



High-throughput sequencing of cytosine methylation in plant DNA

Thomas Hardcastle

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Cytosine methylation is a significant and widespread regulatory factor in plant systems. Methods for the high-throughput sequencing of methylation have allowed a greatly improved characterisation of the methylome. Here we discuss currently available methods for generation and analysis of high-throughput sequencing of methylation data. We also discuss the results previously acquired through sequencing plant methylomes, and highlight remaining challenges in this field.

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