

# How to build a plant

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Dr. Sarah Hake and her colleagues, George Chuck, Hector Candela-Anton, Nathalie Bolduc, Jihyun Moon, Devin O'Connor, China Lunde, and Beth Thompson, have taken advantage of the information from sequenced grass genomes to study how the reproductive structures of maize are formed. Dr. Hake, of the Plant Gene Expression Center, USDA-ARS, who is the 2007 recipient of the Stephen Hales Prize, will be presenting this work at the opening Awards Symposium of the annual meeting of the American Society of Plant Biologists in Mérida, Mexico (June 27, 3:10 PM).

Maize was first domesticated in the highlands of Mexico over 6,000 years ago and is now one of the most important crop plants in the world. It is a member of the grass family, which also hosts the world's other major crops including rice, wheat, barley, sorghum, and sugar cane. Maize has a rich genetic history, which has resulted in thousands of varieties or landraces. Scientists at CIMMYT, Centro Internacional de Mejoramiento de Maíz y Trigo, the International Maize and Wheat Improvement Center, work to preserve the ancient varieties that represent adaptations to different environmental conditions such as different soils, temperature, altitude, and drought. These traits are expressions of different genes and groups of genes that scientists hope to utilize to keep up with changing climatic conditions and global food supply.

Dr. Hake and her colleagues have utilized this rich genetic history of maize to characterize how maize plant architecture is initiated and regulated. They have focused on plant stem cells, the groups of self-renewing cells, called meristems, which are located at the tips of plant shoots and roots. In particular, these scientists have studied the plant's flower structures, which become the corn grain or cob. They have used the numerous mutants generated in the complex maize genome to specify the gene networks and biochemical pathways that determine how the maize inflorescence is built. They have also made use of the genetic information from the already sequenced rice and

Arabidopsis genomes as well as that emerging from the maize genome sequencing project. Up until recently, the thale cress, Arabidopsis, has been the most widely used model organism in plant biology because of its small size and fast generation time. However, says Dr. Hake, "Plant biology has benefited tremendously from Arabidopsis, but when we start to think about morphology, additional model organisms will be useful. Maize is a good model for the grasses because of the ease of genetics in maize, the recently sequenced genome, and the diversity between inbreds."

Meristems are classified as determinate or indeterminate. Indeterminate meristems are groups of cells that are self-renewing and continue to produce structures like stems, branches, leaves, and flowers throughout the life of the plant. Determinate meristems are groups of cells that are gradually consumed after producing a certain number of structures and organs. The maize inflorescence is a good model for studying plant development because it contains both kinds of meristems. Maize is also a good model system because its genetic complexity makes it highly amenable to mutation and it is transformable, allowing the generation of many different mutant lines and genetic backgrounds.

Hake and her co-workers have used maize mutants to dissect flower, grain, and leaf development in this and other grasses. For example, they cloned and characterized the barren inflorescence2 (*bif2*) and ramosa2 (*ra2*) mutants and determined their functions in the formation of axillary meristems, those that produce branches and flowers. Phylogenetic analyses showed that both *bif2* and *ra2* are highly conserved among different grass species.

Maize has two separate inflorescences—the male tassel or pollen-producing flowers, and the female flowers that produce the kernel-bearing ears. Both sets of flowers begin as bisexual but with development, the female structures in the tassel and the male structures in the ear are arrested. By

analyzing the mutant tasselseed4 (t4), Hake and her colleagues found that the t4 microRNA is important in determining the sex and cell fate of the groups of cells forming tassels and ears. Analyses of the mutant Corngrass1 (Cg1) demonstrated that this gene functions in production of mature leaves, while the mutant exhibits the architecture and structures of the juvenile plant.

Through their work with maize mutants, Hake and her colleagues have begun to assemble a representation of the networks of genes and the developmental and metabolic pathways that determine how plants are constructed. Through comparative phylogenetic analyses, they have shown the evolutionary conservation of these traits in other cereals crops, thus laying the groundwork for crop and yield improvement in other food plants as well.

Source: American Society of Plant Biologists

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