FAIRBANKS, ALASKA—At Evolution 2005, from 10–14 June, evolutionary biologists, natural historians, and systematists shared results about fungi, mice, yeasts, and other organisms.

Fungal Trees Grow Faster With Computer Help

Researchers trying to determine the relatedness of organisms are finding it hard to keep up with the torrent of DNA sequence data gushing from biology's spigots. Now, two new computer programs are coming to the rescue, at least for biologists constructing the fungal family tree. One program, created by Frank Kauff of Duke University in Durham, North Carolina, and his colleagues, helps validate, assemble, and keep track of raw data from fungal DNA sequencing efforts. The other, developed by David Hibbett of Clark University in Worcester, Massachusetts, automatically retrieves fungal DNA sequences from the public archives and incorporates the data into an ever-improving phylogeny of this diverse group of microorganisms. Both efforts are part of the "Assembling the Fungal Tree of Life" project begun in 2003 and may be bellwethers of taxonomy's future. "It's great to have this all automated," says Michael Donoghue, a botanist at Yale University. "It means that progress can be made while we sleep."

Fast track. New computer programs are automating the classification of mushrooms and other fungi.

Molecular studies now dominate fungal systematics, but the plethora of data they provide has not necessarily brought clarity. There are hundreds of published family trees for the fungi or their various branches, and many conflict with one another. Yet no one has really tried to piece together where the discrepancies lie. That's where automated computer analyses will help, says Hibbett, a fungal systematist.

Among other fungal projects, Hibbett's lab focuses on mushroom-forming varieties, which make up an estimated 20,000 of the more than 70,000 known fungal species. To deal with the ever-growing number of DNA sequences for this group, Hibbett's program, which he dubbed mor, sifts through GenBank for newly deposited data on a single gene, called *nuc-lsu rDNA*, in mushrooms. If a researcher has deposited a new sequence of this gene for a species, the computer program compares it with other deposited copies of the gene for that species, weeding out any redundancies. It then compares the best version with the sequence of the gene in other species and uses the differences to adjust the branches of the fungal family tree. It even assigns names to new subgroups as needed. So far, mor has 2401 sequences representing 1899 mushroom species in 562 genera, Hibbett reported in Fairbanks, Alaska.

"It's one of the first attempts to automate large-scale phylogenetic analysis," says Roderic Page, a systematist at the University of Glasgow, United Kingdom.

Although fungal experts may need that help more than most—these organisms are among the most diverse and the most difficult to sort out—Hibbett's approach should also be portable. "It's easy to see how it could be expanded to fit other organisms," says David Baum, a botanist at the University of Wisconsin, Madison. Adds Donoghue, "I'd love to have something like this for plants."

Kauff's program, dubbed WASABI for Web Accessible Sequence Analysis for Biological Inference, comes into play before fungal family trees are created. In essence, it ensures that such trees sprout from good seeds. The consortium working on the fungal tree of life project is sequencing eight genes in 1500 different fungi, and WASABI rates the accuracy of each newly submitted DNA sequence. The program also pieces together short fungal DNA sequences into ever longer ones and compares these so-called contigs with existing sequence information. This all happens automatically, providing researchers with one place to find refined data that originated from various consortium members. Finally, WASABI archives its manipulations and analyses of the raw information. "WASABI considerably reduces the time users would otherwise have to spend," verifying and piecing together sequences, says Kauff. "The speedup is many orders of magnitude."

Together with other consortium members, Hibbett and Kauff have already published one 588-species fungal tree, with all the major branches, such as the mushrooms, represented. The goal is to have the 1500 under study linked up in the proper relationships by 2006. Says Baum, "Fungal systematists are really leading the pack in terms of their critical use of cutting-edge analytical tools."

Color Genes Help Mice and Lizards

The light-skinned deer mice (*Peromyscus polionotus*) found along Florida's shoreline didn't always have such a bleached-out look. It took the beach rodents less than 5000 years to go from brown to blond; the darker look may have provided camouflage in the dense fields in which they used to dwell, but on the white sand, it would have made the mice a conspicuous meal for predators. At the meet-

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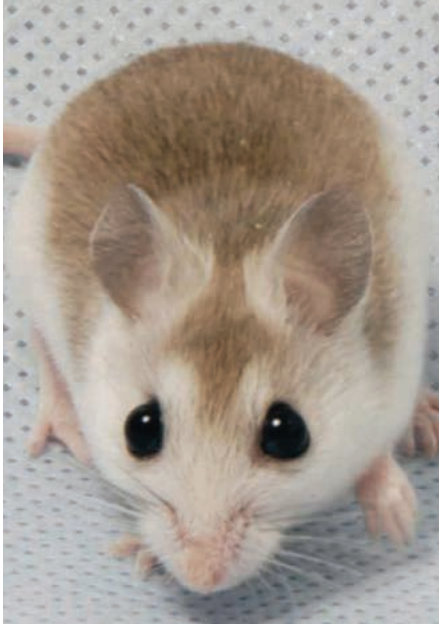

Beached and bleached. Interacting pigment genes helped whiten—and camouflage—mice migrating onto dunes.

ing, a research team described how a key gene aided the animal's colorful transformation. And another group reported that changes in the same gene helped lizards evolve a similar adaptation.

