Proceedings of the Joint Congress SIBV-SIGA
Pisa, Italy – 19/22 September, 2017
ISBN **978-88-904570-7-4**

Poster Communication Abstract – 6.24

CHARACTERIZATION OF AtAPOSTART DOUBLE MUTANTS

AIELLO D., PELLEGRINI L., MARCONI G., ALBERTINI E.

Department of Applied Biology, University of Perugia, Borgo XX Giugno 74, 06121 Perugia (Italy)

apomixis, Arabidopsis thaliana, APOSTART, methylation, polyploidy

Apomixis is a naturally occurring mode of asexual reproduction in flowering plants, that allows the inheritance, perpetuation of the maternal genome through seed by circumventing genome re-assortment due to meiosis and fertilization. The use of apomixis in agriculture relies upon the idea of fixing indefinitely superior genotypes (i.e., F_1 hybrids) through seeds without loss of heterosis due segregation. This possibility holds enormous economic and social potentials in agriculture and food production. The impact of apomictic crops in agriculture would be comparable to, or even greater than, the Green Revolution, especially in Third World. In fact, it has been estimated that the use of apomixis technology in the production of hybrid rice could provide benefits exceeding 1.8 billion Euros per year; results even greater could be reached in potato with a benefit of 2.3 billion Euros per year.

We isolated in *Poa pratensis* a gene named *APOSTART* that shown a relation with the programmed cell death, generally involved in the non-functional megaspore and nucellar cell degeneration events that permit enlargement of maturing embryo sacs. In *Arabidopsis thaliana*, *APOSTART* is located next to an unknown gene that is strongly similar to a *MOB*1 (*MPS-ONE-BINDER)*, a gene involved in the formation of the unreduced egg cells. APOSTART protein share three different domains; one of these is of extreme interest because the human START domain, was discovered in the genetic product of *StAR*, a gene involved in human congenital lipoid adrenal hyperplasia which results in a reduced aldosterone synthesis and in male pseudo-hermaphroditism.

Previous results suggested a possible role of APOSTART in apomixis. To better understand this function we are characterizing *Arabidopsis thaliana APOSTART* members. *PpAPO* shares high homology with the Arabidopsis protein At5G45560, thus renamed *AtAPOSTART*1 (*AtAPO*1), and with *EDR*2 (Enhanced Disease Resistance 2) renamed *AtAPO*2. In order to verify if *AtAPO*1 and *AtAPO*2 have additive or redundant roles we generated and analyzed the atapo1-2 double mutants. Some double mutant plants appear smaller than the parental lines, as well as the developing siliques do. Moreover, high variability in plant size and time of flowering was found between and within mutant lines. This could be due to either polyploidy or genomic imprinting. With the aim of shedding light on this phenomenon: i) a genome-wide as well as *APOSTART* promoter-specific methylation analysis, were carried out; ii) chromosome number was estimated. Overall results in terms of methylation changes and ploidy level in Arabidopsis double mutants are reported and critically discussed.