# Divergence of DNA methylation and gene expression in *Setaria viridis* accessions under drought stress

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## Abstract

DNA methylation is one of the main epigenetic mechanisms involved in gene regulation. A better understanding of this can provide insights into regulatory mechanisms underlying abiotic response. The DNA methylation pattern in the genome of two accessions of *Setaria viridis* (A10.1 and Ast-1) submitted to drought stress was investigated. The experiment was performed in three biological replicates, and the drought stress treatment was applied for 5 days in plants at the booting stage. The treatments consisted of (*i*) moderate stress and (*ii*) field capacity. For DNA methylation analysis, genomic DNA was isolated and treated with bisulphite. The QC of the data was performed using FastQC and mapped through BSMAP v1.0. The unique and aligned reads served as input in the Methylkit (v1.7.4). 11-35 million high-quality reads were obtained, reflecting > 40-fold of genome coverage from each sample. We identified methylated C residues at least five read depth. The frequencies of mCs were similar in Ast-1 with moderate stress and control condition (named Ast1_MS with 5.85% and Ast1_CC with 6.04%), lower in A10 under moderate stress (A10_MS with 4.78%) and higher in A10.1 in well-irrigated conditions (A10_CC with 6.24%). From the total mCs, the highest fraction was CG (62-68.3%), followed by CHG (34.3-41.3) and CHH (2.9-4.7%) in both conditions tested. DNA methylation is concentrated in the pericentromeric regions of chromosomes compared with the end, indicating methylation of repetitive sequences. A considerable number of mCs was found in the intergenic region, followed by promoter, intron and exon regions. Evaluation in genes and transposable elements (TEs) revealed higher methylation at genes for CHG and CHH, and higher at TEs for CG. A large number of GCs was located within gene body and the frequency of CHG and CHH was considerably higher in the upstream and downstream regions. A total of 18.458 differentially methylated regions (DMRs, 10.818 hyper and 7.640 hypomethylation) were identified between A10.1 and Ast-1 accessions, 36 DMRs (9 hyper and 25 hypomethylation) in Ast-1 between drought *vs* control and 150 DMRs (58 hyper and 92 hypomethylation) in A10.1 between conditions (q-value <0.01). Gene ontology revealed that most of the genes involved in fiber organization, transmembrane transport and response to stress. High correlation was observed between methylation and gene expression by qPCR. These results provide insights in the interplay among DNA methylation and gene expression and suggest a role in abiotic stress adaptation in different genotypes.

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**Palavras-chave:** methylomes. TE methylation. whole genome bisulphite sequencing. differential methylation.

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