Dynamics of post-translationally modified histones during barley pollen embryogenesis in the presence or absence of the epi-drug trichostatin A

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Despite the agro-economic importance of pollen embryogenesis, the mechanisms underlying this process are still poorly understood. Pollen embryogenesis is based on the switch from a gametophytic pathway towards an embryogenic pathway. Though morphological and cellular changes that occur during the induction of embryogenesis have been well described [1], remarkably little is known about the underlying cell biological mechanisms. Using indirect immunostaining, we recently described the dynamics of post-translational histone modifications (histone H3K4me2, H3K9ac, H3K9me2, and H3K27me3) and chromatin marks (RNA polymerase II CDC phospho Ser5, and CENH3) during regular barley pollen development [2]. We here show that epigenetic profiles change significantly early in barley pollen embryogenesis from whereon the profiles remain unaltered until the multicellular stage. The most remarkable effect of embryogenesis is the general redistribution of modified histones from the nucleus into the cytoplasm which may be a consequence of ongoing mitotic activity. Application of the histone deacetylase inhibitor trichostatin A stimulated pollen embryogenesis when used on pollen with a gametophytic style chromatin pattern. However, when this drug was administered to embryogenic pollen, the chromatin markers reversed towards a gametophytic profile, embryogenesis was halted and all pollen invariably died.

References

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