

Genomes and Epigenomes: Beyond the DNA sequence

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ABSTRACT

The success of the sequencing projects on model plants such as *Arabidopsis* and Rice has created wide-spread interest in exploring the epigenome in order to elucidate how plant cell execute the information kept in the genome.

Although all nucleated cells effectively contain the same genome, they contain very different epigenomes depending upon cell type, developmental stage, sex, age and various other parameters. Genes constitute only a small portion of the total genome: indeed, non coding DNA which contains introns, repetitive elements and active transposable elements, requires effective mechanisms to be silenced on the long term. Cell differentiation and development are controlled through temporal and spatial activation and silencing of specific genes. Among others, gene regulation is controlled by epigenetic mechanisms. Epigenetics is the study of heritable changes in gene function which occur without a change in the DNA sequence. In plants, although epigenetic mechanisms help to protect cells from parasitic elements, this defense can complicate the genetic engineering process through transcriptional gene silencing.

The genomes are tagged by methylation of DNA cytosine. To understand the biological significance of this epigenetic mark it is essential to know where in the genome it is located. New techniques are making it easier to map DNA methylation patterns on a large scale and the results have already provided surprises. In particular, the conventional view that DNA methylation functions predominantly to irreversibly silence transcription is being challenged. Not only is promoter methylation often highly dynamic during development, but many organisms also seem to target DNA methylation specifically to the bodies of active genes.

This complexity makes it intrinsically difficult to precisely define 'an' epigenome, let alone 'the' epigenome.

What is clear, however, is that in order to unravel any epigenome, existing and novel high-throughput approaches on the DNA, RNA and protein levels need to be harnessed and integrated.