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.

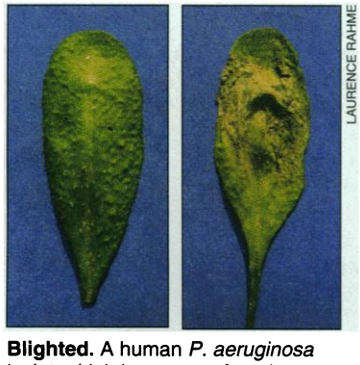
–James Glanz

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

Bernice Wuethrich is a free-lance writer in Washington, D.C.