bidopsis extracts along with COP1, an indication that the two proteins do in fact associate in plant cells. The researchers also studied the overall gene expression profiles of plants with deficiencies in photoreceptors and COP1, and the similarities they found further the circumstantial case for a link between the two proteins.

Based on the data, the team members propose that blue light alters cryptochromes so that they can attach to COP1. This stops the protein from its normal business of tagging HY5 and other transcription factors for degradation. As a result, the gene-transcribing machinery, which is ready and waiting in the nucleus, can respond almost instantaneously to light-signal changes.

Plant researchers say that this three-step COP1 pathway is unexpectedly simple: Experience with other signaling pathways shows that there could easily have been a dozen regulators between cryptochromes at the cell surface and COP1. But the short pathway is not the end of the story.

For one, cryptochromes are not the only photoreceptors involved in photomorphogenesis. Red light receptors called phytochromes control another short pathway that also regulates the light response on time scales as short as those of the new cryptochrome pathway. Indeed, the two pathways may be connected, because Cashmore showed a few years ago that phytochromes can directly interact with cryptochromes. In addition, plant geneticist Chentao Lin of the University of California, Los Angeles, found a protein, SUB1, that now looks like it might modulate the COP1 cascade.

–JOSH GEWOLB

ECOLOGY

Field Test Backs Model for Invader

MADISON, WISCONSIN—The growing threat from invasive species has spurred researchers to try to forecast whether a newcomer species will fade into oblivion or become the next kudzu. To do so, scientists have devised computer models for target species. Here at the annual meeting of the Ecological Society of America last week, a researcher at Washington State University in Pullman presented results that meld such modeling with field tests of a weed currently plaguing the southeastern United States. And although the results are grim, they demonstrate the importance of attacking weeds early in their invasion, before they take hold.

The work involves the Chinese tallow (*Sapium sebiferum*), introduced in the South as an ornamental tree in the 1770s and outlawed in recent years by the state of Florida because of its invasiveness. Robert R. Pattison, who works in plant ecologist Richard N. Mack's group in Pullman, began by plugging the temperature and moisture conditions of the plant's native range in China into a commercially available computer model called CLIMEX. When he applied the same parameters to other parts of Asia and Australia, the model—which has been widely used, to predict the distribution of introduced biocontrol agents—generated a map that corresponds to areas where the tree has indeed invaded. When Pattison applied the model in the United States, it showed that Chinese tallow has a potential that is "well beyond its current range" in the South, he told those attending the meeting. The model predicts that the weedy tree could live as far north as Illinois and New Jersey and in scattered spots along the West Coast.

Pattison then took a novel step: putting the forecast to a test in the field. "That's what is nice about it," says ecologist Erika Zavaleta of Stanford University, who studies invasive species and global change. Pattison planted Chinese tallow seedlings at seven eastern research sites, all within the U.S. range predicted by the model. The seedlings, now leafy 2-meter saplings, have thrived in the 2 years since planting at sites as far away from the current range as Maryland. The plants did well in both dry and moist areas, and did especially well when planted at sites with an open canopy. "They grew like crazy," says Pattison.

The field results suggest that the model lacks other variables that might account for why the plant has not yet spread to Maryland and other northern regions in the 200 years it has been in the United States, says Zavaleta. Still, she says, Pattison's work in coupling field testing with modeling "is really valuable at giving a rough cut" of a plant's potential distribution.

That forecast is also heavily influenced "by what people plant," says Pattison. Chinese tallow's recent appearance in the wild in California, he says, is a likely result of its popularity among backyard gardeners.

Unfallow tallow. Seedlings of the Chinese tallow tree invade a natural area in Australia.

CREDIT: (BOTTOM) GOOLSBY/USDA/ARS

–CHRISTINE MLOT

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HUMAN GENOME

Less Can Be More, U.K. Study Finds

HINXTON, U.K.—In addition to setting a scientific milestone, the publication of competing drafts of the human genome sequence last February marked a struggle for priority in which the rival groups tried to undermine each other's claim by challenging the quality of the results. Now, the first formal comparison of the public and private genome maps confirms that there are indeed major differences between the data sets. And it suggests that the version produced by Celera Genomics of Rockville, Maryland, is more accurate.

