NewsBytes

Modeling Sex's (Evolutionary) Appeal

Sex is a costly undertaking. Finding partners takes time and energy. Sexual contact can transmit disease. And if reproductive success is measured by how many genes you pass on, females would be better off reproducing asexually. But sex must be beneficial in some way—besides being fun—since so many plants and animals do it without going extinct. A new computational model described in the March 2, 2006, issue of *Nature* confirms one existing theory about why sex is advantageous on the genetic level.

"This is very difficult to measure in real organisms," says **Ricardo Azevedo, PhD**, assistant professor of biology and biochemistry at the University of Houston. "But things that take years or decades in the lab take only hours in the computer."

Evolutionary biologists have posited several reasons for the success of sexual reproduction. The mutational deterministic hypothesis suggests that sex helps remove harmful mutations from a population because offspring receive genes from two parents. But the benefits of mutation purging can only overcome the costs of sex if the rate of harmful mutations is high. Multiple mutations must also be more harmful than would be expected from their individual effects, a condition known as negative epistasis. Azevedo's model suggests that the mutational deterministic hypothesis may be true.

Azevedo along with **Christina Burch, PhD**, assistant professor of biology at the University of North Carolina, Chapel Hill, and three graduate students created a model that treats each "organism" as a network of interacting genes. The network is expressed as a matrix of numbers (positive, negative or zero) representing the effect of each gene on the activity of every other gene in the organism. Large populations of sexually and asexually reproducing cyber-organisms (networks) were created with different rates of spontaneous mutation. In the first part of the simulation, each organism's genes interact. Organisms that produce stable patterns of gene expression produce offspring in the second part of the simulation; unstable networks don't—natural selection at work. When the populations reached equilibrium in their sensitivity to mutations, the sexual populations had become more insensitive to mutations than asexual popula-

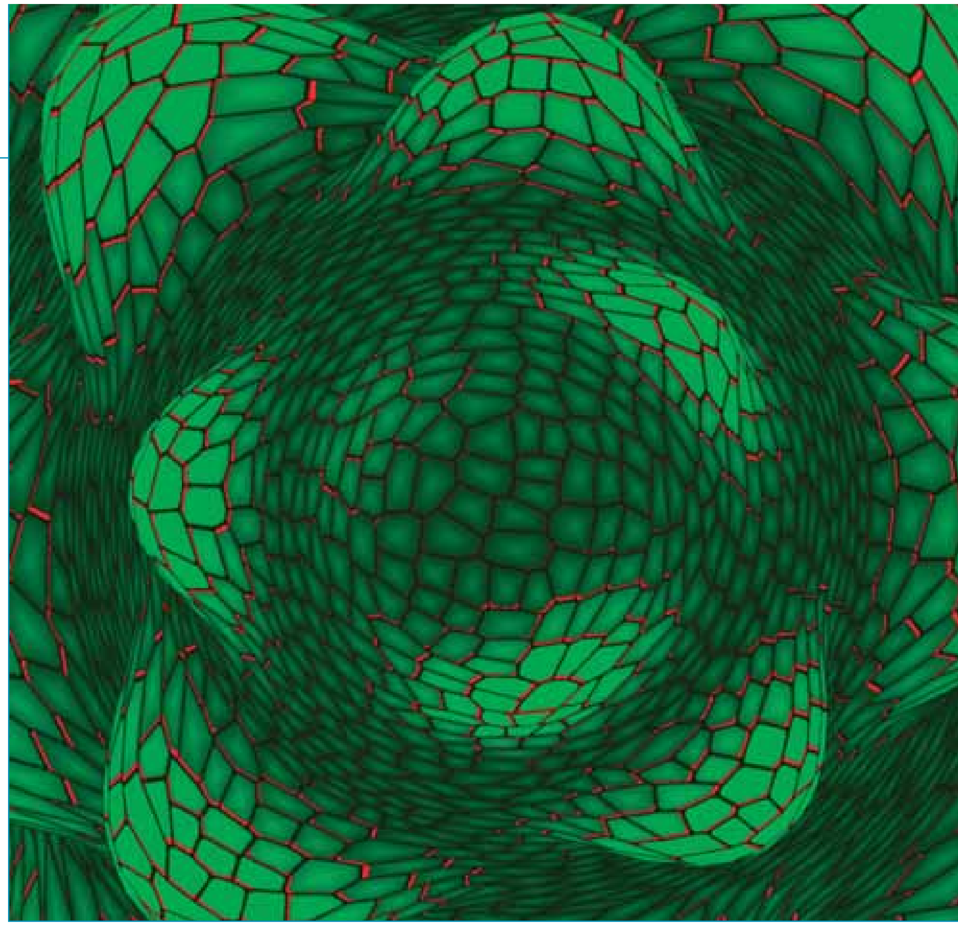
tions and had also evolved negative epistasis. Compared to asexual creatures, they more effectively purge negative mutations from the gene pool.

