teins, as well as many more protein kinase genes than expected. Because protein kinases are involved in cell signaling pathways, "there are an awful lot of ways *Arabidopsis* cells are talking to each other and getting information from outside the cells," says Elliot Meyerowitz, a geneticist at the California Institute of Technology in Pasadena.

Another intriguing find is that the set of genes for cell-to-cell communication varies dramatically between *Arabidopsis* and humans. By contrast, many genes involved in basic cell functions, such as cell division, tend to be conserved among species—in other words, a yeast gene might work just as well in *Arabidopsis*—suggesting that the genes existed in a common ancestor of all organisms. But not so the cell communication genes. "[That] fits with the idea that multicellularity evolved separately [in plants and animals]," says CSHL's Robert Martienssen, a plant geneticist.

These are the first of many insights expected to pour out of the genome, not just for learning about *Arabidopsis* but also about other plants. With this genome in hand, plant biologists should be able to find key genes in other plants far more easily. As Bevan points out, such insights may lead to the development of crops better suited to developing countries, plants designed to soak up more carbon dioxide, or other applications that cannot yet be imagined. For that reason, he predicts, the genome sequence from this tiny plant "will have as much impact as the human genome."

–ELIZABETH PENNISI

ARABIDOPSIS

ECOLOGY

Stalking the Wild Mustard

Arabidopsis thaliana **is not just for molecular biologists anymore. A few intrepid ecologists and evolutionary biologists are now touting its merits**

Several years into his Ph.D. studies, Massimo Pigliucci realized he had a problem. He wanted to study how the environment interacts with a species' genetic makeup over time, and he had been focusing on *Lobelia*, a tall, native perennial much studied by ecologists. But *Lobelia* "was hard to use," he recalls, because little was known about its genetics. So Pigliucci shifted to a small weed typically studied by molecular and developmental biologists rather than ecologists. His committee at the University of Connecticut was appalled. The weed, *Arabidopsis thaliana*, "wasn't a real plant" as far as his advisers were concerned. And, they asserted, it had no intriguing features worthy of ecological or evolutionary investigation.

A decade later, Pigliucci, now at the University of Tennessee, Knoxville, and a small but growing number of other plant ecologists and evolutionary biologists are proving those advisers wrong. They have searched the globe for natural variants of this weed and of its relatives, which will enable them to probe the evolutionary history of this plant (see sidebar). Bucking the trend among field biologists to focus on wild flora in pristine places, these researchers are capitalizing on decades of intensive research on *Arabidopsis*. Thousands of research papers have already examined the physiology, development, biochemistry, and genetics of this plant. Indeed, this week the full genome sequence of *Arabidopsis* is being published—the first complete sequence of any plant (see *Nature*, 14 December, p. 796, and this issue of *Science*, p. 2105). Now it's time for more ecologists and evolutionary biologists to make use of these data, says Thomas Mitchell-Olds, an ecologist-turned–quantitative geneticist at the Max Planck Institute of Chemical Ecology in Jena, Germany. For instance, he and others want to tease out how genetic variation helps *Arabidopsis* thrive under different conditions.

Even mainstream ecologists are beginning to see the potential of this lowly weed. Stanford plant ecologist Harold Mooney, for one, is convinced that *Arabidopsis* will help evolutionary biologists and ecologists answer numerous other questions, and he is encouraging his colleagues to take a chance on this unlikely plant. Specifically, says Mooney, *Arabidopsis* offers "an incredible opportunity" for them to understand the genetic basis of the traits they study. Until now, researchers have had trouble connecting the genotype—an organism's particular mix of genes—with its phenotype—how that organism develops and acts. But with *Arabidopsis*, "you can precisely answer this question, because it's got great genetics," says Michael Purugganan, an evolutionary geneticist at North Carolina State University in Raleigh.

A very real plant. Much used in the lab, *Arabidopsis thaliana* also thrives in the wild, where it is providing insights into how plants adapt to different environments.

CREDIT: MICHAEL PURUGGANAN AND JOHANNA SCHMITT

Those great genetics include not only the sequence but also mutants that *Arabidopsis* biologists have developed for almost every gene. By growing these mutants—or natural variants—under different conditions, Pigliucci and other plant ecologists are homing in on the genes responsible for specific traits, such as the timing of flowering or the production of protective compounds. The sequence information "allows us to plan our experiments more carefully and analyze our data more thoroughly," says Naohiko Miyashita, a population geneticist at Kyoto University, who switched from *Drosophila* to *Arabidopsis* 6 years ago.

