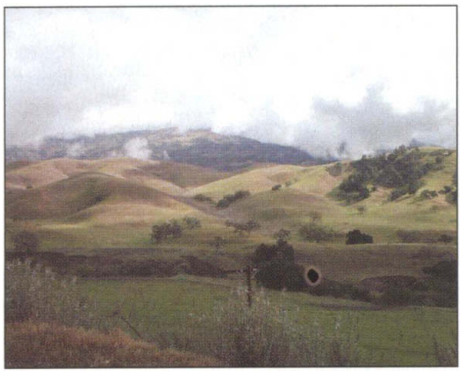


Vanquished invaders. At this reserve dominated by exotic grasses, adding lots of native seeds to plots allowed native grasses to return.

In a 5-year series of experiments on plots in former crop fields at Sedgwick Reserve near the Southern California coast, Seabloom's team ruled out the first and third possibilities. Mixtures of exotic annuals such as black mustard, ripgut grass, and soft chess used less water, nitrogen, and sunlight than a mix of five native perennials such as California brome and purple needlegrass. And the natives were able to retake patches of exotic grasses if the researchers planted more native seeds, showing that the exotic plots weren't impregnable. Seed abundance was the crucial factor, Seabloom says.

The next step is to figure out how to parlay that knowledge into a viable restoration strategy. Californians have tried to restore grasses by adding lots of native seeds, but few seedlings survive, says Rice. Seabloom's plots were "pretty artificial," because exotics had not built up seed banks in the soil, says Carla D'Antonio of UC Berkeley. "These are not your typical grazed grasslands with tens of thousands of seeds per meter squared," she says. And the influence of seed abundance might not be as great as in locations with climates different from those tested in Southern California, Rice says.

Seabloom agrees that "we definitely need to do follow-up work in different conditions," including in fields where exotics have been growing for a long time. But even if his team hasn't found a quick fix for restoring grasslands, the experiment might lay the groundwork for more sophisticated approaches. "By understanding the mechanisms," Seabloom says, "you're always going to be better off."

–**JOCELYN KAISER**

MEETING PLANT TISSUE CULTURE AND BIOTECHNOLOGY

Getting Down to Bare Wood And Overcoming a Barrier

ORLANDO, FLORIDA—From 23 to 28 June, roughly 1000 scientists, half of whom came from outside the United States, gathered here to learn about the latest research on plant biotechnology. Among the new findings: a gene that might make it easier to regenerate whole plants from cultured cells and an analysis of the loblolly pine genome that might help researchers identify the genes that guide plant development.

Loblolly Pine Genome Analyzed

To the casual observer, the model plant *Arabidopsis thaliana* and the loblolly pine (*Pinus taeda* L.) have little in common. *Arabidopsis* is a tiny flowering annual with a life cycle measured in weeks; the loblolly pine, a commercially important tree that provides 58% of the timber harvested in the United States, grows as high as 50 meters and can live for centuries. Yet new results described at the meeting by Ronald Sederoff, a tree molecular geneticist at North Carolina State University (NCSU) in Raleigh, indicate that the genomes of these two species are surprisingly alike.

"We've said all along that *Arabidopsis* is a model for flowering plants," says Eliot Meyerowitz, a plant molecular biologist at the California Institute of Technology in Pasadena. "It may go further than that" and serve as a model for all seed-bearing plants, including more primitive species such as the loblolly and other conifers that don't have flowers.

Sederoff, graduate student Matias Kirst, and their colleagues, both at the NCSU Forest Biotechnology Group and the Center for Computational Genomics at the University of Minnesota, Minneapolis, came to their conclusion by producing and analyzing expressed sequence tags (ESTs) from the loblolly pine. ESTs are DNA copies of fragments of an organism's messenger RNAs and thus represent the genes active in its tissues. To better understand the gene changes that distinguish woody plants such as the loblolly from herbaceous ones such as *Arabidopsis*, the team focused primarily on ESTs from the pine's wood-forming tissue.

