

10th International Conference on
Genomics and Molecular Biology

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6th International Conference on
Integrative Biology

May 21-23, 2018 Barcelona, Spain

Time-series experiment reveals new epigenetic signature and a gene regulatory network involved in early response to salinity stress in *Arabidopsis* T87 cells**Marta Koblowska**

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One of the major abiotic constraints affecting plant growth is soil salinity. Despite many years of studying the molecular basis of plant response to high salinity, we still have gaps in our understanding of complex mechanisms underlying plant tolerance to salinity. To advance our knowledge about the early stages of plant cell response to salinity, we carried out a time-series experiment during the first 100 minutes of high-salt stress. As the most suitable model for performed studies, we chose *Arabidopsis* T87 cell line, offering a relative cellular homogeneity comparing to a mixture of cells building the whole seedling or their organs. Our previous results describing nucleosomal response to high salinity, cold and abscisic acid (ABA) showed that *Arabidopsis* T87 cell line is a very convenient model to analyze stress response at the cellular level. To establish if frequent passages had an impact on T87 cells genome, we characterized a genetic variation in T87 cells. Apart from our previous data demonstrating that phosphorylation of histone H3 (H3S10ph) is a nucleosomal marker of cells standard behavior under stress, we also showed a novel histone modification, H4K16ac to be a valid epigenetic signature of plant stress response. Transcription profiling of T87 cells led to identification of previously unrecognized genes, strongly activated during first few minutes of salinity stress. Time-series transcriptome analysis during salinity stress followed by Bayesian network modelling recognized a set of hub genes directing the early response of plant cells to salinity stress.

Biography

Marta Koblowska is currently the Director of the Laboratory of Bioinformatics and Systems Biology at the Faculty of Biology, University of Warsaw. Since 2008, she is the Head of the Laboratory of Microarray Analysis, in the Institute of Biochemistry and Biophysics, Polish Academy of Sciences. Her main research interests focus around chromatin function in regulating gene expression changes in plant adaptation to stress conditions. Her group recently showed that plant specific histone deacetylase HD2C interacts with BRM-containing SWI/SNF chromatin remodeling complex and both are involved in mediating the heat stress response in *Arabidopsis*.

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