



RESEARCH PROFILE

David Jackson

Studies in plant genetics are teaching us about how organisms develop

It's a late summer afternoon and many members of the faculty at Cold Spring Harbor Laboratory are busy at their computers or huddled over experiments in fluorescent-lit laboratories. David Jackson and several of his postdocs are no less engrossed in their work, yet we find them outdoors on this beautiful day, in the middle of a sun-drenched field just up the road, beyond the mudflats of the lower harbor. They are carefully examining specimens of *Zea mays* — maize, a.k.a. corn — planted in long, ruler-straight rows.

Jackson, a member of the CSHL faculty for a dozen years and a professor since 2006, studies genes that influence the shapes that plants take. Finding odd-looking ears and tassels in maize — respectively, the plant's female and male floral structures, or inflorescences — has proven a productive jumping-off point. Each year, in fact, Jackson and a few members of his

team make pilgrimages to vast corn-growing regions of the American Midwest and Mexico, looking for maize mutants that are the products of natural variation.

Learning from mutations is a time-honored procedure in plant research, and one with immense implications for genetics. "Going all the way back to Mendel, plant breeding has led the way in our efforts to understand the secrets of development and the underlying principles of inheritance," Jackson observes. Perhaps the most famous of CSHL's plant breeders was Barbara McClintock, who grew corn next to Carnegie Library in the 1930s and '40s en route to her Nobel-winning discovery of bits of DNA that propagated themselves, seemingly at random, across the chromosomes — what she called "jumping genes" and others later called transposons.

Technology has dramatically changed what happens after interesting specimens are gathered from the field. "Until recently, we've been very focused on finding interesting genes, one by one," says Jackson. For example, a gene in corn called *TILLERED1*. In 2007, Jackson discovered that it encodes a protein that regulates other genes, which turn out to be responsible for how and when branching takes place. *TILLERED1* was notable because Jackson's team found that it responds to light, suggesting one way in which plants adjust to environmental conditions.

Like many of the discoveries his lab is making, the *TILLERED1* insights have potentially interesting applications in agriculture. Those possibilities can be expected to multiply as new tools, especially new imaging technologies and very fast gene sequencers, "are now enabling us to see how groups of genes work together," according to Jackson.

Gene interactions play a fundamental developmental role in all organisms. Jackson's work on plant architecture therefore is only an aspect of a diverse body of work that has also provided insights about how developmental signals are propagated in plants, particularly in the inflorescences that give rise to the seeds valued by agriculturalists and upon which billions of the planet's hungry people depend.

'Taking things to pieces'

Dave Jackson loved nature as a child, and could often be found hiking the English countryside on the outskirts

of Lancaster, in the northwest, where he grew up. He took inspiration from his father, an engineer with a big workshop at home. "In the basement there were tools everywhere and we used to fix things — or, in my case, take them to pieces and not be able to fix them again," Jackson remembers. "I always wanted to know how things worked."

He was an undergraduate at the University of Leeds in the mid-1980s, interested in biotechnology, although not specifically in plants until hearing a talk at the Royal Society, at which the doctoral thesis of a student named Robert Martienssen was discussed. Ten years later, Martienssen would be instrumental in bringing Dave Jackson to CSHL, following Jackson's Ph.D. at John Innes Institute, the center of plant genetics research in England, and a fruitful period of postdoctoral research at U.C. Berkeley.

At Berkeley, Jackson became involved in work on a maize gene called *KNOTTED1*. His mentor, Sarah Hake, had succeeded in showing the gene was involved in development of the maize plant, but also

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Channels of communication

Since 2005, Jackson and colleagues have made some interesting discoveries about those tiny conduits, the plasmodesmata. They've revealed that the KN1 protein, encoded by *KNOTTED1*, has not two but at least three potential destinations in plant stem cells located in meristems. A portion of the KN1 protein's structure called a homeo-domain enables it to bind specific DNA sequences, accounting for its function as a regulator of developmental genes. KN1 can also bind to its own RNA and enter plasmodesmata, acting as a signal. And when it interacts with a protein called MBP2C, it becomes anchored in the cytoplasm, preventing it from acting as a signal (presumably in response to a developmental cue).