At the Genome Informatics Conference here on 9 August, Colin Semple, head of bioinformatics at the Medical Research Council's Human Genetics Unit in Edinburgh, described an analysis of a 6.9-megabase stretch of chromosome 4 (4p15.3 to p16.1), a region implicated in bipolar disorder. At least 96% of this challenging region had been sequenced independently by Kathy Evans and her group at the University of Edinburgh using a map-based method.

Semple's team compared the sequences published by Celera, the publicly funded Human Genome Project (HGP), and the Evans team. Contrary to speculation, Celera's approach of breaking the whole genome into random fragments for sequencing yielded better data than the map-directed approach used by HGP. For this swath of DNA, Celera made half as many "misassemblies"—putting a fragment in the wrong order, or flipping it—as the public effort did, logging 2.08 misassemblies per megabase. However, Semple's team found that the Celera stretch is still full of holes: Celera had sequenced only 23% of the region, while HGP had managed 59% of it. Celera has "the best quality data, possibly as a result of having so little sequence in it," says Semple. He notes that his group analyzed data that were publicly available as of 1 September 2000, so both sequences undoubtedly have been polished since then. And it's unknown whether the accuracy rates in this chromosome 4 region can be extrapolated to other regions.

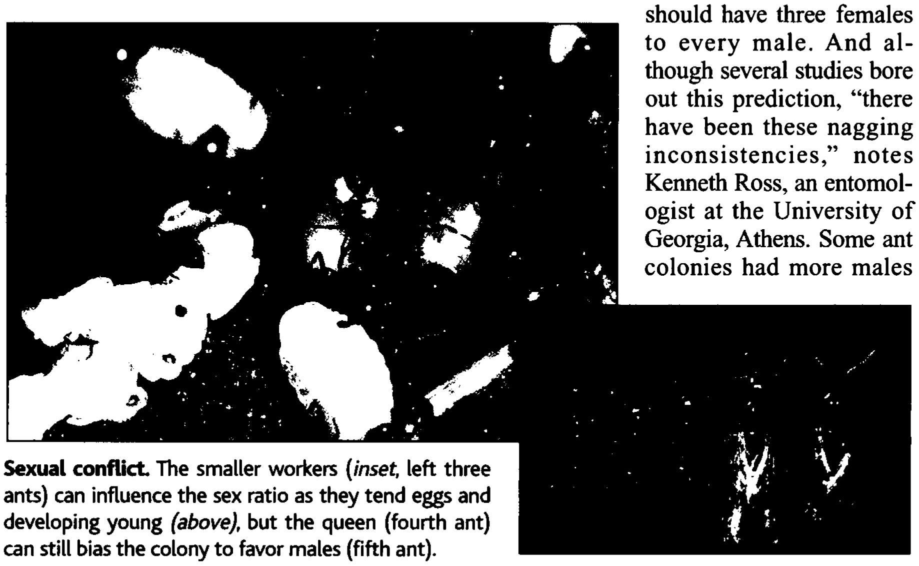
Semple's presentation provoked surprisingly little rancor at the meeting, sponsored by the Wellcome Trust and Cold Spring Harbor Laboratory, which was a mostly cordial affair punctuated by hearty laughs in response to inside jokes and kooky names for genome annotation algorithms such as FANTOM (for functional annotation of mouse). Indeed, the comparative study's implications depend on one's point of view. "It's a question of whether you want Havarti or Swiss cheese. The public assembly doesn't have that many holes, but the holes it does have are much bigger," says Jim Kent of the University of California, Santa Cruz, author of the computer program used for the initial assembly of the HGP genome sequence. Kent advises scientists considering a subscription to Celera's database to take a utilitarian approach. First they should examine the region of interest in the public database, he says: "If it's in good shape, then praise the lord they've just saved themselves $20,000." **–BEN SHOUSE**

Ben Shouse is an intern in the Cambridge, U.K., office.

