close funding levels for individual investigators, but the typical award is about $1 million annually. Wiley also receives $350,625 in annual National Institutes of Health grants awarded through Harvard that don't expire until 2005 and 2006.

The news about Wiley has devastated the close-knit structural biology world. "It's a shock for everybody," says NIAID structural biologist David Garboczi, a former Wiley postdoc. But besides cooperating with the investigation, there is little that scientists can do. "Playing Hercule Poirot from one's desk in Cambridge is not very useful," says Harrison.

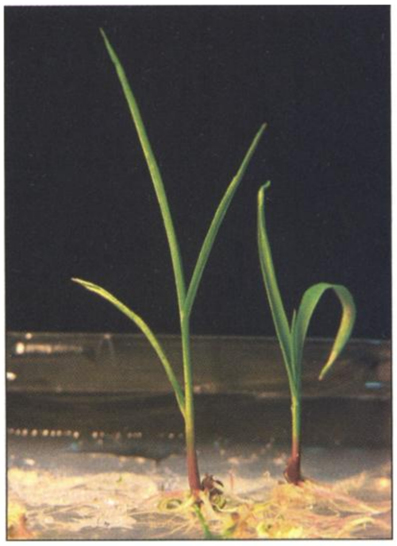
–**JOSH GEWOLB**

MICROBIAL GENOMES

New Genome a Boost To Plant Studies

Molecular biologists have bared the soul of one of nature's best genetic engineers. On pages 2317 and 2323, two teams describe the genome sequence of *Agrobacterium tumefaciens*, a soil microbe whose ability to transfer DNA into plant cells has transformed plant and crop science.

Some 25 years ago, researchers realized they could take advantage of the microbe's route of infection to ferry foreign genes into plants. *Agrobacterium* has been "the workhorse of the agrobiotech industry" ever since, says Joe Ecker, a plant scientist at the Salk Institute for Biological Studies in La Jolla, California. The new sequence data have already revealed clues about *Agrobacterium*'s astounding ability to parasitize plants and should help both academic and corporate researchers better harness its talents, says Ecker. The data also reveal unexpected hints about the microbe's origins, says Andrew Binns, a molecular geneticist at the University of Pennsylvania in Philadelphia. Binns, along with Mary-Dell Chilton, now with Syngenta in Research Triangle Park, North Carolina, and others, helped launch *Agrobacterium* as a full-fledged genetic engineer in the 1980s.



DNA transformer. Researchers have deciphered the genome of the bacterium that helped transfer herbicide resistance genes to this corn plant.

Two independent teams tackled the 5.67-million-base genome. Steven Slater, a bacterial geneticist at Cereon Genomics Inc. in Cambridge, Massachusetts, and his colleagues worked with about a dozen undergraduates at the University of Richmond in Virginia. The other effort was led by microbiologist Eugene Nester at the University of Washington, Seattle. After reading about each other's projects on the Web, both teams agreed to publish their results back to back.

Agrobacterium infects wounded plants, causing disease in some 600 species, including cherries, grapes, and roses and other ornamental plants. Infection leads to tumorlike growths called galls that typically form at the base of the plant. So-called crown gall disease "can cause very serious economic damage," says Nester, destroying whole vineyards, for example.

During the process of infection, *Agrobacterium* transfers some of its DNA to the plant host. When the bacterial DNA is incorporated into the plant's genome, the plant produces growth hormones, and these, in turn, stimulate gall formation. The tumors make novel carbon compounds—again thanks to newly acquired *Agrobacterium* genes. By feeding off these compounds, *Agrobacterium* is able to outcompete any other microbes that colonize the gall.

Although agricultural scientists have piggybacked on this process to transfer genes that make plants hardier and resistant to salt, cold, viral disease, and insect pests, a lot remains to be learned about the infection process. Often, gene transfer is not very efficient, for example. "We felt that there were many questions that could be approached only if we knew the sequence," says Nester, who recruited the University of Washington's Maynard Olson and his team to do the actual sequencing. Both Nester's and Slater's groups are combing through the newly discovered repertoire of 5400 genes looking for those involved in DNA transfer. "It's an area that's ripe for exploration that could lead to ways [to do] more efficient transformation," says Binns.

Agrobacterium's genes are distributed on four pieces of DNA: a linear and a circular chromosome that carry the run-of-the-mill housekeeping genes, and two smaller pieces of circular DNA called plasmids. "All four of these DNA molecules play a role in the interaction with the plant," Slater reports. His team was particularly intrigued by genes for enzymes that suggest *Agrobacterium* feeds off the plant's own nutrients, including cellulose and peptides. Researchers have suspected that this thievery was occurring but had lacked definitive proof. And Nester's group found that *Agrobacterium* doesn't use the usual array of genes that many plant pathogens use to gain access to their hosts. It lacks the so-called type III secretion system responsible for pathogenicity in many bacteria and instead has three versions of type IV; Nester wants to know why this pathogen is different.

The sequence also revealed a closer kinship than researchers had expected with rhizobium bacteria, symbionts that cause plants to form nodules on their roots. Rhizobium bacteria flourish in nodules, producing ammonia in return for the plant's hospitality, whereas *Agrobacterium* sponges off the plant without apparently giving anything in return. A comparison between the new sequence and that of the recently sequenced *Sinorhizobium meliloti* (*Science*, 27 July, p. 668) revealed that "big chunks of DNA are essentially the same in both," Nester reports.

Thus, the two could have a recent common ancestor and might belong to the same genus. At first glance, says Binns, because *Agrobacterium* has some of the genes needed for nitrogen fixation, it seems that it might have evolved from a primitive rhizobium. Alternatively, gene transfer between the two species might explain some of the shared genes, he adds. Whatever the explanation, these very different lifestyles "have occurred without a whole heck of a lot of change in the whole genome."

–**ELIZABETH PENNISI**

MAMMALIAN EVOLUTION

Placentals' Family Tree Drawn and Quartered

A nearly 240-year-old statistical technique has helped sort out the evolutionary history of the broad class of mammals that give birth to live, fully developed young. As William Murphy and Eduardo Eizirik of the National Cancer Institute (NCI) in Frederick, Maryland, and their colleagues report on page 2348, the technique places placental mammals in four major groups. The researchers propose that these groups arose in large part because of the breakup of the giant landmasses that predated modern continents, and that placental mammals in what is now Africa have the most ancient ancestors.

Those conclusions are likely to prove controversial. Researchers are sharply divided on where and when mammals arose; two distinct camps disagree by at least 35 million years. The new work "adds more ammunition" to the case for an early divergence of mammals, notes J. David Archibald, an evolutionary biologist at San

CREDIT: D. W. WOOD ET AL.