"If the conditions in the model are real, then when sex evolves it creates conditions that help sustain itself over time," Azevedo says.

"The prevalence of sex begs to be studied," comments **Andreas Wagner, PhD**, an associate professor of biology at the University of New Mexico. "To the extent that an abstract model can tell you anything about the evolution of sex, [Azevedo and Burch] have made an important contribution." But, he says, he'd like to see the work confirmed in living systems.

Azevedo agrees this paper is a first step. He is trying to make the model more applicable to multicellular organisms while his collaborator, Burch, conducts experiments with viruses in order to confirm the model's results.

—Linley Erin Hall



A computer simulation of the growing tip of a seedling of **Arabidopsis thaliana**, *viewed from above. PIN1 proteins (red) facilitate transport of the plant hormone auxin (green), which in high concentrations promotes budding of leaves, seen here bulging out from the stalk. The feedback interaction of the protein and hormone produce the characteristic spiral pattern of leaves that form as the plant grows. Movies simulating the development of four different leaf arrangements can be seen in the paper's supplemental material online at http://www.pnas.org/cgi/content/full/0510457103/DC1#M1.*

Modeling Whorls of Leaves

The petals of every flower and the leaves sprouting from every plant stalk have characteristic arrangements, a phenomenon called phyllotaxis. For two centuries, botanists have puzzled over the force driving such regularity.

"If you want to understand how plants acquire their form, this is one of the very key questions," says **Przemyslaw Prusinkiewicz, PhD**, professor in computer science at the University of Calgary in Alberta, Canada. He and his colleagues recently presented a new cellular-level computer model of the process. The work appeared in the January 31, 2006, issue of the *Proceedings of the National Academy of Sciences*.

Previous experimental work by Prusinkiewicz's Swiss collaborators had shown that a plant hormone, auxin, plays a crucial role in phyllotaxis, as does a protein called PIN1, which regulates the transport of auxin. The team hypothesized that there was a feedback mechanism in which the distribution of auxin determined the location of the PIN1 proteins, the position of which, in turn, governed the flow of auxin.

They devised a computer model to test the theory quantitatively by simulating the properties of individual cells during the growth of a small flowering plant of the mustard family, *Arabidopsis*.

The model assumes that the tip of the stem develops at the same time that the pattern of leaves is forming, all of which relates to the pattern of cell division. The results of the simulation confirmed that the proposed interplay of auxin and PIN1 on the molecular level could produce the characteristic spiral leaf pattern found in *Arabidopsis*, but also yielded some surprises.

Though the researchers initially assumed auxin was produced in the basal tissues of the stem and flowed up to the growing tip, they were only able to get the leaf patterns observed in nature when they altered the model to have auxin produced locally at the tip.

They also found that by varying the parameters of the model, they could produce the leaf patterns found in other plants, which, Prusenkiewicz says, "reinforces our belief that what we have shown is actually true, and it is not just true in *Arabidopsis*, but also in other plants."

By varying the parameters of the model, the researchers produced the leaf patterns found in various plants.

Prusenkiewicz characterizes their model as part of a broader inquiry into how genes and molecular level processes determine the macroscopic forms of organisms, which he calls "one of the most fascinating questions in developmental biology right now."

—Louis Bergeron, MS