Rodney Mauricio, an ecological geneticist at the University of Georgia, Athens, is using *Arabidopsis* to look at how insect pests affect the evolution of plants. Although he complains about how delicate this weed is—for his next experiment he recently planted 4800 seedlings, each no bigger than a thumbtack—he's one of the pioneers in using *Arabidopsis* in the field. Over the past decade he and his colleagues have established that insect pests prompt plants to develop tiny hairs called trichomes and that these have a "cost": The hairier plants produce fewer seeds. "It's a fairly important adaptive story," Mauricio notes. Now he's tracking down the genes responsible for trichome growth and density. Says Mauricio, "The idea is to move toward a complete understanding of evolution from the ecological side to the molecular side."

Arabidopsis Kin Help Keep Genetics Studies All in the Family

An unobtrusive weed often found at roadsides and other disturbed sites has risen from its humble roots to become *the* model organism, or "lab rat," for studying plant molecular biology. Now, the far-flung relatives of that weed, *Arabidopsis thaliana*, are slowly becoming celebrities as well. By comparing the genetic makeup and characteristics of *A. thaliana* to its cousins, evolutionary biologists can discern how the plant has changed through time.

Before doing so, researchers first needed to clarify *Arabidopsis*'s family ties. Over the past few years, teams led by Marcus Koch of the University of Agricultural Science in Vienna and Thomas Mitchell-Olds, a quantitative geneticist at the Max Planck Institute of Chemical Ecology in Jena, Germany, have done so. Working with evolutionary biologist John Bishop, now at Washington State University in Vancouver, they analyzed ribosomal DNA sequences and various gene sequences from well-studied *Arabidopsis* species and from species in closely related genera, such as *Arabis*, *Cardamine*, and *Capsella*. This work, reported in several journals in 1999 and 2000, has led to a new family tree: *Arabidopsis* now has 10 species, with *A. lyrata* and *A. halleri* being the most closely related to the "lab rat."

But there's a problem in studying these relatives: The molecular tools developed for *A. thaliana* don't necessarily work on them. Mitchell-Olds and researchers at six other European labs have spent the past 2 years adapting these tools for some of the kin. The researchers have cut the related genomes into malleable chunks and cloned them. They are also developing genetic maps, essentially a series of DNA landmarks along the chromosomes, of several relatives to enable investigators to track down genes more easily. Others are making sure that techniques for introducing or altering genes in *A. thaliana* work in these cousins as well. The ultimate goal, says Mitchell-Olds, is to provide plant biologists, especially evolutionary biologists, with the molecular and genetic equipment necessary for analyzing species that split off from the *A. thaliana* line 5 million, 10 million, and 30 million years ago. "We're hoping that researchers who want to make a close or distant comparison can get the stuff they need from a stock center," several of which already exist, says Mitchell-Olds.

Already, these relatives are proving their worth. One drawback to *A. thaliana*—at least in some eyes—is that it is a selfing plant that fertilizes its flowers with its own pollen, thereby creating stands of identical plants. *A. thaliana*'s closest cousin, *A. lyrata*, provides a great alternative. Although it looks much like *A. thaliana*, it is not selfing; instead it has large flowers that attract insects carrying pollen from other plants. Another advantage is that, unlike *A. thaliana*, *A. lyrata* is not an invasive weed—in other words, it stays put. That means *A. lyrata* has had millions of years to coevolve with the local pests, whereas *A. thaliana* largely hasn't.

Mitchell-Olds and Bishop have used *A. lyrata* and other kin to examine the evolutionary history of a family of antifungal proteins called chitinases. Meanwhile, at the University of Oulu in Finland, Outi Savolainen, who coordinates the European consortium on *Arabidopsis* evolutionary genetics, has been looking at various populations of *A. lyrata* to probe the genetics of flowering time in this species. This work should complement research in the United States on flowering times in *A. thaliana* (see main text).

And these are just the beginning. *Arabidopsis*'s sister genus *Arabis*, for example, contains a species that fungal pathogens infect. After infection, the pathogens force the plant to produce an orange pseudoflower—orange because it's covered with spores that are then carried away by pollinators deceived by the fake blossom. "We may be able to apply *Arabidopsis* information to eventually understand how that pathogen takes over that plant," Bishop suggests.

