



Researchers map citrus greening gene

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Researchers have a new tool to combat citrus Huanglongbing, a disease also known as citrus greening that is threatening the nation's \$2.2 billion citrus industry.

Agricultural Research Service scientists have sequenced the genome of the bacterium *Candidatus Liberibacter asiaticus*, which causes HLB, according to a news release.

The bacterium resides in the plant's phloem—tissues that carry nutrients throughout the plant. With the nutrient pipeline clogged, the trees eventually die.

Plant pathologist Yong-Ping Duan and research leader David Hall, at the U.S. Horticultural Research Lab in Fort Pierce, Fla., have sequenced more than 95 percent of the bacterium's genome and have posted results in GenBank, an online database of genetic resources.

They are working to sequence the remaining 5 percent. Once they are complete, they and fellow researchers will be able to study the organism's biological features more closely and possibly unlock the mystery of how it spreads.

They also should be able to identify key genes that would help control the disease.

The Asian citrus psyllid picks up the greening bacterium while it is in an immature stage and then spreads it as an adult during feeding. The insect is found throughout much of the Southeast, as well as in Texas and Southern California.

Citrus greening was discovered in Florida in 2005 and is now found throughout that state's citrus belt. It also has been discovered in three separate residential trees in Louisiana. Those trees have been destroyed.

Citrus trees can be infected for two years before characteristic yellow shoots and mottled leaves appear. Infected trees produce unmarketable, bitter fruit and typically die in five to seven years.

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