This spring, Jackson led a team that discovered a gene called *GAT1* that instructs cells to produce a protein found mainly in meristems. The protein, an antioxidant, relieves cellular stress; its impact in meristem cells is to improve the flow of traffic through the tiny plasmodesmata. It's a mechanism, says Jackson, by which the channels change their structure in response to environmental cues as development unfolds.

that it acted, in a manner not yet understood, as a signal. In its developmental role, *KNOTTED1* was a transcription factor that encoded a protein, KN1, which moved into the cell nucleus to regulate other genes. What made it interesting, says Jackson, was its separate role in signaling between cells. He wanted to study that role.

This work continued after Jackson was brought to Cold Spring Harbor Laboratory by Martienssen and Winship Herr, the founding dean of CSHL's Watson School of



Biological Sciences, in 1997. In tracing the path of the KN1 signal, Jackson's attention was drawn to tiny channels called plasmodesmata which connect plant cells. These minuscule conduits — numbering in the hundreds or thousands in each cell — carry nutrients between cells and serve as pathways for viruses.

Inside the meristem

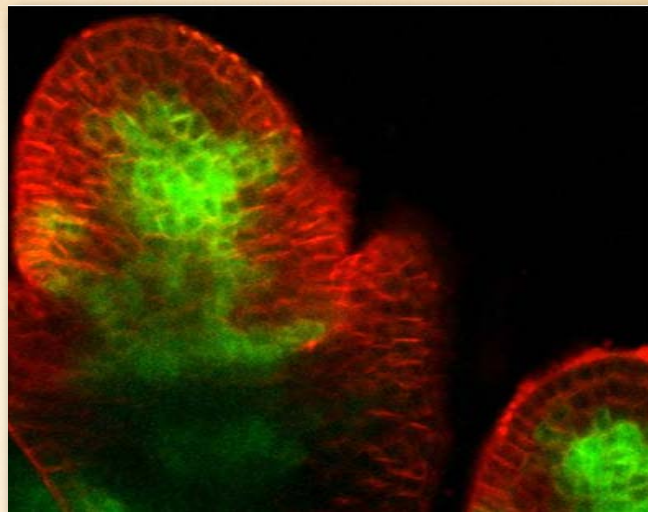
His work in the intervening years has brought to light new knowledge about the plasmodesmata, particularly about their previously unrecognized importance in signaling. Using maize and another plant, a cress called *Arabidopsis*, as models, Jackson and colleagues have focused on communities of stem cells in plants called meristems, situated at the growing tips of shoots and roots. In maize, the shoot meristem, which gives rise to leaves and flowers (tassels and ears), is a niche containing hundreds of stem cells. It's where *KNOTTED1* expresses the protein KN1. It's also where a gene called *RAMOSA3* is expressed, a gene first identified, by Jackson, several years ago.

RAMOSA3 is remarkable because it encodes an enzyme that has proved to have a very important role in maize development — it controls branching in inflorescences. What makes this extraordinary is the fact that the encoded enzyme was known previously for a very ordinary function: the removal of phosphate groups from sugar molecules. "The fact that this gene could be controlling something so important as plant morphology was really incredible," says Jack-



Creating new imaging tools

Jackson and colleagues have made important contributions to the broader research community by developing genetic tools that provide the means with which to observe processes not previously seen in living plants. Under an NSF grant, Jackson is creating 100 maize plant lines that express fluorescent proteins across the full spectrum of cellular "compartments." These have yielded images that are not only beautiful to behold but also productive of new knowledge about how plant cells work. The recent *Science* poster on the maize genome (see p. 13) includes a Jackson image (below) revealing proteins called expansins (green) being expressed in the wall of maize meristem cells (red) just as those cells prepare to grow out into new organs.



son. "But now we're doing the interesting part: trying to figure out how this thing is working — how this ordinary enzyme gained such a vital function. Finding something unexpected like this is what keeps us going in science." **Peter Tarr**



Maize milestone

A major multi-institutional effort in which three CSHL scientists played important roles culminated in late November with publication in *Science* of a reference genome for maize. (Part of an accompanying informational poster is reproduced below.) Doreen Ware, Rob Martienssen and Richard McCombie were co-principal investigators on the project, which Ware calls "a landmark." Ware's lab focused on annotation of the genome, the rough equivalent

of an extensive reference manual that will help guide future research. Ware also co-lead a parallel effort simultaneously reported in *Science* to generate the first haplotype map of maize. The HapMap gauges diversity in the maize genome by comparing 27 distinct maize lines with the reference version; it sheds new light on subjects ranging from the evolution of maize and other plants to the adaptation of maize to environmental changes, including global warming.

