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Mathematics Helps Provide New Biological Insights

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Results obtained by solving millions of copies of model equations

COLUMBUS, Ohio, April 28 -- Researchers at The Ohio State University (OSU) are applying the power of supercomputers to a small plant in the mustard family to better understand how complex genetic processes can lead to different types of cells.

Dan Siegal-Gaskins, a postdoctoral fellow affiliated with the Mathematical Biosciences Institute and the Grotewold Lab in OSU's department of Plant Cellular and Molecular Biology, is leveraging resources at the Ohio Supercomputer Center (OSC) as part of a larger study of cell differentiation in the model plant *Arabidopsis thaliana*.

Known commonly as thale cress or mouse-ear cress, *Arabidopsis* has one of the smallest genomes in the plant kingdom and plays a role in developmental biology similar to that of mice and fruit flies. The small size and short growing period of *Arabidopsis* makes it particularly well-suited for genetic studies.

At a specific phase of *Arabidopsis* leaf development, cells on the surface of the leaf receive genetic instructions to become either one of the majority 'pavement' cells or a large hair-like cell known as a trichome. The specific function of trichomes is unclear, although they may be involved in preventing infection, protecting delicate tissues on the underside of the leaf, or reducing the amount of water lost to evaporation.

To better understand how cells develop into trichomes, Siegal-Gaskins, colleague Kengo Morohashi and Principal Investigator Erich Grotewold are focusing on relationships between three proteins that figure prominently in determining a cell's fate. Most importantly, the researchers are supplementing traditional benchwork with mathematics to better understand the proteins' functional relationships.

The mathematical model Siegal-Gaskins constructed consists of seven differential equations and twelve unknown factors. For his preliminary studies, he turned to OSC to choose

random values for the unknowns and solve the equations for millions of different random value sets.

"Due to the large range of possible parameters and the complexity of the problem, we took advantage of OSC's parallel processing capabilities and the MATLAB computing environment," Siegal-Gaskins said. "This process was repeated for five million randomly-chosen parameter sets, and the set that gave us the closest agreement with experimentation was kept."

To meet the challenge of processing the millions of iterations, Siegal-Gaskins accessed OSC's IBM Cluster 1350. The center's flagship supercomputer system, nicknamed the Glenn Cluster, features 9,500 cores, 24 terabytes of memory and a peak computational capability of 75 teraflops -- which translates to 75 trillion calculations per second.

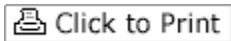
"Dr. Siegal-Gaskins is leveraging high performance computing (HPC) to better understand biological systems at the cellular and molecular level," said Yuan Zhang, client and technology support engineer at OSC. "His project is especially well-suited for the Glenn Cluster, which is largely dedicated to research in the biosciences, and MATLAB features many tools for numerical computations."

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