

Reducing CO₂ Loss From Tillage

When a farmer tills a field, some carbon dioxide in the soil escapes to the atmosphere. Agricultural Research Service (ARS) scientists in Auburn, Alabama, are seeking methods of reducing this CO₂ loss because the loss of carbon in this gas form may be harmful to the environment and to soil productivity.

Plant physiologist Stephen A. Prior and agricultural engineer Randy L. Raper are the leaders of this project at the National Soil Dynamics Laboratory. The main factors they scrutinized were time of year (spring vs. fall tillage) and implements used. The scientists looked at loamy sand soil in east-central Alabama to see how much CO₂ escaped during plowing of a grain sorghum field.

With fall tillage, the amount of CO₂ lost depends specifically on the type of implement used. Disking caused more CO₂ release than chisel plowing because disking causes greater soil mixing. Plots of land that were not tilled had low levels of CO₂ loss similar to the fields that were chisel-plowed because less residue was incorporated into the soil.

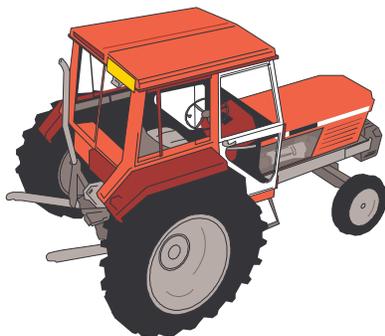
“Our research shows that fall tillage equipment that maintains surface residue and minimizes soil disturbance helps reduce CO₂ loss,” Prior explains.

Simply waiting until spring to till also reduced CO₂ flux. Leaving crop residue in place over the winter months and postponing tillage until spring slows residue decomposition and protects the soil during winter rains.

Sequestering carbon reduces the rate at which the atmosphere’s CO₂ concentration increases. Carbon dioxide and several other gases trap heat near the Earth’s surface and may contribute to global warming.

This work fits into Raper’s research to develop implements and cropping systems that minimize residue burial. He has also found that the amount of residue buried increases substantially for disks as speed or depth of tillage increases. His advice? “Park the disk and use the chisel, if you have the choice.”—By **David Elstein**, ARS.

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Fingerprinting a Killer—A Nematode Killer, That Is

A new genetic fingerprinting method is now on hand to identify *Pasteuria* bacteria that kill soybean cyst nematodes—culprits behind \$324 million to \$1.4 billion in annual yield losses.

ARS nematologist Greg Noel and colleagues devised the method to help resolve confusion about *Pasteuria*’s taxonomic classification and, in turn, speed efforts to identify strains with the greatest potential as nematode biocontrol agents. (See “Soybean Cyst Nematodes, Look Out!” *Agricultural Research*, September 1997.)

Conventional methods involve collecting “endospores”—*Pasteuria*’s infectious stage—from nematode specimens so that ribosomal DNA (deoxyribonucleic acid) can be extracted from the bacterium using centrifugation, heat, enzymes, and other chemicals. It’s a laborious, time-consuming affair, however, partly because at least 1 million endospores are needed to yield enough DNA to analyze. Contamination by other bacteria is also a problem.

With the new method, which includes use of DNA-multiplying technology called polymerase chain reaction (PCR), “We can extract ribosomal DNA from a single, infected nematode that has several hundred to a few thousand endospores,” says Noel, who’s in ARS’s Soybean/Maize Germplasm, Pathology, and Genetics Research Unit in Urbana, Illinois. His colleagues are Ndeme Atibalentja, at the University of Illinois at Urbana-Champaign, and Aurelio Ciancio, Institute of Plant Protection, Bari, Italy.

For years, says Noel, researchers used morphological, developmental, and pathological characteristics to describe and classify *Pasteuria*’s four known species. Now, comparing differences in the bacteria’s ribosomal DNA is deemed more precise.

Although the approach is widely used, Noel felt there had to be an easier way of extracting the DNA from endospore-infected nematodes. Instead of using conventional methods, his group used “glass bead beating.” This procedure involves crushing a nematode specimen so that any DNA within it, including that from *Pasteuria*, is released into solution. Lab-built molecules called primers are then added. They bind with specific fingerprint regions on *Pasteuria* DNA so it can be multiplied by PCR, cloned, and sequenced for identification.

Noel’s group has already used the method to confirm the identity of *P. nishizawae* in an Illinois soybean plot, marking the first report of this promising biocontrol species in U.S. soils.—By **Jan Suszkiw**, ARS.

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