Researchers have studied the genetics of color in lab mice for decades, implicating more than 100 genes, half of which are now sequenced. But Hopi Hoekstra, an evolutionary biologist at the University of California, San Diego, says she "wanted to see what kinds of genes are involved" in shaping color patterns in nature.

In the southeastern United States, deer mice living in forests and dense fields have brown backs and light gray underbellies. But their cousins living on the vegetation-sparse white dunes on islands along the Gulf Coast have lost most of the brown on their backs, and their bellies look bleached. The beach mice have also dropped a characteristic dark stripe running down their face for a more muted look that helps camouflage the animals in their burrows.

To get at the genetics behind such adaptations, Hoekstra and her colleagues bred male beachcombers with female forest mice and vice versa. They now have 600 second-generation mice. "We see a lot of variation in pigmentation" among the animals, says Hoekstra, estimating that about a dozen genes control the pattern of colors distributed across the rodent's flanks, faces, tails, and other body parts. With these crossbred mice, she began testing whether various genes shown to have roles in coloration in lab mice are involved in the beach mouse's new look. "Hoekstra can ask where in the pathway natural selection is working," notes Johanna Schmitt, an evolutionary biologist at Brown University in Providence, Rhode Island. By happenstance, Hoekstra and her colleagues scored a hit with *Mc1R*, a gene involved in the switch between light and dark pigments. A single base change in the gene resulted in the Mc1R protein having abnormally low activity, causing less melanin to be made in the beach mice and resulting in whiter fur. In fact, the change in just this one gene accounts for 34% of the color variation in beach mice, Hoekstra reported. Hoekstra's postdoc Cynthia Steiner subsequently showed that a second gene called *agouti* is more significant for patterning than overall color.

Further analyses indicate that the two genes influence each other, a process called epistasis, in defining the overall patterns of body coloration. "It's the interaction that explains the variation" in color from body part to body part, Hoekstra notes.

Lizards from White Sands, New Mexico, also seem to have exploited changes in *Mc1R* to transform themselves from dark brown to light-colored, Erica Rosenblum of the University of California, Berkeley, reported. She studied three distantly related lizard species that have moved into the dunes in the past 600 years. Rosenblum found that all three had mutations in the gene, dramatically reducing their colors. "What is most striking is the repeating pattern as different species converge on the same phenotype," says Hoekstra.

Lizards and mice are far apart on the tree of life, and scales and fur bear little resemblance, but the metabolic pathways to produce melanin pigment in both animals are very similar. As a result, "it may be evolutionarily 'easy' to evolve color and color pattern differences" by means of the *Mc1R* gene, says Rosenblum.

Wine Yeast's Surprising Diversity

Since the days of the pharaohs, the yeast *Saccharomyces cerevisiae* has enabled us to make bread, as well as wine, beer, and other alcoholic beverages. More recently, it has become a model organism for cell and molecular biologists. Yet it has barely been studied outside the lab. Now, a research team has begun to trace the genetic diversity of this simple eukaryote in the wild.

Evolutionary biologist Jeffrey Townsend of the University of Connecticut, Storrs, and his colleagues have identified several distinct *S. cerevisiae* strains from forests and vineyards in Italy and the United States. Different strains found on grapes from different vineyards "may in part be responsible for the distinctive tastes of naturally fermented wines," Townsend speculates.

Until recently, yeast researchers paid little mind to grapes, thinking that any yeasts on the grapevines were escapees from the nearby vats, where the microbes are often added for the fermentation process. That thinking came into question, however, in 2004, when Paul Sniegowski of the University of Pennsylvania in Philadelphia discovered *S. cerevisiae* just below the bark of oak trees and in the soil around the base of these trees, establishing that this organism had a broader distribution beyond rotting fruit and vineyards. He "demonstrated that there are isolated, variant populations of *S. cerevisiae*," says Townsend.

Sniegowski's finding led researchers to wonder how many yeast strains there are in the wild, how the oak strains are related to those in vineyards, and whether one is derived from the other. While working in John Taylor's lab at the University of California, Berkeley, Townsend and graduate student Erlend Aa of the University of Tromsø in Norway compared DNA of 15 *S. cerevisiae* strains from Italian vineyards—primarily from grapes used in Chianti wine—with two lab samples and a strain from crushed grapes used to make wine. They also analyzed yeast strains provided by Sniegowski that were found on and near oak trees.

Aa sequenced four genes from each yeast and found 78 single-base differences

Unexpected diversity. Once thought to be one strain worldwide, *S. cerevisiae* species collected from oaks and vineyards are quite distinctive.

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