

CHARACTERIZATION OF APOSTART MEMBERS: DOES APOMIXIS RUN STRONG IN THIS GENE FAMILY?

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By avoiding the genome re-assortment due to meiosis and fertilization, apomixis is a naturally occurring mode of asexual reproduction in flowering plants. Due to this mechanism, the inheritance and perpetuation of the maternal genome through seed is assured. In apomictic vs. sexual *Poa pratensis* cDNA AFLPs revealed a different expression of a gene, later named APOSTART, putatively involved in programmed cell death. Such a gene could be hence involved in the degeneration of non-functional megaspores and nucellar cell, permitting the enlargement of maturing embryo sacs. PpAPOSTART shares high homology with two *Arabidopsis thaliana* proteins: AtAPOSTART1 and AtAPOSTART2. In order to verify if AtAPOSTART1 and AtAPOSTART2 have additive or redundant roles we generated and analysed two *Atapo1/Atapo2* double mutant lines. Both seem to germinate slower and plants appear smaller than the wild type, showing a high variability between and within mutant lines.

We are investigating the expression levels for AtAPO1 and AtAPO2 in many tissues through qRT PCR, their cellular localization through fusion with fluorescent proteins, their function during meiosis and embryo development through crosses with specific marker lines (e.g. markers for the first precursor of the female germline and the product of meiosis) and their interaction with new putative interactors to better dissect the molecular network they might be involved in.

Thus far, results in terms of the phenotypic and expression analysis in the *Arabidopsis* double mutants are reported and critically discussed.