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Journal

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Title:

DNA demethylation and heterochromatin remodelling upon heat stress

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Meeting:

COST action TD0905 "Epigenetics-Bench to Bedside"

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Abstract:

Conversion of environmental signals into epigenetic information is thought to occur widely but has been poorly studied as yet. It is proposed that changes in the expression of molecules involved in chromatin remodelling or their modification might play a role in this process. Here we study remodelling of heterochromatin upon heat stress in the red flour beetle *Tribolium castaneum* (Tenebrionidae, Coleoptera), one of the most important stored products pest. We show that the expression of abundant satellite DNA TCAST which is located within the constitutive pericentromeric heterochromatin, is strongly induced following heat shock and is accompanied by increase in repressive epigenetic modifications of histones at TCAST regions. Upon recovery from heat stress, the expression of satellite DNA-associated siRNAs as well as histone modifications is quickly restored. Bisulphite sequencing of TCAST satellite DNA reveals cytosine methylation not only restricted to CpG sites but also found at CpA, CpT and CpC sites, and preserved within heterochromatin during all developmental phases. The level of methylation decreases after heat shock depending on the duration and results in a complete demethylation after prolonged treatment. Our results indicate that heat shock induced satellite DNA demethylation and expression affect epigenetic state of constitutive heterochromatin in insects. It can be hypothesized that transient remodelling of heterochromatin is part of a physiological gene expression program activated under stress conditions. We propose the existence of a negative-feedback mechanism in which satellite DNA-associated siRNAs induced by heat stress, repress their own transcription by providing additional H3K9me3 anchorage sites for the chromodomain protein such as HP1, and in this way restore heterochromatic state.

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