

Crunching New Data on Walnut Genes

Many things make a walnut wonderful—its rich taste, smooth texture, and, of course, its heart-healthy compounds. Now, ARS scientist Mallikarjuna Aradhya and his University of California-Davis colleagues have embarked on a 4-year study to identify walnut seedlings that have about a half-dozen traits valued highly by those who grow—and those who eat—walnuts. Those traits range from the plumpness of the kernel to the time of year the tree comes into leaf—a feature useful for avoiding frost damage and some diseases.

The scientists intend to home in on the traits via genetic markers, called “single nucleotide polymorphisms” or SNPs, that they will create.

Ideally, walnut breeders will use the markers in what’s known as “marker-assisted breeding.” The approach enables them to identify superstars while those trees are still very young. That’s a huge advantage when breeding English walnuts—America’s favorite. This species takes several years to begin bearing marketable nuts.

The collaboration will also yield several different kinds of genetic maps and, in all, is expected to provide the most comprehensive picture ever offered of walnut’s little-known genetics. More than 600 trees are being grown especially for the research, which is sponsored by ARS, the Folsom, California-based Walnut Marketing Board, and the university.

Aradhya says the markers will be invaluable for profiling the genetic makeup of the 1,680 walnut trees in the nation’s official walnut collection, located just outside of Sacramento, California. He’s a geneticist for this splendid array of the planet’s wild and domesticated walnuts, officially known as the ARS National Clonal Germplasm Repository for Tree Fruit and Nut Crops and Grapes.—By **Marcia Wood**, ARS.

*Mallikarjuna Aradhya is with the USDA-ARS National Clonal Germplasm Repository for Tree Fruit and Nut Crops and Grapes, 3201 Straloch Rd., Davis, CA 95616; phone (530) 752-9392, fax (530) 752-5974, e-mail malli.aradhya@ars.usda.gov. **

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New DNA Markers for Rice Blast-Resistance Gene

Rice blast fungus (*Magnaporthe grisea*) causes blast disease (also known as “rotten neck disease”), which has a catastrophic effect on rice. Rice blast disease—found in 85 countries worldwide—causes huge crop losses annually and is estimated to destroy enough rice to feed more than 60 million people. The fungus can infect the roots, leaves, and stems of the plant. Once embedded, the fungus can produce structures that can also invade the plant’s vascular system—blocking transport of nutrients and water and producing lesions on the aerial plant parts.

Scientists at the Rice Research Unit in Beaumont, Texas—led by plant molecular geneticist Robert Fjellstrom and research leader Anna McClung—have found genetic markers that tag a disease-resistance gene that has been effectively used to combat a broad-spectrum of races of *M. grisea*.

Rice blast is found in 85 countries.

These DNA markers are linked to the *Pi-z* blast-resistance gene in rice. This gene confers resistance to many forms of the blast fungus, so these markers are quite valuable for selecting and breeding disease-resistant rice cultivars. Because the resistance genes are natural, their use represents an environmentally friendly way to combat the disease.

The markers presented in this research are located closer to the *Pi-z* gene than previously developed ones. This close proximity makes the new markers extremely accurate in predicting the presence of this useful gene. Rice breeders have already been able to use these markers to select for highly resistant rice cultivars in California (M-207 and M-208) and Texas (Presidio).

Preliminary analysis of a cross between the cultivars Zenith and Pi-2, which carry the *Pi-z* and *Pi-2* resistance genes, respectively, indicate that the genetic factors encoding their separate resistance reactions are not the same but are very tightly linked. The *Pi-z* markers reported here provide rice breeders and geneticists with a valuable tool for marker-aided selection of the *Pi-z* gene. Most of the *Pi-z* marker alleles are unique to the *Pi-z* gene, making them easy to select for the *Pi-z* gene within most genetic backgrounds.—By **Alfredo Flores**, ARS.

*Robert Fjellstrom and Anna M. McClung are in the USDA-ARS Rice Research Unit, 1509 Aggie Dr., Beaumont, TX 77713; phone (409) 752-5221, fax (409) 752-5720, e-mail bob.fjellstrom@ars.usda.gov, anna.mcclung@ars.usda.gov. **