Linker histones - their roles beyond the chromatin architecture

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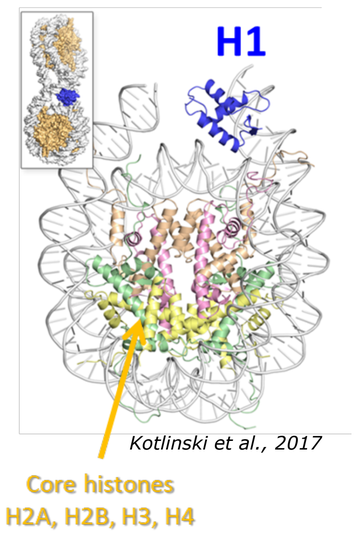
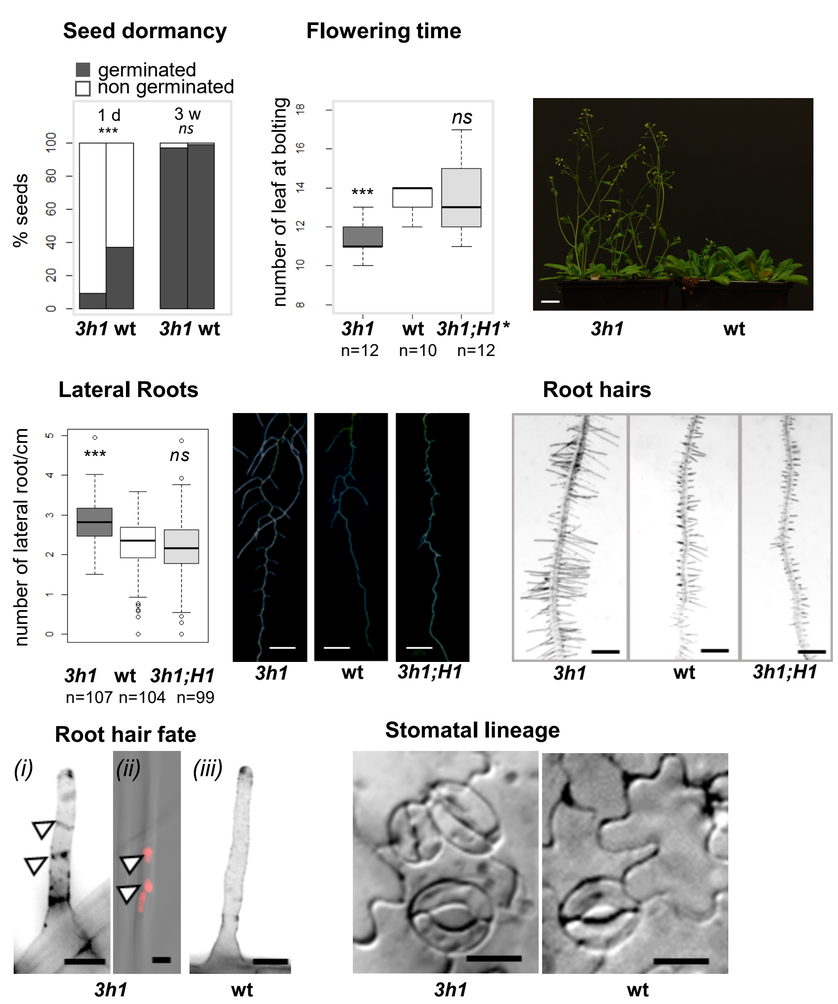
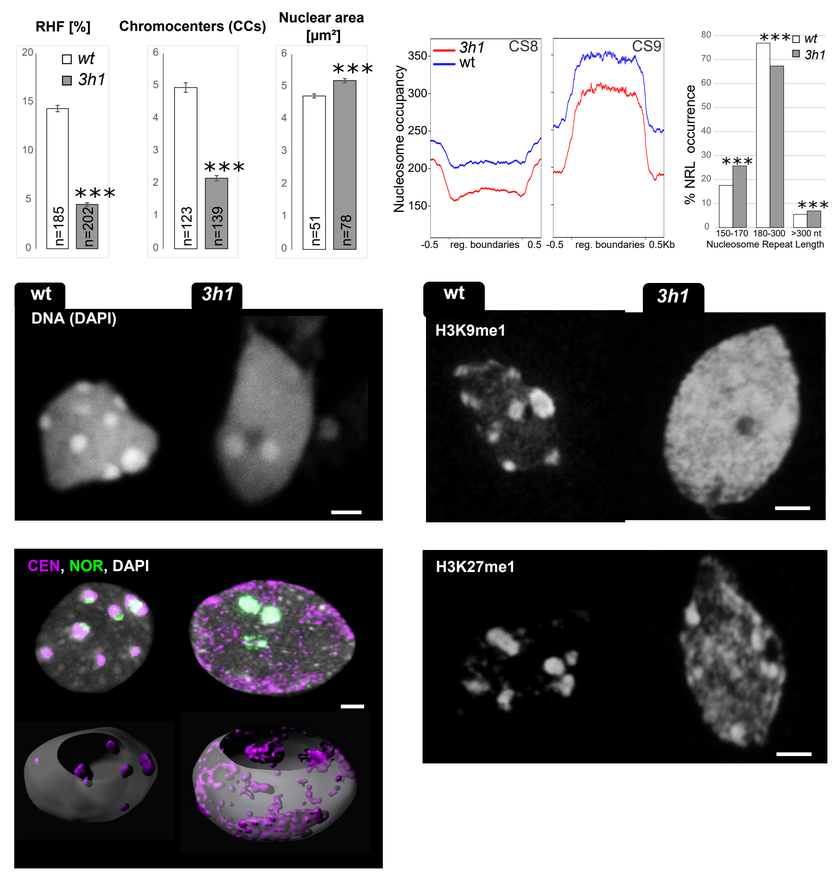


