Proceedings of the 50th Italian Society of Agricultural Genetics Annual Congress
Ischia, Italy – 10/14 September, 2006
ISBN 88-900622-7-4

Poster Abstract – D.07

MORPHOLOGICAL AND FUNCTIONAL ANALYSIS OF MALE AND FEMALE GAMETOPHYTES OF *PETUNIA HYBRIDA MEI2* AND *MIP1* RNA INTERFERENCE PLANTS

M. PURELLI*, G. GALLA**, M. VIVIANI*, S. ZENONI*, A. PORCEDDU***,
G. BARCACCIA**, G.B TORNIELLI*, M. PEZZOTTI*

*) Scientific and Technological Department, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy
**) Department of Environmental Agronomy and Crop Science, University of Padova, Viale dell'Università 16, I-35020 Legnaro, Padova, Italy
***) Istituto di Genetica Vegetale CNR, Perugia, Italy

Petunia hybrida, mei2, mip1, meiosis, RNAi

The plant life cycle alternates between a diploid sporophyte and a haploid gametophyte. Meiosis in plants represents the transition from the sporophyte to the gametophyte generation. In higher plants, meiosis takes place in specialized cells called sporocytes, which are formed in anthers and ovules. Many of the genes encoding basic structural components of meiotic machinery common to all eukaryotes are highly conserved also in yeast and other organisms. For instance, in *S. pombe*, an eukaryote organism considered as a model for studying meiosis, the genes *mei2* and *mip1* play a fundamental role in this process. In particular, MEI2, an RNA-binding protein, is responsible for the synthesis of pre-meiotic DNA in the cytoplasm, whereas in the nucleus it promotes the first meiotic division. MIP1 is a WD-repeat protein that interacts weakly with MEI2 in the cytoplasm, likely helping MEI2-folding, but its function remains unknown and may be more complex.

The aim of this work is to elucidate the role of *mei2* and *mip1* genes in the meiosis process of *Petunia hybrida*. To gain further insights of their biological role, the two genes were isolated, molecularly characterized and a loss-of-function approach was carried out.

A post-transcriptional gene-silencing of both *mei2* and *mip1* genes was induced independently in plants of *Petunia hybrida* cv. Mitchell by means of RNAi technique. No visible phenotypic alterations were observed in the silenced plants. Therefore, *mei2* and *mip1* RNAi plants were crossed to generate single plants with double interference. The cytohistological characterization of embryo sac and pollen development in T2 double silenced plants is reported and discussed. Patterns of megagametogenesis and microsporogenesis were investigated, and functional analysis of pollen viability and embryo sac fecundity was also performed. The role of *P. hybrida mei2* and *mip1* genes is also reviewed.