

DNA hypomethylation is the plausible driver of heat stress adaptation in *Linum usitatissimum*

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Abstract

Heat stress has a significant impact on the climatic adaptation of flax, a cool-season economic crop. Genome-wide DNA methylation patterns are crucial for understanding how flax cultivars respond to heat adversities. It is worth noting that the DNA methylome in flax has yet to be investigated at the nucleotide level. Although heat stress above 40°C caused oxidative damage in flax leaves, 5-azacytidine, a hypomethylating agent, reduced this effect by 15%–24%. Differences in the expression of the *LuMET1* (DNA methyltransferase) gene suggested that DNA methylation/demethylation may play a major role in the flax heat stress response. Thus, whole-genome bisulfite sequencing-derived DNA methylation profiles in flax, with or without heat stress and 5-azaC, were developed and analyzed here. In response to heat stress, a high percentage of significant differentially methylated regions (DMRs), particularly hypomethylated DMRs, were identified in the CHH nucleotide sequence context (H = A/T/C). Some of these DMRs overlapped with transposable element insertions. The majority of DMRs were discovered

this study are crucial for understanding and identifying the key players in heat stress response in flax, which will help in developing climate-smart flax varieties.

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DATA AVAILABILITY STATEMENT

Raw reads of whole genome bisulfite sequencing and other associated data generated in the present study can be accessed from the NCBI Gene Expression Omnibus under the accession number GSE185571. Other data are available in the article supplementary material.

Supporting Information

| Filename | Description |
|--------------------------------|---|
| ppl13689-sup-0001-TableS1.docx | Word 2007 document , 14.3 KB Table S1 |
| ppl13689-sup-0002-TableS2.xlsx | Excel 2007 spreadsheet , 30.4 KB Table S2 |
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| ppl13689-sup-0006-SupInfo.docx | Word 2007 document , 4.1 MB Figure S1 Figure S2 Figure S3 Figure S4 Figure S5 Figure S6 |

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