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The dynamics of genome-wide DNA methylation during heat stress in *Arabidopsis thaliana*

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Environmental stresses are one of the most important factors affecting the growth and development of plants. Recent studies have shown that epigenetic mechanisms are crucial in plant adaptation to stressful conditions. Understanding the role of DNA methylation modulation under stressful conditions, such as high temperature, will allow a better understanding of the mechanisms of plant response to environmental factors. Using whole-genome bisulfite sequencing on DNA extracted from leaves of wild-type Arabidopsis seedlings subjected to high temperature we analyzed the dynamics of DNA methylation at seven time points including control conditions, heat stress treatment and recovery. Results that we obtained show a gradual reduction in the level of methylation with the duration of the experiment. Most changes in DNA methylation level occurring only after treatment discontinuation and transfer to control condition. Despite the fact that the effect of DNA methylation reduction is visible globally, it refers to a very specific genes, largely related to the response to stress. Among differentially methylated genes there are those encoding heat shock proteins, genes associated with translation elongation and many genes with a documented role in response to abiotic stress. In our studies we showed, at base-resolution level, that DNA methylation level changes under the influence of heat stress and that those changes mainly concern reduction in DNA methylation. Considering the fact that changes in the level of DNA methylation was related to specific genes involved in the response to stress we assume that we observe active demethylation phenomenon caused by heat stress.

Biography

Urszula Korotko is a PhD student at University of Silesia in Katowice. She is a co-author of 5 papers in reputed journals. Beyond the academic experience, she has also experience in working in companies from the bioinformatics industry.

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