The researchers ultimately produced and sequenced some 60,000 ESTs, representing about 12,000 genes, roughly one-half of the total number in *Arabidopsis*. They found that 90% of the loblolly genes apparently have counterparts in *Arabidopsis*. "The closer we looked, the fewer differences we found" between the *Arabidopsis* and loblolly pine genomes, says Sederoff. Given that the last common ancestor of the two species dates back roughly 300 million years, he adds, the finding indicates that the protein-coding portions of their genomes have been highly conserved.

The finding suggests that a relatively small number of genes could determine whether a plant species grows as a tall, woody tree or a small, herbaceous plant, Sederoff notes. This difference might also be due to the influence of regulators, which can mediate between environmental factors and functional genes, turning them on and off as needed.

Indeed, there is evidence for that idea. Several years ago botanist Simcha Lev-Yadun of the University of Haifa, Israel, found that he could trigger the formation of woody roots and stems—albeit matchstick-sized ones—in *Arabidopsis* by pruning the flowers every day. Two years ago, molecular biologist Eric Beers of Virginia Polytechnic Institute and State University in Blacksburg repeated the work, using the resulting wood to build a miniature Adirondack chair.

This shows that *Arabidopsis* does in fact carry the genes for wood formation, as suggested by the Sederoff team's results. It should now be possible to track down those genes and see how they are controlled in a species much more amenable to study than the majestic loblolly pine.

Genetic cousins? Despite its normal herbaceous nature, *Arabidopsis*, like the loblolly pine, has the genetic potential to produce wood, here used to make a tiny Adirondack chair.

CREDITS: (TOP TO BOTTOM) ANDREW BORCHER/UC SANTA BARBARA; E. BEERS/VIRGINIA TECH

Gene Might Aid Plant Regeneration

Researchers seeking to genetically engineer new plant strains often run into a major obstacle: how to grow whole plants from cells into which they have introduced a new gene. So far, that's been much more of an art than a science, as researchers have had to resort to laborious trial-and-error methods to find just the right culture conditions. Now, a new development might help solve this hitherto intractable problem.

At the meeting, Qi-Wen Niu, a postdoc in Nam-Hai Chua's lab at Rockefeller University in New York City, reported that he and his colleagues have identified a gene in the model plant *Arabidopsis* that can, when overexpressed, cause ordinary somatic cells to develop into embryos. The result, Chua suggests, is like converting plant cells to stem cells. (The results also appeared in the May issue of *Plant Journal*.) The finding could help "transform cell culture studies from an empirical to a more targeted, experimental discipline," says Indra Vasil, a plant biologist at the University of Florida, Gainesville.

The gene, dubbed *pga6* (for *plant growth activation 6*), is not the first one found to have this ability. About 5 years ago, Tamar Lotan, then working in the laboratory of John Harada at the University of California, Davis, found that overexpression of the *lec1* gene has a similar effect, but the frequency of embryo production was low. In contrast, *pga6* triggers the formation of copious numbers of somatic embryos that develop into fertile plants.

Niu, Chua, and their colleagues, including Rockefeller's Giovanna Frugis and Jianru Zuo of the Institute of Genetics and Developmental Biology in Beijing, discovered *pga6* using a method called activation tagging. This involves introducing into plant cells foreign DNA containing a regulatory element known as a promoter that enhances gene activity in response to chemicals, the hormone estradiol in the Chua team's case.

The researchers then exposed cells containing the DNA to estradiol and looked for any changes produced when genes near the inserted promoters increased their activity. Some of the transformed cells produced numerous somatic embryos—an effect the group traced to the *pga6* gene. The researchers also showed that when they turned off *pga6* expression by removing estradiol from the culture medium, the somatic embryos germinated into morphologically normal and fertile plants.

Further work by Chua and his colleagues showed that *pga6* is identical to the *WUSCHEL* gene, which was originally identified about 5 years ago by Tom Laux's team at the University of Freiburg in Germany. Laux and his co-workers found that *WUSCHEL* is important for normal development of zygotic embryos—those produced sexually when pollen fertilizes a plant's ovules—but they did not find any relation between *WUSCHEL* and somatic embryo formation. Now that the Chua team has made the connection, plant researchers might be able to increase the efficiency of their genetic engineering efforts by temporarily upregulating the *pga6* gene in the plant cells they are transforming.

