

UNRAVELLING THE FUNCTION OF THE HISTONE DEACETYLATION MACHINERY DURING STRESS TRANSCRIPTIONAL RESPONSES IN *ARABIDOPSIS THALIANA*

FASANO C.*, DONALD N.**, CARR C.**, HERZYK P.***, AMTMANN A.**, PERRELLA G.*

*) ENEA, Trisaia Research Centre, 75026 Rotondella (Matera), Italy

**) Plant Science Group, Institute of Molecular, Cell and Systems Biology (IMCSB), University of Glasgow, Glasgow G12 8QQ, UK

***) Glasgow Polyomics, Wolfson Wohl Cancer Research Centre, University of Glasgow, Glasgow G61 1QH, UK

epigenetics, abiotic stress, plant development, transcriptomics, protein complex

In order to survive to stressful environments, plants must adjust and adapt to different variations that can often lead to loss in germination and growth.

Histone deacetylation represents a regulatory process that mediates stress transcriptional responses in plant development. In yeast and mammals, Histone Deacetylases (HDACs) are known to operate within multi-protein complexes formed among others, by a catalytic subunit, a co-repressor and several histone-binding proteins.

Histone Deacetylase Complex 1 (HDC1) is a recently discovered component of the HDAC complex that directly interact with HDACs and is able to promote histone deacetylation. During plant growth HDC1 operates as a rate-limiting factor by determining a series of downstream processes in a quantitative manner, including germination, vegetative growth and flowering¹. Truncation of HDC1 full-length protein to the ancestral core domain RXT3 revealed that such domain can stimulate seed germination in presence of NaCl or ABA. In addition, HDC1, together with HDACs, is able to bind to a wide range of proteins, including co-repressors, histone binding proteins and the linker histone H1².

Here, we describe a comprehensive transcriptome analysis of different HDC1 lines of *Arabidopsis thaliana*, and we reveal HDC1 function during germination in response to salt stress. By combining chromatin immunoprecipitation with next generation sequencing (ChIP-Seq), we show that HDC1 can deacetylate DNA regions under stress conditions. Furthermore, the over-expression of the RXT3 domain appears to be sufficient in remodulating the expression of HDC1 targets. Interestingly, ChIP PCR analyses on specific loci revealed that HDC1 and H1 can determine histone acetylation and methylation levels of promoter elements of responsive genes.

Altogether our results further elucidate the histone deacetylation mechanisms regulating seed germination and address the causal link between chromatin modifications and transcriptional responses. Finally, we propose that the HDC1-H1 complex might function as a hub for the establishment of different epigenetic marks.

¹: G Perrella et al., (2013) *Plant Cell*. 25(9):3491-505; ²: G Perrella et al., (2016) *Plant Physiol*. 171(1):62-70.