develop closer university ties but remain independent. Lippmaa says his camp "wants to renovate Soviet-constructed science without destroying the science."

A handful of institutes are already integrated. For instance, the Estonian Biocentre and the Institute of Molecular and Cell Biology, which share a building, already have close ties with Tartu University, and they plan to break ground later this month on an adjoining 1000-square-meter lab, including a transgenic animal facility, funded by a Swiss private charity. For Aaviksoo, the time has come to have other institutes, including those a couple hours' drive away in Tallinn, answer to the university.

"Research institutes are cut off from young, ambitious people," says Mart Ustav, a molecular virologist at the Institute of Molecular and Cell Biology. Moreover, says Aaviksoo, placing the institutes under university administration would help integrate the institutes' 750 scientists and the university's 200 full-time researchers. Without administrative changes, he argues, "we can never achieve integration of functioning research teams."

Lippmaa says that he does not want to perpetuate the Soviet-style system in which many scientists "spent their creative years shuffling for positions" as lab chiefs or directors. Rather, he says, the institutes and the university must strive for "an association on equal terms." He compares Estonia's institutes to U.S. national laboratories such as Lawrence Berkeley, which are affiliated with universities but retain independence to plan their research. Lippmaa says, however, that his proposal has been rejected by the education ministry.

So far, Lippmaa's close ties to Estonian's Prime Minister Tiit Vahi have forestalled any government action on Aaviksoo's proposal. Top Estonian scientists and policymakers are working hard to find a compromise, but in the meantime this bitter dispute has sapped the momentum of Estonia's reform process. But that may not be all bad. Villems says that many Estonian scientists, dizzy from the pace of reforms, "just want to stop and catch their breath for a while."

–Richard Stone

PLANT GENETICS

First Global Sequencing Effort Begins

The list of organisms whose DNA is being cranked wholesale through U.S. genome sequencing labs includes a worm, bacteria, fruit flies, and humans. Notably absent are plants—until now. Last week the U.S. government ended the omission by putting up $12.7 million to begin large-scale sequencing of *Arabidopsis thaliana*, a small, flowering member of the mustard family. The awards will allow the United States to join other countries already sequencing *Arabidopsis* in an international collaboration to decipher the plant's entire genome by 2004.

The initiative is being hailed by scientists who use *Arabidopsis* as a model organism. "I've been hoping for this," says one grantee, Steve Rounsley of The Institute for Genomic Research (TIGR) in Rockville, Maryland, who studies the plant's flowering genes to understand the molecular basis of flower development. "There's a huge number of *Arabidopsis* researchers out there who will get a head start by identifying many genes." The information should provide insights into basic cell processes and plant development and help researchers bioengineer more desirable crops and foods. For plant biologists, who have lagged behind biomedical researchers in using model organisms, "this will make it much clearer how a model system will help," says Oklahoma State University plant scientist David Meinke.

The 3-year awards are being funded with $9.5 million from the National Science Foundation (NSF), $2.1 million from the Department of Energy (DOE), and $1.1 million from the Department of Agriculture (USDA). The winners (see table) include some groups already using the fastest automated methods to do human genome sequencing. "We are thrilled," says Meinke, who helped organize the competition. "We were concerned that some of the major sequencing labs would have their hands full and wouldn't want to expand."

Arabidopsis has several features that make sequencing its genome a worthwhile challenge. At 120 million base pairs (only 3% of the length of the human genome) distributed over five chromosomes, it is thought to be the smallest genome of any flowering plant, with the least amount of noncoding sequences. What's more, the plant's rapid growing cycle—6 weeks—and large number of mutants make it a good experimental model.

Sequencing *Arabidopsis* should have a significant impact on plant science because all 250,000 species of flowering plants, from corn to tulips to cherry trees, are genetically very similar. A gene transferred from one plant into another usually continues to operate in the same way, explains plant scientist Chris Somerville of the Carnegie Institution in Stanford, California, a co-investigator on one award. DOE hopes that similarity will aid its search for plants bioengineered to clean polluted soil by absorbing toxins, and to provide biomass that can replace fossil fuels.

M. YANAFSKY/UC SAN DIEGO

The *Arabidopsis* community began preparing for the sequencing effort 6 years ago when, with NSF support, it started a multinational project to begin analyzing cDNA clones and to set up stock centers and a World Wide Web database (http://genome-www.stanford.edu/Arabidopsis/). This project, now chaired by Meinke, laid the groundwork for the *Arabidopsis* Genome Initiative, which involves the U.S. labs, a consortium of 17 European labs, and one Japanese lab. Armed with the new funding, U.S. scientists expect to sequence about half of the genome; the European and Japanese labs, some of which have already begun sequencing, will do the other half. "In a way, the sequencing is just the final step," Somerville says.

The collaborators met in August in Washington, D.C., where they pledged to coordinate their efforts to avoid duplication and to post their data on the Internet as quickly as possible in a form easily used by all plant scientists. An international project isn't "necessary," says Satoshi Tabata of the Kazusa DNA Research Institute in Chiba, Japan, but "by doing it that way, the data obtained become more 'common' to all the researchers in the world. I think that is very important."

The group expects to cover about 40% of the genome, with 99.99% accuracy, in the first 3 years of the effort. They will need additional funding to finish the project.

–Jocelyn Kaiser

SEQUENCING THE *ARABIDOPSIS* GENOME

Lead Scientist	Laboratories	Estimated Funding	Chromosome	Rate (kb/mo)
Richard McCombie (Cold Spring Harbor)	Cold Spring Harbor Lab; Washington U.; Applied Biosystems, CA	$4.2 million/ 3 years	4, 5	150
Ron Davis (Stanford)	Stanford U.; USDA/ UC Berkeley; U. Penn.	$3.8 million/ 3 years	1	150
Craig Venter (TIGR)	The Institute for Genomic Research, Md.	$4.7 million/ 3 years	2	220
Satoshi Tabata (Kazusa Institute)	Kazusa DNA Research Institute, Chiba	$4.5 million/ year	3, 5	500
Mike Bevan (John Innes Center)	17-lab consortium of European Union	$7.5 million/ 2 years	4, 5	200

SOURCE: MULTINATIONAL *ARABIDOPSIS* STEERING COMMITTEE