

ANNOTATION AND EXPRESSION OF FDM-LIKE GENES IN SEXUAL AND APOMICTIC *H. PERFORATUM* ACCESSIONS

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Apomixis is an asexual reproductive strategy that permits to the inheritance of the maternal genome over generations without genetic recombination events. From a biological point of view, this modality of asexual reproduction by seed could be the consequence of heterocronic expression of genes involved in fundamental aspects of sexual reproduction, such as meiosis and spore selection, leading to the formation of functional un-reduced gametes which retain the ability to form an embryo eventually bypassing double fertilization. Although this process is well documented in many flowering plants, and despite its revolutionary potentials in plant breeding strategies, the genetic control of apomixes is still not properly understood. Recently, a number of independent studies on sexual model species provided experimental evidences linking single components of apomixis to the deregulation of genes involved in the RNA-directed DNA methylation pathway (RdDM). RNA-directed DNA methylation refers to a specific process in which small interfering RNAs produced by the RNA interference pathway guide de novo methylation of cytosines at the homologous DNA region, thereby regulating the expression of specific genes. Remarkably, gene expression studies in the apomictic model species *Hypericum perforatum* corroborate the hypothesis that miss expression of genes involved in this pathway is functionally associated with early events of apomixes in this species. The aim of the present research is a better understanding of the role of a class of genes involved in the RdDM known as Factor of DNA Methylation (FDM), in the frame of ovule cell fate change, megagametogenesis and, ultimately, aposporous apomixis. To this end, computational investigations were performed in order to annotate the *H. perforatum* FDM genes. The expression of these genes in *H. perforatum* pistils and ovules was studied by qPCR and ISH assays on sexual and apomictic accessions. Furthermore, *Arabidopsis thaliana* knock out lines were characterized in order to elucidate the role of specific genes in relation to gametophyte and/or seed formation. All data will be presented and critically discussed as they prove a better understanding of molecular bases of apomixes in *H. perforatum*.