domesticated sunflower remains at San Andrés, which date to 4700 years ago. Some archaeologists have argued that the sunflower was domesticated in eastern North America (*4*). The new data challenge this idea [the complete details are due to appear soon (*9*)]. This is all the more interesting because molecular studies of extant wild sunflower populations from several different regions of North America, including ones near the archaeological sites in question, could not identify the wild progenitor (*9*). However, additional studies using different genetic markers are needed.

We could resort to the unsatisfying explanation that, although other wild sunflower varieties are common in the United States, the wild ancestor may be extinct. But perhaps molecular biologists have not yet sampled the right spot. Wild Mexican sunflowers are distributed a few hundred kilometers directly north of San Andrés but were not included in the molecular analyses (see the figure). If future work identifies them as credible ancestors to the domesticated species, this would provide strong support for Pope *et al.*'s hypothesis for a Mexican origin of sunflower, but a separate origin in North America would still be possible.

The Mexican sunflower data clearly bear importance for the question of whether eastern North America was an independent center of plant domestication. During the past 10 to 15 years, scholars have been building a case for such a scenario (*4*). Eastern North America stands in dramatic contrast to the other independent centers because it arose much later, about 5000 years ago, with sunflower and squash (*Cucurbita pepo* L.) consistently among the oldest components of the plant assemblages (*4*).

Now that a North American origin for sunflower is under reexamination, attention will also turn to what seems to be the earliest plant in the complex, squash. Some controversy already surrounds it because, as with sunflower, investigators are not willing to rule out the possibility that squash was a product of Mexico, where evidence for the domestication of *C. pepo* is 10,000 years old (*10*). The story is more complicated because of the probability of two separate domestication events of the *C. pepo* variety of squash (*4*), but again, molecular studies indicating where these events most likely took place remain to be carried out. A more complete answer will rest on such molecular studies and their convergence with future archaeological work in northeastern Mexico and the eastern United States.

Students of prehistoric agriculture have proposed numerous explanations for its beginnings, many of which rely on either the influence of the ecological changes that occurred globally at the end of the last Ice Age or processes operating from within human social systems involving the emergence of power and prestige (*2*). Identifying the regions where plant domestication arose independently, and regions where it did not, is crucial for our understanding of why and how agriculture emerged. More surprises are sure to come our way.

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PERSPECTIVES: CLIMATE CHANGE

# Where Has All the Carbon Gone?

**Steven C. Wofsy**

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Emission rates of $CO_2$ from combustion of fossil fuel have increased almost 40 percent in the past 20 years, but the amount of $CO_2$ accumulating in the atmosphere has stayed the same or even declined slightly. The reason for this discrepancy is that increasing amounts of anthropogenic $CO_2$ are being removed by forests and other components of the biosphere (*1*). It is estimated that more than 2 billion metric tons of carbon (2 Pg C)—equivalent to 25 percent of the carbon emitted by fossil fuel combustion—are sequestered by forests each year. Inverse models for studying atmospheric concentrations of $CO_2$ suggest that mid-latitude forests in North America and northern Eurasia (*2, 3*) are crucial carbon sinks that remove this $CO_2$ from the atmosphere. But analyses of forest inventories (which measure forest areas and timber volume) seem to indicate that forests sequester much smaller amounts of carbon (*4, 5*). Thus we have a mystery: If our forests are sequestering billions of tons of carbon annually, why can't we find it? Evidently, we have not been looking in the right places.

One place to look is in the organic matter of forests that is not considered commercially valuable and so is not normally reported in forest inventories. Such organic matter includes woody debris, soil, wood products preserved in landfills, and woody plants that have encroached on grasslands because of the long-term suppression of natural fires (see the figure, this page). According to Pacala *et al.* on page 2316 of this issue (*6*), more than 75 percent of the carbon sequestered in the United States is found in organic matter that is not inventoried. When all major sequestration processes are counted, the range of values for uptake of $CO_2$ by U.S. forests is 0.3 to 0.7 Pg ($10^{15}$ g) of carbon per year. This number is similar to that calculated from inverse models, and is compatible with direct carbon flux measurements and ecological data.

**The fate of sequestered carbon.** Uptake of atmospheric $CO_2$ by vegetation and soils in the United States, partitioned according to the ultimate fate of the sequestered carbon in the environment [adapted from (*6*)]. The total uptake of carbon in the continental United States is between 0.3 and 0.6 Pg C per year, equivalent to 20 to 40 percent of fossil fuel emissions worldwide.

Asia is another place to look for forest carbon sinks, as Fang *et al.* (*7*) demonstrate on page 2320 of this issue. They report that forests in China have sequestered substantial quantities of $CO_2$, despite population pressure, rapid expansion of industry, and a relatively small base of forest land (~100 million ha with 4.5 Pg C in China, versus 250 million ha with 12 Pg C in the continental United States) (*8*). Reforestation and afforestation (the planting of new forests) have been national policies in China since the late 1970s, motivated by the desire to restore degraded ecosystems for flood and erosion con-

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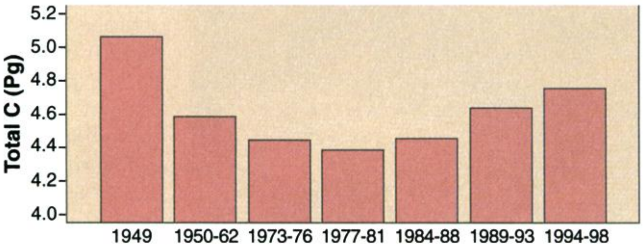
trol, to protect water supplies, and to produce wood for fuel. Reforestation and afforestation policies have reversed the sharp decline in Chinese forests (see the figure, this page). Planted forests now account for 20 percent of the total organic matter and 80 percent of sequestered carbon in China.

