Fruitful

Disease-Resistance Findings



The Japanese crab apple (Malus floribunda) is resistant to apple scab disease.

n 2007, cherries, red raspberries, and apples earned U.S. producers some \$3.1 billion. Research by ARS computational biologist Angela Baldo indicates that these three members of the Rosaceae plant family share key genetic traits for disease resistance. Her findings could help plant breeders develop more robust varieties of these popular fruits.

"We can survey the genetic makeup of a single plant fairly easily. But we run into a bottleneck when we try to figure out which genes are represented in multiple cultivars," says Baldo, who works at the ARS Plant Genetic Resources Unit (PGRU) in Geneva, New York. "So we need to use tools that allow us to survey plant collections quickly and find accessions that are good candidates for breeding programs."

Plants in the Rosaceae family—which has been evolving over millions of years—share disease-resistance genes found in many other plants. These genes are active in pathogen recognition, cellular signaling, and protein interaction.

One class of these resistance genes is called "resistance gene analogs" (RGAs) and is characterized by two protein sequences at either end of the gene. One of the sequences is a nucleotide-binding site, and the other is a leucine-rich region.

Scientists have already developed methods to use these protein sequences—called "motifs"—for generating molecular markers that can be used to locate and map these resistance genes and others nearby. Using RGAs, researchers have located resistance genes in soybeans, potatoes, barley, rice, peas, and other crops.

First Steps in Raspberry Resistance

Baldo worked with several colleagues to capture a collection of RGAs in red raspberry (*Rubus idaeus*). Using 175 RGAs already available for other Rosaceae species, they identified motifs that could be used to develop molecular markers to pinpoint similar sites in red raspberry. Then they extracted DNA from the red raspberry cultivar Latham—which is known for its resistance to *Phytophthora* root rot, a significant pathogen of the berry—and began their search.

Using this approach, the research team found 75 red raspberry RGAs. Most were unique—but they were anywhere from 50 to 87 percent similar to the RGAs from other Rosaceae species.

In addition, one of the red raspberry RGA markers was linked genetically to *Phytophthora* root rot resistance. This discovery might someday help plant breeders develop hardier—and more marketable—varieties of red raspberry.

To date the most effective way of managing this pathogen has been to develop disease-resistant raspberry varieties. But the fruit quality of most disease-resistant types is not as commercially appealing as berries produced by more susceptible raspberry cultivars.

"Now we have some idea of where we can start looking for disease-resistance traits," Baldo says. "Even though we only surveyed a small portion of the *Rubus* genome for disease-



The European crab apple (Malus sylvestris) can be found from Scandinavia to Greece.

PEGGY GREB (D1400-1)



The research team located three new groups of disease-resistance genes in the wild apple collections.

resistance sites, we found 75 RGAs. If we expand our search, it's possible we could find many more."

Checking Out Cherries

Cherry breeders are also cheering on Baldo's RGA research. She contributed to the identification of 90 RGAs from sweet and sour cherry cultivars that have different levels of resistance to cherry leaf spot and powdery mildew.

The cherry RGAs were compared with other rosaceous RGAs that researchers have already linked with resistance to a range of pathogens. These threats include powdery mildew, sharka—also known as "plum pox"—bacterial spot, *Phytophthora* root rot, apple scab, and nematodes.

ARS plant physiologist Gayle Volk prepared the genetic materials for the cherry RGA study. She works at the ARS National Center for Genetic Resources Preservation in Fort Collins, Colorado, where she helps maintain the viability of the plant accessions.

Volk is especially pleased with findings about possible links between sharka, which infects most stone fruit tree species, and powdery mildew, which affects a wide range of horticultural and ornamental plants. "Preliminary studies suggest there may be similarities between peach RGAs that are linked to sharka and cherry RGAs that are linked to powdery mildew," she says. "If we can confirm this with additional research, it could save a lot of genetic mapping for disease resistance."

More Than Cherries and Berries

Baldo also helped search for RGAs in some 300 wild apple accessions maintained at the PGRU and else-

where. "Brambles and trees in the Rosaceae family diverged a long time ago, and I wanted to start piecing together a history of resistance genes in this family," she says.

The wild apple collection was enticing for other reasons as well. "Traits for wild apple trees are not well known, because they're not in commercial production," she says. "This kind of study helps us identify what varieties to focus on for additional sources of disease resistance in breeding."

Initial results are promising for computational biologists and plant breeders alike. Using existing Rosaceae RGAs, Baldo's team located three new groups of resistance genes in the wild apple collections. Plans are under way to map these genes and assess their links

PEGGY GREB (U1403-1)

The wild apple (Malus sikkimensis) is native to temperate and tropical Asia.



Computational biologist Angela Baldo studies wild apples in the ARS collection to identify new disease-resistance genes. She also develops software methods to put these genes in context within the entire Rosaceae family, which includes apples, pears, peaches, strawberries, brambles, and ornamental roses.

to regions of the apple genome that convey resistance to fire blight, apple scab, and powdery mildew.

Baldo has also begun to collaborate with plant breeders and geneticists in South Africa, Italy, and New Zealand on surveying disease resistance in apples. All three countries produce apples as an export crop—as does the United States, which exports about one of every four apples harvested.

"RGAs can help us survey fruit crops and tag resistance gene regions," Baldo says. "But we can also use them to survey larger germplasm collections to look for ancestors of these resistance genes and add to our knowledge of how these genes evolved in

the Rosaceae family."—By **Ann Perry,** ARS.

This research is part of Plant Genetic Resources, Genomics, and Genetic Improvement, an ARS national program (#301) described on the World Wide Web at www.nps.ars.usda. gov.

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