Proceedings of the 52nd Italian Society of Agricultural Genetics Annual Congress
Padova, Italy – 14/17 September, 2008
ISBN **978-88-900622-8-5**

Poster Abstract – D.53

ISOLATION AND CHARACTERIZATION OF GENOMIC REGIONS CONTAINING APOSTART IN *POA PRATENSIS* L.

MARCONI G., RAGGI L., COLLANI S., ALBERTINI E., FALCINELLI M.

Department of Applied Biology, University of Perugia (Italy)

APOSTART, apomixis, meiosis, genomic libraries, promoter

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, by using this strategy, we have isolated a gene which we termed APOSTART and which shows both a different expression between apomictic and sexual genotypes and a flower-specific localization.

For these reasons we have created 3 genomic libraries using 2 apomictic and 1 sexual genotypes with three aims: i) to isolate DNA regions containing APOSTART members/alleles; ii) to identify genes linked to APOSTART and iii) to sequence regions upstream APOSTART to verify the presence of promoter, 5’-UTR and of possible enhancers.

Here we describe the screening of these genomic libraries for clones carrying the APOSTART gene and the full-length clone sequencing. The bioinformatic characterization of these clones is reported and discussed.