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Tomato pathogen genome may offer clues about bacterial evolution at dawn of agriculture

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The availability of new genome sequencing technology has prompted a Virginia Tech plant scientist to test an intriguing hypothesis about how agriculture's early beginnings may have impacted the evolution of plant pathogens.

Boris Vinatzer, assistant professor of plant pathology, physiology, and weed science in the College of Agriculture and Life Sciences, has received a $1 million, five-year Faculty Early Career Development (CAREER) award from the National Science Foundation (NSF) to investigate the pathogen that causes bacterial speck disease of tomatoes and to develop a new undergraduate course in microbial genomics.

"Little is known about how plant pathogens, which were adapted to natural mixed-plant communities in pre-agriculture times, evolved into today's highly aggressive pathogens of crops cultivated in monoculture," Vinatzer said. "To fill this void, this project aims at identifying the molecular evolutionary mechanisms that allow pathogens to specialize to specific plant species and to become more aggressive."

In 2007, Vinatzer sequenced the genome of a Pseudomonas syringae pv. tomato strain using technology from the Virginia Bioinformatics Institute (VBI) at Virginia Tech and funding from the university's Institute for Biomedical and Public Health Sciences. The tomato pathogen was the first genome to be sequenced on the new Roche GS-

FLX™ machine, which VBI had just purchased with Virginia's Commonwealth Research Initiative funding.

"That sequence, in addition to other preliminary data, allowed me to develop a hypothesis on the evolution of plant pathogenic bacteria since the beginning of agriculture," Vinatzer said. "The hypothesis is that plant pathogenic bacteria evolved from relatively weak pathogens that caused disease in many plants to specialized highly virulent pathogens of single crops after entire fields of the same plant species became available to them in agricultural fields. Importantly, understanding the mechanisms pathogens used to adapt to crops in the past will help us predict how they might change again in the future and allow us to breed or engineer crops for long-lasting disease resistance."

Vinatzer's approach combines comparative evolutionary genomics, population genetics, and microbial genetics and leverages the latest advances in the biological sciences and the computer sciences. He is collaborating with João Setubal, associate professor and deputy director at VBI.

Source: Virginia Tech

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