EVOLUTIONARY BIOLOGY

Queens, Not Workers, Rule the Ant Nest

Queen fire ants not only populate their colonies, but they can also influence its sex ratio by limiting the number of female eggs they produce. This finding, reported on page 1308 by evolutionary biologist Laurent Keller of the University of Lausanne, Switzerland, and his colleagues, is contrary to expectation. Most entomologists thought that the workers, the queen's female daughters who actually raise the colony's young, determine the ratio of males to females, as they have the ability to kill or starve unwanted eggs.



Sexual conflict. The smaller workers (*inset,* left three ants) can influence the sex ratio as they tend eggs and developing young *(above),* but the queen (fourth ant) can still bias the colony to favor males (fifth ant).

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But, says Lotta Sundström, an evolutionary biologist at the University of Helsinki, Finland, "this is really the first experimental test of who determines [sex] ratios." The results are "compelling," adds Jon Seger, an evolutionary biologist at the University of Utah in Salt Lake City.

The idea that the female workers should shape the relative proportions of females and males in *Solenopsis invicta* ant colonies dates back to work done 25 years ago by Harvard's Robert Trivers and Hope Hare. They predicted that worker females would favor females over males for evolutionary reasons: Insect males develop from unfertilized eggs and carry just one copy of every chromosome, while the females arise from fertilized eggs and have two copies, one from each parent.

This so-called haploid-diploid system of sex determination skews the relatedness of the offspring such that sisters have more genes in common and, therefore, are more closely related to one another than to their brothers. Thus, while queens benefit equally by producing sons or daughters, worker females should prefer to raise sisters so they can pass on more of their genes. Trivers and Hare's subsequent analysis of sex ratios—using the relative dry weights of males and females in preserved ant, bee, wasp, and termite colonies in museum collections—supported an apparent bias in favor of females among these social insects. In contrast, solitary species tended to have the usual one-to-one proportion of females to males.

To reflect the degree of genetic relatedness between the two sexes, ant colonies should have three females to every male. And although several studies bore out this prediction, "there have been these nagging inconsistencies," notes Kenneth Ross, an entomologist at the University of Georgia, Athens. Some ant colonies had more males than predicted, and fire ants sometimes even had colonies with many more males than females. Keller and his colleagues decided to try to find out why.

In 1999, they collected 24 fire ant colonies, each of which had a queen. The researchers reared those colonies in the lab for at least a week, then counted the number of males and females among 100 individuals selected from each colony. Eleven turned out to have mostly males, and 13 consisted almost entirely of females. The researchers then switched queens from male-dominated colonies with queens from female-dominated ones.

ScienceScope

Genome Buzz An international attack on the genome of the mosquito that carries the malaria parasite (*Science,* 9 March, p. 1873) got a big financial boost last week—and a new partner.

The U.S. National Institute of Allergy and Infectious Diseases awarded $9 million to Celera Genomics Group of Rockville, Maryland, to swat the sequence of *Anopheles gambiae,* the primary malaria vector in sub-Saharan Africa. Researchers hope the sequence will reveal molecular targets for drugs and other antimalaria strategies. The company expects to have the mosquito's 260 million DNA base pairs sequenced by spring 2002, giving researchers access to the genomes of all three players in the disease: humans, the mosquito vector, and the *Plasmodium* malaria parasite itself.

Climate Upheaval Despite spending 40 years in the United States, prominent climate modeler Syukura Manabe thought he knew what to expect when he decided to return to his native Japan in 1997 and join the Frontier Research System for Global Change, whose centerpiece is a massively parallel supercomputer called the Earth Simulator. But the climate for cooperative research proved so unreceptive that the former head of the U.S. government's Geophysical Fluid Dynamics Laboratory in Princeton, New Jersey, is headed back across the Pacific to his adopted home.

"To use such a huge machine, you need a lot of scientists working together. But that type of collaboration is very hard to accomplish in Japan, especially by an outsider," says Manabe, who earned his Ph.D. at the prestigious University of Tokyo before coming to the United States in 1958.

Manabe, who turns 70 next month, says that he's spent a "very productive" 4 years in the Frontier program, which is funded by both the marine science and space agencies. "But it's time to slow down," he says, "and hand over the job to a younger scientist who can communicate better with everybody involved." He expects that person to be someone who's spent his career in Japan.

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