Linker histones (H1) belong to major constituents of plant and animal chromatin besides the core nucleosomal histones. H1 variants appeared early during evolution as lysine-rich, proto-linker histones found in the ancestral eukaryotes such as protists but not Archaea (Kasinsky, Lewis et al. 2001). In contrast to core nucleosomal constituents H1 form a highly divergent class of histones (Kasinsky, Lewis et al. 2001).

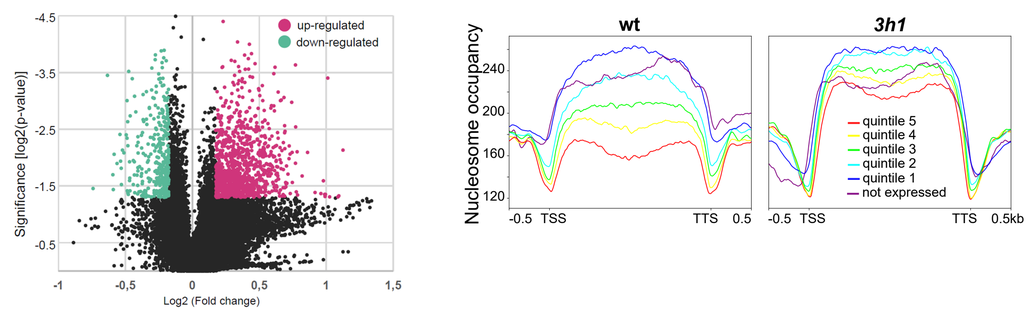
H1-deficient plants are viable yet show mild phenotypes.



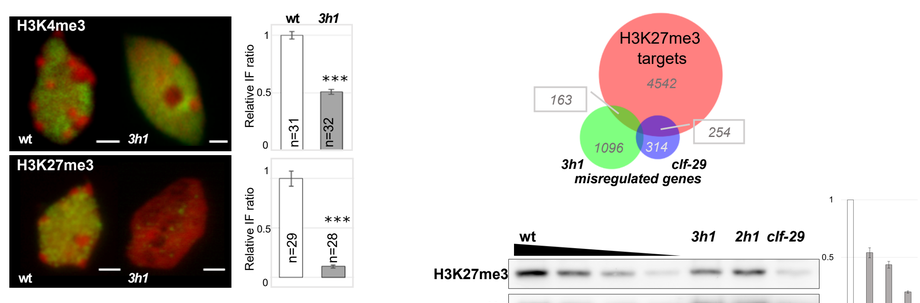
H1 variants are necessary to form compact heterochromatin domains but are dispensable for TE silencing and peripheral positioning of chromocenters



H1 loss-of-function allows identifying both H1-sensitive and H1-independent genes



H1 depletion impairs the distribution of H3K27me3 and to a lesser extent of H3K4me3



Conclusion

H1 variants have a profound impact on the molecular and spatial (nuclear) chromatin organization in Arabidopsis with distinct roles in euchromatin and heterochromatin and a dual causality on gene expression. Phenotypical analyses further suggest the novel possibility that H1-mediated chromatin organization may contribute the epigenetic control of developmental and cellular transitions.

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