

Genome-wide DNA methylation perturbations in rice regeneration

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Abstract

Rice cultivars display significant differences in callus regeneration efficiency that can also impact transformation. DNA methylation as an epigenetic factor comprises a cumulative record of cultural environments leading to somaclonal variations and potentially affects regeneration. We generated stage-associated methylomes and transcriptomes of the embryo, induced calli, sub-cultured calli, and regenerated calli (successful and failed regeneration) of IR64 and TNG67. Through extensive bioinformatic analysis integrating methylomes and transcriptomes, we found that stage-associated changes are evident by the increase in the DNA methylation upon induction and decline upon regeneration. These changes in the methylome are largely random, but a few regions are consistently targeted at the later stages of culture. A subset of cultivar-associated differentially methylated regions also showed stage-associated changes, suggesting an association between DNA methylation and the regeneration programs of both rice cultivars. Finally, we identified stress-responsive genes enriched in both stage-associated differentially methylated and expressed genes, and the early onset of trehalose and abscisic acid bioprocesses may contribute to the resilience of TNG67 during regeneration.

Keywords: DNA methylation; *Oryza sativa*; regeneration efficiency; RNA-Seq; somaclonal variation; tissue culture; WGBS