It is the past decisions on land use that drive $CO_2$ uptake by forests today in both the United States and China. But the policies of the two nations are very different in character and intent. In the United States, land use decisions are largely private matters driven by socioeconomic trends. Marginal agricultural land has been abandoned in the face of intensification and industrialization of agriculture. Timber harvesting has responded to market pressures. Fires have been suppressed to protect private and public property, with ambiguous long-term effects on atmospheric $CO_2$. For instance, increases in combustible material in fire-prone areas must be addressed lest conflagrations lead to disaster and, incidentally, to a rapid return of sequestered carbon to the atmosphere. In China, afforestation and reforestation are government policies intended to enhance forests, but were never intended to reduce the rate of increase in atmospheric $CO_2$. In neither country has sequestration of carbon been included as a factor in land use decisions.



**Boosting carbon stocks.** Changes in carbon stocks (the amount of sequestered carbon) in Chinese forests over the past half-century (*7*).

The reports by Pacala, Fang, and their colleagues help to demystify the low rate of accumulation of atmospheric $CO_2$. In addition, these authors demonstrate the potential benefits associated with managing forest resources not only for promoting traditional uses (production of fiber, flood control) but also for slowing the rise in atmospheric concentrations of $CO_2$. Forests cannot miraculously stop an increase in $CO_2$ in the atmosphere, but they can significantly mitigate the rate of increase for many decades to come. The opportunities are balanced by the risks of inaction or regressive policies that could promote the release of carbon currently stored in forests, halting or reversing the benefits of forests acting as carbon sinks.

These new studies on carbon sequestration help to provide the rationale for sensible national and international policies regarding forests and the $CO_2$ cycle. We need to develop a scientific basis for measuring and improving the properties of forest carbon sinks (*9*). The United States should join with other countries to provide sensible incentives for land use decisions, from the tropics to the boreal zone, that optimize the many benefits of forests, including their ability to sequester anthropogenic $CO_2$.

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PERSPECTIVES: MICROBIOLOGY

# The Great Escape

**Graham F. Hatfull**

Lytic bacteriophages are parasitic viruses that infect and replicate inside bacteria. But these skilful parasites face a conundrum: How can their progeny escape from bacteria so that they can go forth and multiply? Most bacteria are surrounded by a tough wall composed of a cross-linked peptide-sugar (peptidoglycan) matrix that protects the bacterial membrane and helps to maintain the microbe's shape (see the figure) (*1*). Building and maintaining this peptidoglycan matrix is problematic for bacteria because the wall must be strong enough to withstand the osmotic pressure from within yet flexible enough to be constantly remodeled as the microbe divides and grows. On page 2326 of this issue, Bernhardt and colleagues (*2*) report that some bacteriophages have adopted strategies to block enzymes in the peptidoglycan synthesis pathway, skillfully exploiting the bacteria's need to continuously synthesize these molecules.

One obvious way to disrupt bacterial walls is to smash through them. Most double-stranded DNA phages exercise this option—they produce an endolysin that rips apart the peptidoglycan matrix. The bacterial membrane beneath the matrix, however, presents a barrier that separates these muralytic enzymes from their targets (see the figure). Undaunted, these phages also produce a holin protein that permeabilizes the membrane and lets the endolysin wrecking crew gain access to the peptidoglycan matrix (*3*). Lysis of the bacterial wall needs to be closely coordinated with virus replication and the assembly of viral progeny because premature rupture would be suicide for the phage offspring (*4*). As always, timing is everything.

According to Bernhardt and co-workers, lytic phages with smaller genomes, such as the RNA phage Qβ (*2*) and the single-stranded DNA phage ϕX174 (*5*), use a very different strategy for escaping from their bacterial hosts. These phages encode neither an endolysin nor a holin and have no way of attacking preexisting bacterial wall structures (*2*, *5*). Instead, they interfere with the bacterial enzymes that make precursors of the peptidoglycan murein, a key component of bacterial walls. The resulting lack of coordination between peptidoglycan synthesis and bacterial wall construction leads to weaknesses in the wall, which collapses owing to osmotic pressures from within.

Phage ϕX174 makes a single lytic enzyme, protein E, which is associated with the bacterial membrane (*6*). This lysin blocks the activity of MraY, a bacterial membrane protein that catalyzes the transfer of murein precursors to lipid carriers so that the precursors can be transported through the membrane. Phage Qβ does not encode a single protein with a dedicated lytic activity, but rather produces a multifunctional $A_2$ maturation protein. Present as a single copy in the capsid coat of the phage, this remarkable 41-kilodalton polypeptide is necessary not only for lysis of bacteria but also for binding of the bacteriophage to the bacterial sex pilus during infection (*7*).

Like protein E of phage ϕX174, $A_2$ specifically interferes with bacterial wall biosynthesis, but acts at an earlier stage by inhibiting the MurA enzyme. Bernhardt *et al.* (*2*) show that this inhibition is membrane-independent and appears to involve a direct interaction between $A_2$ and its MurA substrate. This is supported by their finding that $A_2$-resistant *Escherichia coli* mutants have a single amino acid substitution in a region on the surface of MurA that

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