

DOWN-REGULATION OF A HISTONE DEACETYLASE AFFECTS MALE MEIOSIS IN *ARABIDOPSIS*

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Recent studies showed that histone post-translational modifications (HPTMs) are associated to meiotic events including homologous recombination, cohesion, chromosome segregation. Our previous work in *Arabidopsis* evidenced that histone acetylation is required for meiotic recombination and chromosome segregation in male meiosis (*Perrella et al. Plant J 2010, 62: 796*). Histone acetylation is a reversible process carried out by two classes of enzymes known as histone acetylases (HATs) and histone deacetylases (HDACs). In this work, we focused our attention on a HDAC recognized as a global regulator that is involved in different physiological and developmental processes in *Arabidopsis*. Down-regulation of this HDAC mediated by antisense RNA and T-DNA insertion caused male and female sterility. In order to elucidate the mechanisms underlying the reduction of plant fertility the functional role of this HDAC was investigated in male meiosis in T-DNA mutant characterized by lower expression level and transcript rearrangement as compared to wild type. Different abnormalities affecting pairing, recombination and chromosome segregation have been observed in the mutant. As compared to wild type meiocytes, homologous chromosomes appeared not fully synapsed in pachytene. At diplotene/diakinesis, two univalents were observed in 17% of male meiocytes indicating a failure of the obligate CO for one chromosome pair. At later stages, uneven chromosome distribution was evidenced, as well. It is likely that the meiotic defects are depending on the histone hyperacetylation caused by HDAC down-regulation.