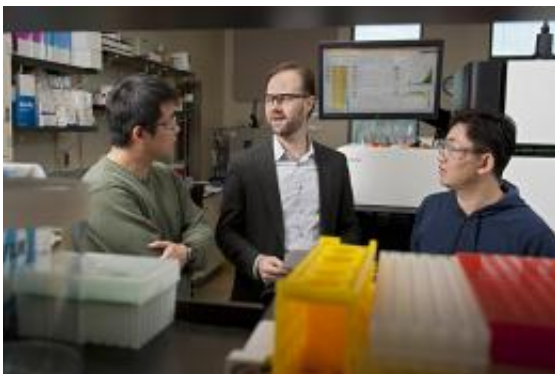


Researchers identify novel regulatory network within legumes

January 30 2012, By Blake Meyers and Laura Crozier



Jixian Zhai (left) with Blake Meyers (center), chair of the Department of Plant and Soil Sciences, and Dong-Hoon Jeong. Credit: Evan Krape and Kathy F. Atkinson

(PhysOrg.com) -- Three collaborating laboratories in the Department of Plant and Soil Sciences at the University of Delaware -- those of professors Blake Meyers, Janine Sherrier and Pamela J. Green -- recently identified a novel regulatory network within legumes, including in alfalfa and soybean plants.

The work was performed predominantly by Jixian Zhai, a doctoral student in the department and was published in the December issue of the prestigious journal *Genes & Development*, one of the top journals in molecular biology and genetics. The genomics project was funded by a grant from the U.S. Department of Agriculture.

Conducting their research at the Delaware Biotechnology Institute (DBI), the investigators set out to get a comprehensive view of how small RNAs function in [legumes](#) and how they might be important to these plant species. They focused their work on the chromosomal sequences (genome) of Medicago, a legume genus that includes both the crop plant alfalfa and the species that was recently sequenced, *Medicago truncatula*.

The researchers sequenced libraries containing millions of small RNAs, important gene regulatory molecules, as well as the genes targeted by these small RNAs. Using advanced computational techniques to categorize the RNA sequences, they identified a novel function for a handful of "microRNAs" -- special small RNAs that direct the targeted destruction of specific protein-coding messenger RNAs.

Among these plant microRNAs, the team determined that many target genes encode NBS-LRRs, or "guard proteins" that function in defense against pathogenic microbe infiltration. These NBS-LRRs function as an immune system to battle pathogens but presumably must be suppressed to allow the interactions with [beneficial microbes](#) for which legumes are particularly well known. The result of this microRNA targeting is a complex network of co-regulated small RNAs that Zhai characterized using a set of computational and statistical algorithms and analyses.

"The NBS-LRRs keep pathogens out, but these plant cells are still allowing beneficial microbes to enter," says Sherrier. "The regulation of genes encoding NBS-LRR proteins has been largely unknown until now."

Over time, these mechanisms have evolved into a more elaborate system in legumes to take advantage of this defense-suppressing system and facilitate the development of nodules, the specialized root structures of legumes in which the beneficial plant-microbe interactions take place.

"We may have found the 'switch' that recognizes good versus bad microbes," adds Meyers, Edward F. and Elizabeth Goodman Rosenberg Professor and chair of the Department of Plant and Soil Sciences.

"These guard proteins usually trigger [cell death](#) when a pathogen is recognized, but the plant cell is triggering cell death when it encounters a 'good' microbe. The circuit we identified may play a role in preventing cell death when the microbe is a friend."

This discovery could ultimately prove important to the improvement of plant-microbe interactions in other crop plants by allowing plants to become healthier by letting in the good microbes, but keeping the pathogens out.

"We didn't expect to find something as exciting as this," says Sherrier. "It's exciting because no one knows about this kind of gene control and also because it is showing us the diverse interaction between plants and bacterium as well as plants and fungi that could help us develop better mechanisms in other plants, like Arabidopsis."

"Beyond the applied significance, the finding that NBS-LRR [genes](#) are key targets opens up a new frontier for basic research," says Green, Crawford H. Greenewalt Professor of Plant and Soil Sciences.

If this diverse regulation of beneficial microbes could be added to other crop plants, it could mean scientists could program the [plants](#) to grow stronger and taller with less water, and even fertilize themselves.

Provided by University of Delaware

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