The Maize Genome

The Domestication of Maize

Corn, also known as maize (from the Spanish *maíz*), was first domesticated nearly 5,000 years ago from teosinte, a wild grass that looked quite different from our modern crop. Teosinte grew in Mexico and Central America as a bushy plant with many spikes, the precursor to our familiar ear of corn. The small teosinte spikes had only two rows of nearly inedible kernels, or seeds, each enclosed by a hard covering. These seeds were not well adapted to being eaten by humans, but they were well adapted to being eaten by birds. The first step in domestication was to select for larger, more edible kernels that remained on the cob for easy harvest. Now these domestic changes counted has been a puzzle for over a century. Scientists are now convinced that humans living in the Toluca River region first began forging teosinte seeds when they noticed new domesticated plants that produced more grain.

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Maize Genetics in the 20th Century

Maize emerged as a model research plant in the early 20th century partly because its domesticated state was ideal for genetic experiments. Controlled genetic crosses were possible because the male (pollen) and female (ovule) parts of the plant were separate. This allowed researchers to study the inheritance of specific traits. The discovery of transposons—pieces of mobile DNA—revolutionized the field of genetics and demonstrated the dynamic nature of the maize genome. By the second half of the 20th century, maize geneticists had studied hundreds of maize genetic gene locations, cloned the first plant genes, and identified transposon-induced genomic rearrangements among closely related maize varieties. Meanwhile, a physical map of the maize genome was assembled, and researchers began to understand the genetic basis of many maize traits. These traits, in turn, were used to study gene expression profiles and other resources, providing the necessary foundation to sequence the maize genome.

The Dynamic Maize Genome

Maize has a strikingly dynamic genome. Two maize varieties show as much DNA sequence variation as that observed between two different species. This gene diversity is a result of maize's history of rapid genome evolution. The maize genome has evolved rapidly, with many genes being duplicated and then diverging. This has led to a high level of genetic diversity within the species. The maize genome is also highly dynamic, with many genes being duplicated and then diverging. This has led to a high level of genetic diversity within the species. The maize genome is also highly dynamic, with many genes being duplicated and then diverging. This has led to a high level of genetic diversity within the species.

Maize Genomics Resources and Genomic Resources

Functional Genomics Resources

Maize Data Center and Resources

Educational Resources on Maize

From Gene Discovery to Application

Early explorers of the Americas took maize back to Europe during the 16th century. Since then, maize has spread globally and is now a major world crop. Maize has increased steadily over the past century as maize became an important source of food, feed, fiber and more recently biofuels. During this period, scientists, breeders, and seed companies worked together to transform basic research in maize genetics into practical applications. One area of particular impact was the domestication of hybrid vigor or heterosis, which results when two parental varieties, both showing recessive features desired for farming, are crossed to produce more robust hybrid offspring. Vigorous hybrids increase crop productivity dramatically and produce more than the sum of their parents. Domesticated maize are still unraveling the underlying molecular basis of heterosis and the sequencing of maize genomes will provide new insights into the process. Scientists have now also used the identification of genes controlling genetic traits that can be incorporated into breeding programs.

The Future

Maize has adapted through domestication to nearly every climate across the globe, and many societies have developed to feed expanding populations of people and livestock. Although breeders and agronomists have increased crop yields over the past century, the world's growing population requires even greater food production. Solutions will be made possible by global cooperation in which scientific and technological progress translates basic discoveries into practical applications. To this end, the genome sequences of maize and other crops are rapidly emerging and will aid in breeding efforts. Soon it will be possible to reconstruct and fully understand the genetic basis for maize growth and development; new tools and methods will be available to researchers to understand the genetic basis of maize growth and development; new tools and methods will be available to researchers to understand the genetic basis of maize growth and development.

Poster content and text: Anne W. Sylvester, Patrick S. Schnable, and Rob Martienssen



Courtesy AAAS