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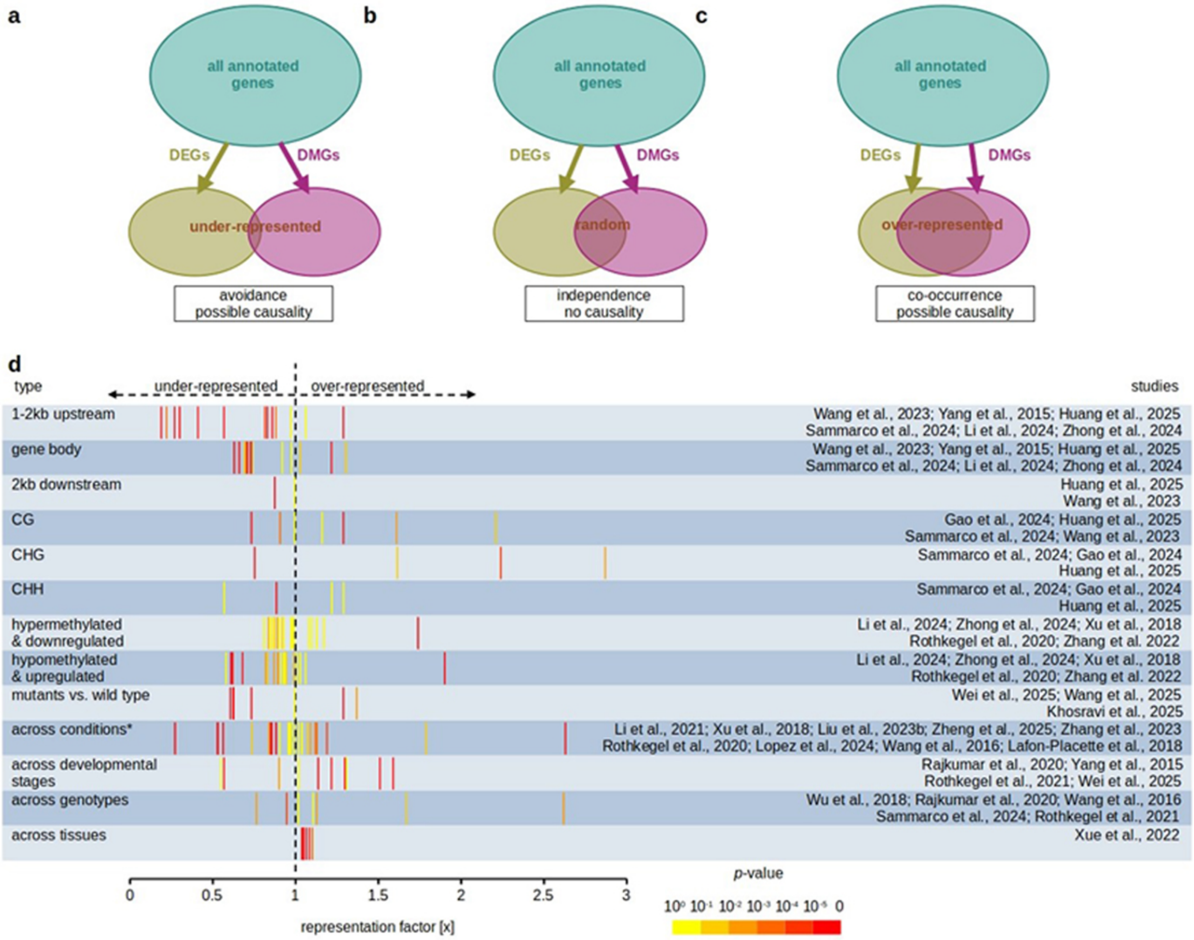
Is transcription directly regulated by DNA methylation in plants?

April 6, 2026



Theoretical and empirical outcomes of comparisons between sets of differentially expressed genes (DEGs) and differentially methylated genes (DMGs). The statistical *significance of the intersection of these sets was assessed by a hypergeometric test. Image courtesy of Peter Civan, French National Institute for Agricultural Research (INRAE).*

Regulation of gene activity—by increasing or suppressing transcription—is key to understanding how cells work and organisms develop, respond to their environments, and differ from each other. Some of this gene regulation is believed to be epigenetic, that is, determined by malleable changes of genetic material—DNA methylation and histone modifications. However, clear associations between DNA methylation and gene expression are difficult to find, and a few known examples should not generalize this relationship.

In a perspective article published in *The Plant Genome*, researchers argue that the link between DNA methylation and transcription is barely apparent on a genome-wide scale—and sometimes inconsistent across species. If DNA methylation regulated gene expression on any meaningful level, changes in DNA methylation would be associated with changes in gene expression. However, the researcher’s statistical assessment of many studies does not support this expectation. In many experiments, genes that change their DNA methylation are statistically associated with a stable transcriptional status, or vice versa.

These observations suggest that the role of DNA methylation in regulating gene expression is minor and quite possibly misunderstood. While some authors enthusiastically anticipate “epibreeding” (harnessing of epigenetic variation in crop breeding), some skepticism about such prospects remains.

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Civan, P., Sammarco, I., & Banouh, M. (2026). The mirage of DNA methylation in transcriptional regulation of plants. *The Plant Genome*, *19*, e70208. https://doi.org/10.1002/tpg2.70208

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