In short, notes Charles Langley, a population geneticist at the University of California, Davis, "there's a lot of cool stuff that can be done."

–E.P.

All in the family. *Arabidopsis thaliana* (top left) and its relatives (left to right), *A. lyrata*, *Arabis holboellii*, *Brassica rapa*, and *Arabis alpina*.

CREDITS: THOMAS MITCHELL-OLDS/MAX PLANCK INSTITUTE OF CHEMICAL ECOLOGY

Another convert is Johanna Schmitt of Brown University in Providence, Rhode Island. She got hooked on *Arabidopsis* when Pigliucci joined her lab as a postdoc 6 years ago. Together, they began to study how the weed reacts to crowding by other plants. When the plant's light-sensing pigments, called phytochromes, are shaded by close neighbors, they somehow trigger rapid growth by the main stem, causing the plant to become tall and gangly and prompting early flowering. Molecular biologists had already tracked down the pigments and their genes; Schmitt, Pigliucci, and colleagues used the *Arabidopsis* strains developed for those molecular studies in their work. By planting the various strains, each of which lacks a gene for a particular pigment, under different crowding conditions, "we were able to measure natural selection on shade avoidance," Pigliucci says.

Purugganan has teamed up with Schmitt's group to track down the genes that regulate when *Arabidopsis* flowers, taking advantage of natural variation in North American populations. In North Carolina, *Arabidopsis* seeds germinate in the fall, forming a small rosette of leaves that hugs the soil and waits out the winter before sending up a stalk and, eventually, flowering. But in harsher climates, nothing happens until spring, when the seeds sprout immediately and flower a few weeks later. In other places, such as Rhode Island (in southeastern New England), Schmitt and her postdocs Lisa Dorn and Cynthia Weinig find stands of *Arabidopsis* where both growth patterns exist.

To understand the variation in this trait,

Grand experiment. A planting of 12,000 *A. thaliana* seedlings.

Weinig and her colleagues from Brown and North Carolina last year planted inbred lines of *Arabidopsis* that differed in particular genes, such as those coding for proteins that sense day length, both in Rhode Island and in North Carolina. They also planted *Arabidopsis* from Rhode Island in North Carolina and vice versa. Over the ensuing months the researchers monitored when these plants sprouted and when they bloomed. They also noted traits such as the number of branches to see how these plants responded to the conditions in each place. Already, intriguing hints are emerging. The preliminary data suggest that, depending on the season, different genes are affected. The team's goal, Schmitt says, is to understand "what are the causes of selection on particular traits in [the] wild, what are the genes underlying individual traits, and how is selection acting on these genes."

Still others are studying how *Arabidopsis* and its bacterial or fungal pathogens coevolve. Ecological geneticist Joy Bergelson of the University of Chicago, for instance, used sequence data to study the R genes that help the plant recognize bacterial pathogens. Next, her group obtained *Arabidopsis* from various sites around the world and assessed their R-gene makeup. Contrary to what they expected, Bergelson and her colleagues have found that different versions, or alleles, of R genes have persisted in these populations for millions of years. That finding, along with other data from Mitchell-Olds's group, indicates that defense-related genes are not in an evolutionary arms race with pathogens, as current dogma predicts. Instead, suggests Mitchell-Olds, the frequency of the different alleles varies from year to year and population to population, enabling the plant to maintain its defenses against numerous threats.

These insights represent just the beginning of what Mitchell-Olds and others expect to gain by moving *Arabidopsis* studies into the field. "Ecologists may like to work in wonderful pristine places," Mitchell-Olds says, "but this is a system where we can get answers."

