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Abstract

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DNA methylation as a possible mechanism responsible for *Haemaphysalis longicornis* response to low temperature stress*

CHUKS FIDELIS NWANADE, ZI-HAO WANG, RU-WEI BAI, RUO-TONG WANG, TIAN-AI ZHANG, JING-ZE LIU & ZHI-JUN YU[1]

Hebei Key Laboratory of Animal Physiology, Biochemistry and Molecular Biology, Hebei Collaborative Innovation Center for Eco-Environment, Ministry of Education Key Laboratory of Molecular and Cellular Biology, College of Life Sciences, Hebei Normal University, Shijiazhuang 050024, China

[1]*Corresponding author: yuzhijun@hebtu.edu.cn; https://orcid.org/0000-0003-0122-7525*

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Abiotic stress is an important factor that can influence the survival and development of ticks. DNA methylation is an important epigenetic modification that has been implicated in the adaptation of plants and insects to abiotic stress, but its role in the response of ticks to abiotic stress remains unclear. Herein, we explore the DNA methylation profile of the tick, *Haemaphysalis longicornis* exposed to low-temperature stress using whole-genome bisulfite sequencing (WGBS). We found that the cytosine methylation level varied depending on the treatment (control at 26 °C and low-temperature stress at 4 °C) and sequence context (CG, CHG and CHH). Moreover, DNA methylation was detected in the 3' untranslated region (UTR) and exon region. In addition, a total of 6,087 differentially methylated regions (DMRs) were identified between the low-temperature and rearing temperature groups, including 3,288 hypermethylated and 2,799 hypomethylated DMRs. Further, Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of differentially methylated genes (DMGs) revealed that most of the DMGs were most significantly enriched in binding, and RNA transport pathways. Taken together, this research enhanced our knowledge of and provided new insights into DNA methylation changes relating to low-temperature stress in *H. longicornis*. It also provided a foundation for future studies of the epigenetic mechanism underlying the responses of ticks to cold stress.

Keywords: *Haemaphysalis longicornis*, epigenetic regulation, DNA methylation, whole-genome bisulfite sequencing, low-temperature stress

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