Two genes better than one for important plant pest

February 1 2011

Researchers funded by the Biotechnology and Biological Sciences Research Council (BBSRC) have revealed a novel molecular mechanism that triggers plant infection by *Pseudomonas syringae*, the bacteria responsible for bacterial speck in tomatoes. The scientists from the Department of Life Sciences at Imperial College London have revealed how two genes in the bacteria work together to launch the infection process that ultimately kills the plant's cells and causes disease, significantly reducing crop quality and yield.

Pseudomonas syringae is responsible for major disease outbreaks in an enormous range of economically important food plants including rice, tomatoes, corn, cucumbers and beans. It is also a problem in wild plants and one *Pseudomonas syringae* type has recently infected half of all chestnut trees in the UK. The researchers hope that by understanding the molecular basis for how the bacteria attack plant cells they will be able to find new targets for pesticides and devise better strategies for disease management.

Speaking about the findings, published today (1 February 2011) in *Nature Communications* Dr Jorg Schumacher, the senior author on the study, explains: "These bacteria have quite a sophisticated system for infecting plants. They use remarkable needle-like structures called pili to penetrate and inject a range of proteins into a plant's cells, which then work to suppress its immune response and kill infected cells. *Pseudomonas syringae* are very versatile bacteria and their pili help them to infect a very large range of plants causing numerous symptoms in

different plants, for example black/brown specks on tomato fruits."

"From what we know, these bacteria only produce their pili and launch infection when they have already invaded the plant tissue. It is unclear how they sense the plant tissue environment that triggers infection, but we do know that the regulatory mechanism that controls pili formation is essential in this process."

What distinguishes *Pseudomonas syringae* from other related pathogens that also use pili to infect plants is that it has duplicated a gene during evolution that is involved in producing the pili. Indeed the researchers have found the duplicated gene in all the strains of *Pseudomonas syringae* they have studied, which makes them think that it is very likely to provide some selective advantage in the infection process. It appears, for example, that this innovation may allow for more subtlety when it comes to whether or not to commit to infection.

Dr Schumacher continues: "The motivation for this study was to find out how having a duplicated gene could provide *Pseudomonas syringae* with the 'edge' in terms of evolutionary advantage. We have studied related systems in other bacteria in great detail in the lab of Professor Martin Buck, where this study was carried out. What we have found here is that the two-gene system in *Pseudomonas syringae* is an evolutionary innovation that had not been described in bacteria.

"With our work and that of others we are able to understand how evolution that happens at the molecular level translates to phenomena we observe in our daily lives. When we see brown leaved chestnut trees next spring, chances are that *Pseudomonas syringae* and the duplicated gene are involved."

Professor Douglas Kell, BBSRC Chief Executive said: "With improvements in imaging and modelling we are now able to look deeper

into cells at how the molecular machines that underlie all life on earth work. But this is not just knowledge for its own sake; a more detailed understanding of how crop pests interact with their hosts will be important for developing more sophisticated methods of controlling them. This is vital to global food security, ensuring that we can provide safe nutritious food to a growing world population."

Provided by Biotechnology and Biological Sciences Research Council