IN BRIEF

Epigenetics and Genetics: Global Profiling in Maize Inbred Lines Examines Variation in DNA Methylation

DNA methylation provided one of the first clues to the mechanisms of epigenetic regulation, explaining mysterious phenomena like transgene silencing in plants and oddities of inheritance in maize (Zea mays) and other species. Further research revealed that genomic DNA, and the histones that bundle it into chromatin, can be modified in different ways; these modifications affect gene expression and can be inherited at variable frequencies. DNA methylation contributes to silencing repetitive sequences, including transposable elements, a crucial function for genome stability in reproductive cells. DNA methylation can also produce regulatory changes in specific genes reviewed in Law and Jacobsen, 2010. Many plant genes also have methylation within their coding sequences, so-called “gene body methylation;” these genes are generally moderately expressed, and the function of gene body methylation remains unclear. Small RNAs, chromatin remodeling factors, methyltransferases, and demethylases all function in the inheritance, de novo addition, and removal of methyl groups on DNA.

Genetic and epigenetic effects do not occur independently. Indeed, some methylation variation is associated with variations in DNA sequence, but other variants have the same underlying DNA sequence as their wild-type alleles and are deemed epialleles. Whether such variation shows a causal effect or results from linkage disequilibrium remains unclear. To examine the relationship between epigenetic regulation and the underlying genetic landscape, Eichten et al. (pages 2783–2797) used methylated DNA immunoprecipitation-chip analysis to locate differentially methylated regions (DMRs) in 51 maize and teosinte inbred genotypes. This genome-wide characterization identified nearly 2000 common DMRs, and somewhat fewer rare DMRs, distributed throughout the genome (see figure). In the examined lines, half of the common DMRs were associated with DNA polymorphisms, which are likely in linkage disequilibrium, and many of these DMRs also had nearby transposable elements, which may affect DMR state. Also, the authors used recombinant inbred lines to show that most of the identified common DMRs are locally inherited. A subset of the common DMRs was associated with changes in the expression of nearby genes, changes that may affect phenotypes. Thus, the authors show a substantial interaction between the DNA methylation state of a region and the underlying genomic landscape, an interaction with likely phenotypic consequences.

Epigenetic variation provides a generally unexploited resource for plant breeders; semistable inheritance makes harnessing of epialleles difficult. However, such epigenetic differences can be important; for example, the authors identified many DMRs between maize and teosinte, DMRs that may have been selected during domestication. Polymorphisms that predict DNA methylation state (whether causal or not), and thus predict gene expression levels, provide a useful breeding tool. A deeper understanding of the relationship between epigenetic variation and the underlying genomic landscape may allow breeders to begin using the flexibility of epigenetic regulation, rather than avoiding its unpredictability.

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