

## COMPARATIVE GENOME ANALYSIS OF APOSTART AND OTHER GENES INVOLVED IN THE CONTROL OF PLANT REPRODUCTION

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### *APOSTART, apomixis, meiosis, genome organization*

*Poa pratensis* L. is a cool-season grass of great importance for forage and turf production in the temperate climates of the world besides it is important for the production of high quality amenity and sport lawns. This species reproduces facultatively through aposporous apomixis and sexual outcrossing. In natural populations plants showing a wide range of combinations of sexuality and apomixis have been found, including completely sexual, intermediate apomictic and nearly obligate apomictic genotypes.

For understanding the molecular genetics of complex traits such as apomixis, the isolation of specific genes is crucial. With this respect, the use of new cloning strategies could provide innovative tools to isolate genes involved in traits of interest. The choice of the right method is related to the kind of information desired.

We have demonstrated that a cDNA-AFLP strategy, applied to developmental staged inflorescences, was useful to identify several ESTs differentially expressed between apomictic and sexual genotypes of *P. pratensis*. In particular APOSTART, SERK and PpMET showed to be putatively involved in the formation of unreduced embryo sacs and in the modification of sexual reproduction.

We performed a comparative analysis based on bioinformatic approaches to investigate on the genome organization of these genes in *A. thaliana* and in other plant species for which genome sequences are today available.

Our goal was to consider genome distribution of this set of genes, possible functional implications and evolutionary relationships.