



How to Fight a \$5 Billion Enemy: Sequencing the Genome of *Phytophthora infestans* and *Phytophthora capsici*

Phytophthora infestans, the pathogen that causes late blight of potato and tomato and was responsible for the Irish potato famine, has re-emerged as a pervasive enemy of potato and tomato production. Worldwide losses exceed \$5 billion a year—making late blight the single greatest pathogenic threat to global food security, as potatoes are the staple food in many countries and the most important non-cereal crop in the world.

Late blight is an expensive disease, as growers must spray fungicides in order to have a viable harvest. However, in many parts of the world, farmers don't have the means to apply chemicals; there, this disease could cause food shortages and hunger. Recent widespread occurrence of new fungicide-resistant strains of this pathogen is another reason to take *P. infestans* seriously, even in countries where farmers can afford to treat their crops with fungicides.

A related pathogen, *Phytophthora capsici*, has become a disease of national economic importance, spreading widely since 1922 when it was first reported in the United States on New Mexico chili peppers. It affects crops such as peppers, cucumbers, squash, pumpkins, and tomatoes. However, research on this pathogen has been negligible.

Sophien Kamoun, a plant pathologist with The Ohio State University's Ohio Agricultural Research and Development Center (OARDC), is the only investigator in the country who is part of two research teams recently awarded \$6.7 million to sequence the genome of *P. infestans* and *P. capsici*—a key step in understanding how these pathogens work and developing new tools to reduce their devastating impact on some of the world's most popular vegetable crops.

OBJECTIVES

The goal of Kamoun and his colleagues is to complete the genetic profile of these two important *Phytophthora* pathogens and interpret the resulting data. These organisms may have as many as 20,000 genes each, and researchers must find the subset of those genes that is important for triggering disease symptoms. Once those genes are identified, they would be able to manipulate them or target them with chemicals. This data would also allow scientists to identify the corresponding resistance gene in the plant.

CHALLENGES

Phytophthora pathogens have presented numerous challenges to farmers and researchers alike. Once thought to be fungi because of their physical resemblance, *Phytophthora* pathogens are actually classified as oomycetes—organisms that are more closely related to brown algae at the molecular level. Because of this fundamental distinction, they function and infect plants differently, posing chemical control challenges and generating new questions as to how exactly they interact with plant hosts.

ACHIEVEMENTS

Kamoun and his colleagues had originally received a four-year \$1.9-million grant from the National Science Foundation (NSF) to crack the genetic code of *P. infestans*. The success of their research led to the recent decision by NSF and the U.S. Department of Agriculture's Cooperative State Research, Education, and Extension Service (USDA-CSREES) to award the project an additional \$3.7 million.

Kamoun's expertise has also been sought for the *P. capsici* project, which was funded in late 2005 at approximately \$3 million by NSF, USDA-CSREES, and the DOE's Community Sequencing Program. What's unique about this project is that the genome of *P. capsici* will be mapped employing a novel DNA-sequencing method developed by Branford, Conn.-based 454 Life Sciences. This will be the first instance in which a eukaryotic (non-viral or non-bacterial) microorganism is sequenced from scratch using 454's technology since it was introduced in 2003—marking the first time a new way to sequence whole genomes became available in more than 20 years.

THE FUTURE

As the link between both research teams, Kamoun sees great promise in having the unprecedented chance to compare the genomes of two major *Phytophthora* pathogens. His efforts will break new scientific ground by making it possible to compare the two species, see what their differences are at the molecular level, and learn what makes one pathogen infect one crop and not the other. This will open up many possibilities for research and ultimately new management options for growers.



This research is supported in part by state of Ohio funds allocated to the Ohio Agricultural Research and Development Center of The Ohio State University.