

Research team unravels tomato pathogen's tricks of the trade

November 3 2011

(PhysOrg.com) -- For decades, scientists and farmers have attempted to understand how a bacterial pathogen continues to damage tomatoes despite numerous agricultural attempts to control its spread.

Pseudomonas syringae pv. tomato is the causative agent of bacterial speck disease of tomato (*Solanum lycopersicum*), a disease that occurs worldwide and causes severe reduction in fruit yield and quality, particularly during cold and wet springs.

In the spring of 2010, for example, an outbreak in Florida and California devastated the harvest in those areas.

"There is not much that can be done from a farming standpoint," said Boris Vinatzer, associate professor of [plant pathology](#), physiology and weed science, and an affiliated faculty member with the Fralin Life Science Institute at Virginia Tech. "First, farmers try to use seed that is free of the pathogen to prevent [disease outbreaks](#). Then, there are some disease-resistant tomato cultivars, but the pathogen has overcome this resistance by losing the gene that allowed these [resistant plants](#) to recognize it and defend themselves. For the rest, there are pesticides but the pathogen has become resistant against them."

So how exactly has the pathogen evolved to consistently evade eradication efforts? This is where science steps in, and a copy of the bacterial pathogen's game plan is crucial.

Thanks to the collaborative work of Vinatzer, Virginia Bioinformatics Institute computer scientist Joao Setubal, assistant professor of statistics Scotland Leman, and their students, the genome of several *Pseudomonas syringae* pv. tomato isolates have been sequenced in order to track the bacterial pathogen's ability to overcome plant defenses and to develop methods to prevent further spread.

Their findings were recently published in the Aug. 25 issue of [PLoS Pathogens](#), a peer reviewed open-access journal published by the [Public Library of Science](#).

The research team has studied the pathogen for nearly five years. In 2007, with resources from the Virginia Bioinformatics Institute and the Fralin Life Science Institute, Vinatzer sequenced the genome of *Pseudomonas syringae* pv. tomato using a Roche GS-FLX™ sequencer at the Virginia Bioinformatics Institute.

In 2008, Vinatzer received a \$1 million, five-year Faculty Early Career Development (CAREER) Award from the National Science Foundation to continue investigation of the pathogen. Shortly thereafter, he brought Setubal, a former Virginia Tech faculty member who recently went to work for the University of Sao Paulo in Brazil, and Leman, onto the project to handle the bioinformatics and statistical aspects of the research, respectively.

First, the scientists needed to map changes in the [bacterial pathogen](#) over large spans of time. They compared DNA sequences of bacteria isolated in multiple years, dating back to 1960 and stored since then in international culture collections. Setubal, along with Nalvo Almeida, an associate professor at the Federal University of Mato Grosso do Sul, provided automated genome annotation and helped Vinatzer with identification and analysis of mutations that distinguished the sequenced genomes.

"One of the questions we asked was, did the bacteria isolated in 2000 directly evolve from the bacteria isolated in 1975, or did they evolve independently from an ancestor that lived further back in time, maybe 100 to 200 years ago?" said Vinatzer.

To answer this question, Leman, Vinatzer, and Rongman Cai of Lixian, China, a Ph.D. student in plant pathology, physiology, and [weed science](#) at Virginia Tech, used statistical methods to correlate the differences in the DNA sequences between the isolated bacteria with the years in which they were isolated to determine if the bacteria progressively became more different from the first bacteria isolated in 1960.

The research team found that the pathogen likely evolved on a relatively recent time scale and continues to adapt to the tomato by minimizing its recognition by the tomato immune system. This suggests that new pathogen variants with increased virulence are spreading around the globe unobserved, presenting a potential threat to biosecurity. Ultimately, it calls for more precise methods of pathogen identification to replace outdated taxonomic descriptions that were established at a time when it was impossible to classify bacteria precisely because the necessary molecular techniques had not been developed yet.

This particular pathogen is important to study because "it has been used as a model pathogen by many labs around the world and is economically significant because it reduced tomato quality and yield," said Vinatzer. He is extending the research project to investigate where the pathogen originally evolved, how it is spreading around the globe, and what can be done to interfere with its spread, including how the tomato might be engineered to be more resistant to the pathogen.

More information: Cai R, Lewis J, Yan S, Liu H, Clarke CR, et al. (2011) The Plant Pathogen *Pseudomonas syringae* pv. *tomato* Is Genetically Monomorphic and under Strong Selection to Evade Tomato

Immunity. PLoS Pathog 7(8): e1002130.
[doi:10.1371/journal.ppat.1002130](https://doi.org/10.1371/journal.ppat.1002130)

Provided by Virginia Tech

Citation: Research team unravels tomato pathogen's tricks of the trade (2011, November 3)
retrieved 25 April 2024 from
<https://phys.org/news/2011-11-team-unravels-tomato-pathogen.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.