–ANNE SIMON MOFFAT

GENOME RESEARCH

NSF's Ark Draws Alligators, Algae, and Wasps

Evo-devo researchers are thrilled about NSF's new grants for genetic studies of neglected species, although there are too many species and not enough money

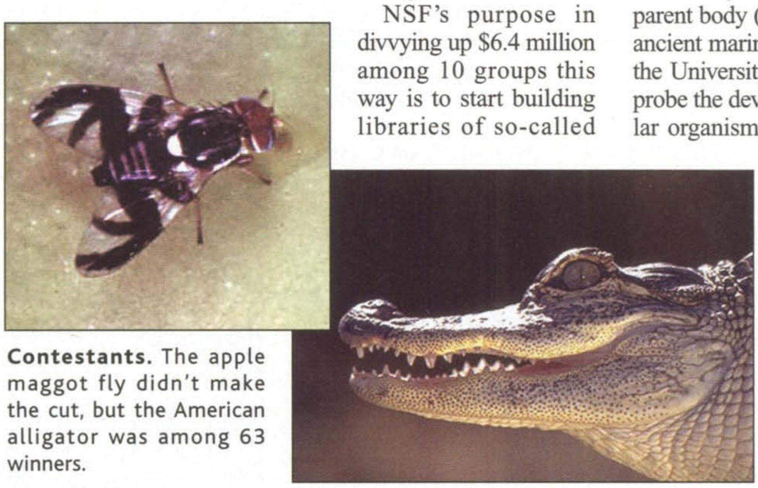
Scott Edwards treks around the world seeking songbirds. He's especially passionate about house finches, a focus of his ornithological research at the University of Washington, Seattle. So how did he end up last month as principal investigator on a genetics project involving a jumble of reptiles—including the relatively obscure (and nearly legless) worm lizard? The answer is simple: Edwards followed the rules set by the National Science Foundation (NSF), embracing species he doesn't normally study, and won a grant.

NSF launched a novel competition a year ago, attempting to boost genetic research on organisms not deemed to be models of human biology and thus not usually funded by biomedical science. The agency decreed that most of the projects should be broad, covering as many branches on the Tree of Life as possible. The call for breadth brought together extended families of organisms that don't always fraternize. In Edwards's case, after reviewers had trimmed his plan, the flightless emu was left as the lone bird to tag along with lizards, a turtle, and an alligator.

NSF's purpose in divvying up $6.4 million among 10 groups this way is to start building libraries of so-called bacterial artificial chromosomes (BACs) for detailed genetic studies of neglected species. BACs are useful for storing and cataloging DNA, essentially as bits of genomes that have been broken into manageable stretches, tagged, and inserted into bacteria. Biologists use BACs to examine genes, compare whole genomes of two or more organisms, and fill the gaps in existing gene sequences. Winners will use the money to pay for BAC libraries covering organisms of interest.

The NSF grant competition electrified a diverse set of biologists and yielded an array of potential new genome projects. The species that came flying, swimming, and slithering out of NSF's award chute last month range from Edwards's worm lizard (*Amphisbaenia alba*) to a butterfly (*Heliconius erato*) and a tiny crustacean with a transparent body (*Daphnia pulex*). A study of two ancient marine animals, led by Rob Steele of the University of California, Irvine, seeks to probe the development of the first multicellular organisms, looking in particular at how and when a family of regulatory genes, called *HOX* genes, evolved. Another, led by Dina Mandoli of the University of Washington, Seattle, will explore genetic diversity in a range of plants, and a third, led by Marian Goldsmith of the University of Rhode Island, Kingston, is comparing genes that govern wing patterning in two moths and a butterfly.

Still, $6.4 million goes only so far. Although NSF initially hoped to fund BAC libraries for 100 organisms—the cost of each depends on the size of its genome—money ran out after 63. Like garnering an invite to the Oscars, earning a spot on that final list demanded lots of politicking and a little luck, which sometimes failed to materialize.



Contestants. The apple maggot fly didn't make the cut, but the American alligator was among 63 winners.

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