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.

–CHRISTINE MLOT

Christine Mlot is a writer in Madison, Wisconsin.

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

CREDIT: (BOTTOM) GOOLSBY/USDA/ARS

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 re-