

Genomes of citrus canker pathogens decoded

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An international team of scientists from Brazil and the United States have completed the draft genome sequences of two strains of the *Xanthomonas* bacteria that cause citrus canker. Citrus canker, a belligerent disease that has plagued plant growers in parts of the United States, South America, and Asia, causes millions of dollars in lost revenue every year for farmers of citrus crops such as oranges, limes, and grapefruit. The genomic information obtained by these sequencing projects, which is described in the journal *BMC Genomics*, suggests possible intervention targets for further experimental investigation.

João Setubal, Associate Professor at the Virginia Bioinformatics Institute and the Department of Computer Science at Virginia Tech, commented: "[Citrus canker](#), which is found in different citrus plants, is effectively a single disease that is spawned by one of three strains of certain species of the *Xanthomonas* [bacterium](#). The [genome sequence](#) of the most virulent of the citrus canker pathogens, *Xanthomonas citri* *subsp. citri*, was completed in 2002, and this was a big step forward in understanding the disease. The two new sequences will provide a welcome boost to citrus canker studies."

Citrus canker has proved difficult to combat despite concerted national disease eradication efforts. The disease produces lesions, blisters, and holes in the stems, leaves, and fruit of citrus crops. While the [bacterial infection](#) of the plant is not harmful to humans, the fruit becomes damaged and infection can lead to leaf loss and premature dropping of fruit. The availability of the genome sequences for the two additional bacterial strains that cause citrus canker means that scientists can now

use key similarities and differences between the three related genomic sequences to zero in on the molecular basis of citrus canker.

Leandro Moreira of the Federal University of Ouro Preto, Brazil, remarked: "There is currently no such thing as a treatment for a plant disease like citrus canker. Infected trees, and others nearby, need to be cut down. Our work is another step in the direction of a more rational and cost-effective way to control and perhaps eradicate this disease."

Researchers have known for some time that the *Xanthomonas* bacteria inject certain proteins called effectors into the plant cells, bringing about citrus canker. Said Setubal: "Our findings have uncovered new effectors that are shared only by the three bacterial strains, and not by other *Xanthomonas* species. These effectors are excellent candidates for further studies."

Differences in the genome sequences of the three bacterial strains are also helping to shed light on why strain A (*Xanthomonas citri subsp. citri*) is more virulent than its strain B and C counterparts (*Xanthomonas fuscans subsp. aurantifolii*) and why it infects more citrus species. Said Boris Vinatzer, Assistant Professor in the Department of Plant Pathology, Physiology and Weed Science at Virginia Tech, who played a key role in the project: "Intriguingly, our sequence data revealed genes that are absent in the genome of the A strain but present in the genomes of *Xanthomonas* strains B and C. These genes may code for effector proteins that are recognized by some citrus species in a way that triggers a resistance response that interferes with disease development in these species. Such genes warrant close attention in future experiments."

In November 2006, The United States Department of Agriculture called for a new disease management plan to be devised for citrus canker after unprecedented hurricanes in Florida and other factors enabled the bacteria to jump significantly beyond the recommended cutting zone

that scientists had thought necessary to prevent spread of the disease under normal weather conditions. It is hoped that the sequence information described in the new study will be used in the future to develop countermeasures and, perhaps, to help engineer citrus species that have long-lasting resistance to citrus canker.

Dean Gabriel, Professor in the Department of Plant Pathology at the University of Florida, Gainesville, who is not an author on the paper, remarked: "The availability of complete genome sequences of pathogens always greatly accelerates research because geneticists can then literally see all of the tools that the pathogen has in its arsenal, both defensive and offensive. This guides future research and control measures. Comparisons by the team behind this study have already resulted in the identification of specific candidate genes that may affect host range on citrus."

More information: Novel insights into the genomic basis of citrus canker based on the genome sequences of two strains of *Xanthomonas fuscans* subsp. *aurantifolii*. BMC Genomics 11: 238. [PMID: 20388224]. www.biomedcentral.com/1471-2164/11/238/abstract

Provided by Virginia Tech

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