IN BRIEF

DNA Methylation in Maize: Toto, I’ve a Feeling We’re Not in Arabidopsis Anymore

The maize (Zea mays) genome is ~20-fold larger than the Arabidopsis thaliana genome (~2500 Mb versus 125 Mb) and packed with transposons and other repetitive sequences. DNA methylation affects the silencing of genes and transposons and may help plant cells manage their repetitive DNA (reviewed in Law and Jacobsen, 2010). In plants, different enzymes and pathways function in de novo DNA methylation, maintenance of DNA methylation in different sequence contexts, and demethylation of DNA.

To examine the effects of alterations in DNA methylation, Li et al. (2014) assembled a set of mutants in maize genes predicted to affect methylation, including homologs of Arabidopsis DNA methylation genes, and mutants from genetic screens, such as mediator of paramutation 1 (mop1), mop2, mop3, transgene reactivated1 (tgr1), and tgr9. Genome-wide bisulfite sequencing showed that these mutants had different, subtle effects on CG, CHG, and CHH methylation and on different types of transposable elements. The mop and tgr mutants did not substantially alter global methylation, but sequence-capture bisulfite sequencing showed that they affect methylation at specific loci (see figure).

Chromomethylase mutants affected CHG methylation genome-wide and altered CHH methylation at specific loci. These differing effects indicate that multiple pathways affect methylation in different sequence contexts in maize.

In one intriguing difference between maize and Arabidopsis, the authors could not isolate double mutants for some maize paralogs that correspond to a single Arabidopsis gene, for example, double mutants of maize zea methyltransferase2 and 5, which affect the maize paralogs of Arabidopsis CHROMOMETHYLASE3 (CMT3). By contrast, Arabidopsis cmt3 mutants are viable. This suggests that DNA methyla-

In RNA-directed DNA methylation (RdDM), transcripts from repetitive elements direct de novo methylation via small interfering RNAs (reviewed in Matzke and Mosher, 2014). To examine the loci undergoing RdDM, Gent et al. (2014) identified RdDM loci by comparing the small interfering RNAs of the wild type and mop1 mutants and confirming the methylation status of the loci by bisulfite sequencing. Micrococcal nucleosome digestion and sequencing of the released nucleosome-sized DNA fragments showed that RdDM loci have relatively accessible chromatin. Chromatin immunoprecipitation showed that RdDM loci have reduced methylation of lysine 9 on histone H3 (H3K9me2), a marker of inactive chromatin. By contrast, RdDM and non-RdDM loci had similar levels of H3K27me2, a marker of silenced genes and transposons. Unlike RdDM loci, maize centromeres and heterochromatic knobs showed high CG and CHG methylation, and H3K9me2 and H3K27me2, but low CHG methylation and inaccessible chromatin. Thus, the RdDM loci showed intriguing similarities to euchromatic regions. Based on this work and other studies, the authors suggest that RdDM loci and other heterochromatic regions differ in Arabidopsis, as they do in maize, perhaps showing that following the yellow kernel road may lead back to Arabidopsis.

Revealing how chromatin modifications, noncoding RNAs, protein regulators, and DNA sequences function together in the genome may seem to be somewhere over the rainbow. However, these studies provide a step forward in understanding how plant genomes balance transcription of genes, and repression of transposons, and the activity of important heterochromatic regions. Oh my!

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