–ELIZABETH PENNISI

CREDITS: (TOP TO BOTTOM) MICHAEL PURUGGANAN AND JOHANNA SCHMITT; UNIVERSITY OF CHICAGO HOSPITALS; GREGORY P. COPENHAVER/UNIVERSITY OF CHICAGO

ARABIDOPSIS
CENTROMERES

A Journey to the Center of The Chromosome

The *Arabidopsis* genome project is the first to give a detailed picture of the centromeres in a higher eukaryote

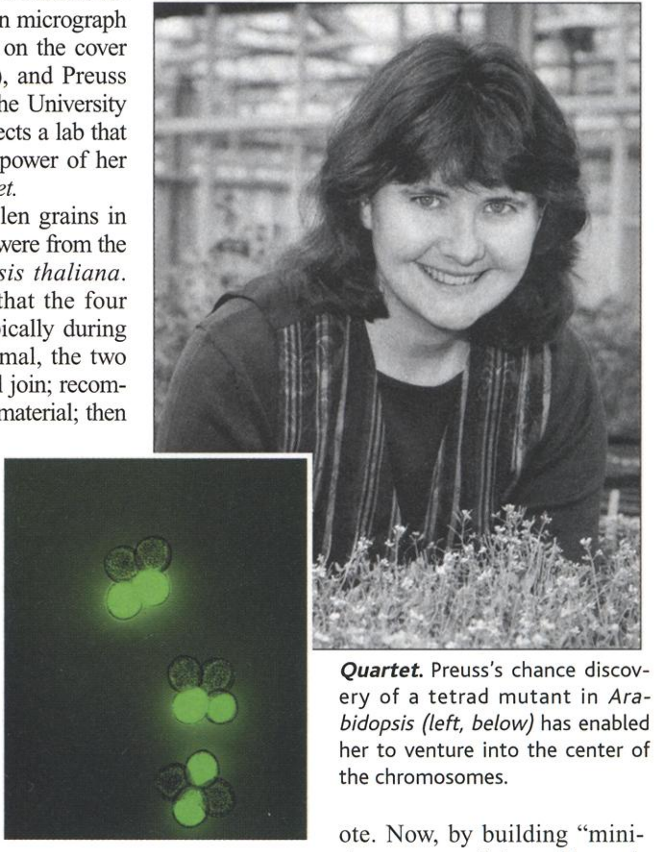
As a postdoc at Stanford University in 1994, Daphne Preuss was examining mutagenized pollen grains under a microscope when she saw it: Amid all the dots of lone pollen, four grains were stuck together, tracing the shape of a tetrahedron. Having written her Ph.D. thesis on yeast, where such tetrads are standard and have been the foundation for its genetic analysis, Preuss knew she was looking at something powerful. "I immediately knew this [mutant] was the key to doing all kinds of genetic analysis" in plants, she recalls. "Life would be different."

That chance finding launched her career as a plant biologist. Some 6 months after she found it, an electron micrograph of the mutant pollen was on the cover of *Science* (3 June 1994), and Preuss was soon on her way to the University of Chicago, where she directs a lab that runs in large part on the power of her mutant find, dubbed *quartet.*

The lemon-yellow pollen grains in which she spotted *quartet* were from the mustard plant *Arabidopsis thaliana*. What was unusual was that the four gametes were joined. Typically during meiosis in a plant or animal, the two chromosomes within a cell join; recombine, or exchange genetic material; then divide and separate twice into four haploid cells—the gametes. Each gamete, whether pollen or sperm, contains half the genetic complement. But in this newfound *Arabidopsis* mutant, the standard diploid cell produces four adjoined haploid cells—a tetrad, as in yeast. By analyzing these four cells instead of random gametes, geneticists can chart recombination events with unprecedented precision. Preuss realized that this four-in-one mutant could reveal what happens during meiosis in plants as it had in yeast. It would also enable her to define the centromeres, which have been defined in yeast but which remain a black box in plants and animals.

The centromere is a crucial stretch of DNA buried in the knotty terrain at the center of the chromosome. It plays a key role in meiosis, pairing up parental chromosomes and hitching them to protein motors that pull the chromosomes apart before cells divide. The dense, central region of the chromosome containing the centromere is readily visible under a microscope. Yet only in yeast have researchers been able to identify the exact DNA sequence of the centromere.

Using the *Arabidopsis* tetrad mutants, Preuss has established where the centromeric region starts and stops on each of the five chromosomes, a first for a complex eukaryote. Now, by building "minichromosomes," she and her colleagues are on their way to pinpointing where and how in that region the proteins attach in meiosis. The research is "blazing trails," says Kelly Dawe of the University of Georgia, Athens, who is developing such minichromosomes in maize.



Quartet. Preuss's chance discovery of a tetrad mutant in *Arabidopsis (left, below)* has enabled her to venture into the center of the chromosomes.

Preuss's lab and *quartet* have also been indispensable to the *Arabidopsis* genome se-