

PLoS Genetics 2009 maize genome collection

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Maize is an important crop in many countries of the world. It is widely used for human consumption, animal feed, and industrial materials. It also is considered an exemplar plant species for studying domestication, molecular evolution, and genome architecture.

[Reference Genome of Maize Published \(w/ Podcast\)](#)

The authors of the research presented in this special collection used the first description of the B73 [maize](#) genome to probe some of the most intriguing questions in genetics and [plant biology](#). The ten papers consider maize centromeres, new insights into transposon types and distribution, the abundance of very short FLcDNAs encoding predicted peptides, and many other "genetic jewels".

The Physical and Genetic Framework of the Maize B73 Genome

Wei F, Zhang J, Zhou S, He F, Schaeffer M, et al.

Wei et al. present a detailed account of how the maize genome was sequenced and how the maize chromosome-based pseudomolecules were constructed. In an approach that can be adopted in other large-genome species, the researchers use a comprehensive physical and genetic framework map to develop a minimum tiling path of over 16,000 BAC clones across the maize B73 genome.

A Genome-Wide Characterization of MicroRNA

Genes in Maize

Zhang L, Chia J-M, Kumari S, Stein JC, Liu Z, et al.

MicroRNAs (miRNAs) are small non-coding RNAs that play essential roles in plant growth, development and [stress response](#). Zhang et al. provide a comprehensive analysis of maize miRNA genes and describe results suggesting that mature miRNA genes were highly conserved during their evolution.

Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome

Wei F, Stein J, Liang C, Zhang J, Fulton RS, et al.

By extensively analysing ~1% of the maize genome, Wei et al. demonstrate the feasibility of refining the B73 RefGen_v1 genome assembly by incorporating optical map, high-resolution genetic map, and comparative [genomic data](#) sets.

A Single Molecule Scaffold for the Maize Genome

Zhou S, Wei F, Nguyen J, Bechner M, Potamousis K, et al.

The construction of the maize optical map represents the first physical map of a eukaryotic genome larger than 400 Mb that was created de novo from individual genomic DNA molecules. "The maize optical map is by far the most complex example of genome analysis via single molecules," says Dr. David Schwartz of the University of Wisconsin-Madison. "It was created using completely de novo techniques which greatly surpass conventional sequencing and all available next-generation sequencing methods and platforms in terms of completeness, speed,

accuracy and cost. This work points the way for new platforms dealing with personal genomics."

Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content

Springer NM, Ying K, Fu Y, Ji T, Yeh C-T, et al.

There is a growing appreciation for the role of genome structural variation in creating phenotypic variation within a species. Springer et al. used comparative genomic hybridization to compare the genome structures of two maize inbred lines, B73 and Mo17, and observed that whole genes are missing in one inbred relative to the other. The data reinforce the view that maize is highly polymorphic (assuming different forms) but also show that there are often large genomic regions that have little or no variation.

Sequencing, Mapping, and Analysis of 27,455 Maize Full-Length cDNAs

Soderlund C, Descour A, Kudrna D, Bomhoff M, Boyd L, et al.

To complement the completion of sequencing the maize B73 genome, Yu, Soderlund and Walbot sequenced 27,455 full-length cDNAs from two maize B73 libraries, representing the gene transcripts from most tissues and common abiotic stress conditions. They discovered about 1,600 unique maize genes, not found in other plant databases, that they anticipate will allow a better understanding of the biology and production of maize and cereal crops.

Loss of RNA-dependent RNA Polymerase 2 (RDR2) Function Causes Widespread and Unexpected Changes in the Expression of Transposons, Genes, and 24-nt Small RNAs

Jia Y, Lisch DR, Ohtsu K, Scanlon MJ, Nettleton D, et al.

Jia et al. focus on a mechanism by which the activity of genes and transposons alike are reined in or left to run free. The mechanism, involving small [RNA](#) molecules and their interactions with chromatin, is known to regulate transposons. Based on these findings, it now appears to influence gene activity as well.

Mu Transposon Insertion Sites and Meiotic Recombination Events Co-localize with Epigenetic Marks for Open Chromatin across the Maize Genome

Liu S, Yeh C-T, Ji T, Ying K, Wu H, et al.

Eighty-five percent of the newly sequenced maize genome consists of transposable elements, restless chunks of DNA that restructure the genome, generate genetic diversity, and influence gene expression patterns. Liu et al. debut a new PCR-based strategy for identifying Mu transposon insertion sites using highly conserved signature sequences from these elements. The finding that both Mu insertions and meiotic recombination sites concentrate in genomic regions decorated with epigenetic marks of open chromatin provides support for the hypothesis that open chromatin enhances rates of both Mu insertion and meiotic recombination.

Exceptional Diversity, Non-Random Distribution, and

Rapid Evolution of Retroelements in the B73 Maize Genome

Baucom RS, Estill JC, Chapparro C, Upshaw N, Jogi A, et al.

Baucom et al. report results showing that the maize genome provides a great number of different niches for the survival and generation of a wide variety of retroelements that have evolved differentially to occupy and exploit this genomic diversity. "This research breaks a lot of new ground in the understanding of what drives the evolution of most of the DNA in a chromosome. Although the work focuses on maize, the results are pertinent across all organisms, including humans."

Maize Centromere Structure and Evolution: Sequence Analysis of Centromeres 2 and 5 Reveals Dynamic Loci Shaped Primarily by Retrotransposons

Wolfgruber TK, Sharma A, Schneider KL, Albert PS, Koo DH, et al.

Because centromeres - the point or region on a chromosome to which the spindle attaches during mitosis and meiosis - consist of highly repetitive DNA sequences, these regions are exceedingly difficult to map and thus usually the last genomic regions to be assembled in [genome](#) projects. Using a comprehensive and general approach for mapping centromeres, Wolfgruber and colleagues precisely mapped all ten maize centromeres, constructed detailed maps of two centromeres, and determined the latter's present-day, as well as historic, boundaries. These findings that centromeres are dynamic loci that can shift over time have provided valuable insights into corn centromere evolution that may prove helpful in the design of artificial chromosomes of corn and other plants.

Source: Public Library of Science ([news](#) : [web](#))

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