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Poster Abstract - B.21

IS THERE ANY FUNCTION FOR *P. HYBRIDA MEI2* AND *MIP1* GENES?

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Meiosis is a key step in the sexual reproduction in eukaryotic organisms. The meiotic events, comprising the meiotic cell cycle, appear to be highly conserved among the various species studied, from yeast to mammalian. In plants, meiosis, in addition to providing an opportunity for genetic recombination, marks the transition from the diploid sporophyte to the haploid gametophyte.

In *S.pombe*, a eukaryote considered as a model for studying meiosis, the proteins mei2 and mip1 are fundamental in this process. mei2, an RNA-binding protein, is responsible for the synthesis of pre-meiotic DNA in the cytoplasm, while, in the nucleus, it promotes the first meiotic division. Mip1 is a WD-repeat protein that interacts weakly with mei2 in the cytoplasm, probably helping mei2-folding, but its function may be more complex.

The aim of this project is to elucidate the role of mei2 and mip1 genes in *Petunia hybrida*. The two genes were previously isolated and molecularly characterized in our group but their function in Petunia hybrida is still unknown. To gain further insight of their biological role a loss of function approach was carried out.

In Petunia hybrida cv. Mitchell post-transcriptional gene-silencing, by RNAi technique of both mei2 and mip1 genes, was induced independently. In this abstract we report the regeneration of the primary-transformed plants and their molecular and phenotypical characterization. The alteration of the expression-level of the endogenous Petunia mei2 and mip1 genes was studied, meiosis was analyzed in the primary transformed plants and their progenies. mei2 promoter region was also studied by fusion with the reporter genes β-glucoronidase (GUS) and GFP.

At the moment no evident phenotype was obtained by the RNA interference technique; the function of Petunia hybrida mei2 and mip1 genes is still to be elucidated.