostriker of Princeton University. The question now, he says, is whether the clouds are associated with faint dwarf galaxies. If large galaxies formed by the merger of small ones, as some theories hold, then some of the "dwarf" galaxies should be left behind in the voids, and clouds may trace them.

So far, the team hasn't spotted any obvious galaxy near their two clouds-in-the-void. But that doesn't mean they aren't there, says Simon Morris of the Dominion Astrophysical Observatory in Victoria, Canada. After all, he says, "you can always postulate galaxies that are fainter" than those you see.

Ostriker thinks a better way to answer the question would be to scan the void clouds for absorption lines characteristic of heavy elements that could only have been made in the nuclear furnaces of stars—a task the observers say is probably beyond present instrumentation. "I wouldn't say, 'No way, José,' " says Shull, but he thinks such measurements will have to wait at least until HST's spectrograph is upgraded in 2 years.

–**James Glanz**

MICROBIOLOGY

Bacterial Virulence Genes Lead Double Life

Soft rot in a sick plant leaf and the infected tissue of a human burn patient's wounds might not appear to have anything in common—but they do. In spite of the vast evolutionary gap between plants and animals, some of the same bacteria may cause both types of infections. And new results from Fred Ausubel's team at Massachusetts General Hospital in Boston show that plants and people fall victim not just to the same organisms, but even to some of the same virulence genes that enable the bacteria to trigger disease (see p. 1899).

Experts in infectious diseases find this discovery intriguing, partly because it may provide a new way to track down the virulence genes of human pathogens: by using plants instead of the tens of thousands of animals that would otherwise be needed to screen for the genes, which encode everything from toxins to regulatory proteins that turn on other genes. "The ease and low cost of the plant model is going to uncover new virulence factors in animal and presumably human infections," predicts microbiologist Barbara Iglewski of the University of Rochester in New York. And that would in turn provide a better understanding of just how the bacteria cause disease, as well as potential new targets for anti-bacterial drugs.

LAURENCE RAHME

Blighted. A human *P. aeruginosa* isolate *(right)* causes soft rot in an *Arabidopsis* leaf.

For the current work, Ausubel and his colleagues chose to focus on the bacterium *Pseudomonas aeruginosa*. Some strains of this pathogen infect plants, causing a disease called "soft rot," in which the leaves turn slimy and decay. But the bacterium is also a leading cause of fatal hospital-acquired infections, especially in burn patients and others with depressed immune systems.

As a first step toward finding out what makes *P. aeruginosa* so broadly infectious, Laurence Rahme, a postdoc in Ausubel's lab, screened 75 isolates of the bacterium, looking for any that could infect both the plant *Arabidopsis thaliana* and mice that suffered a small skin burn. She found two that caused particularly severe soft-rot symptoms in the plant, and one of these also produced 75% mortality in the mice. Rahme then used this strain to test whether two bacterial genes already known to play a role in animal disease (*toxA* and *plcS*) are also required for plant pathogenicity. The answer was yes. Bacteria in which either *toxA* or *plcS* had been mutated caused 40% less mortality in plants than did bacteria with the normal genes.

Conversely, Rahme found that a gene involved in plant disease (*gacA*) is essential for infectivity in animals. "This demonstrates that there's an astonishing evolutionary breadth to the pathogenesis by this bacterium," says Colin Manoil of the University of Washington, Seattle, whose team is also trying to identify *P. aeruginosa*'s virulence factors, although in the nematode *Caenorhabditis elegans*.

The virulence genes must have been honed to attack plants, says microbiologist Stanley Falkow of Stanford University, because *Pseudomonas* only infects people whose immune defenses are already down. But the genes can cause disease across a wide evolutionary range in part because they attack the fundamental machinery of cells, says Ausubel. In infected animals, *toxA* produces a diphtheria-type toxin that inhibits host protein synthesis, whereas *plcS* encodes an enzyme that degrades host membranes.

And when *P. aeruginosa* invades plants, *gacA* helps sense that it is in the host. The gene then responds to that environment by turning on other bacterial virulence genes that attack the host. If the gene works in a similar manner in animals, it may be a good target for anti-microbial drugs, Ausubel says, "because by blocking it you can snuff out the action of a central regulator."

Ausubel now hopes to take advantage of the dual nature of *P. aeruginosa*'s virulence genes by using *Arabidopsis* to screen for additional genes that enable the bacterium to infect animals, a project that will, he says, take several years. A question remains, however, as to whether any virulence genes identified in an experimental system using *Pseudomonas* will also be virulence genes for other human pathogens. Ausubel wagers that at least some will, for instance genes that enable the pathogen to adapt to its host.

Meanwhile, he is hedging his bets by also developing a nematode pathogenesis model in the hopes that it will turn up *Pseudomonas* virulence factors that might not be activated in plants. Both Ausubel's and Manoil's groups have found strains of the bacterium that infect the worm and are working to identify both the genes needed for the infection and their cellular targets in the host. If these efforts succeed, and the discovery of new virulence factors does lead to better antibacterial drugs, then the same versatility that makes *P. aeruginosa* such a wide-ranging pathogen may also lead to its downfall.

–**Bernice Wuethrich**

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