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Poster Abstract - B.14

THE *TERTIA* GENE ENCODING A PUTATIVE ACETYLTRANSFERASE IS INVOLVED IN CHROMOSOME SEGREGATION DURING MEIOSIS IN *ARABIDOPSIS THALIANA*

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activation tagging, meiotic gene

Recently, a considerable progress in the identification of meiotic genes has been ensured by the adoption of *Arabidopsis thaliana* (Ath) as a model plant system (Consiglio et al. 2004 Sex Plant Reprod, 17: 97-105).

The activation tagging realized by a T-DNA vector containing multimerized transcriptional enhancers from CaMV35S allowed us the isolation of dominant mutants with "few seeds" phenotype. The T-DNA insertion in one (b16) of these mutants leads to the overexpression of a gene (*TERTIA*) encoding a GCN-5 related N-acetyltransferase belonging to GNAT family. The *TERTIA* gene, 1319 bp long characterized by five exons, is localized on chromosome 3. This gene shows a similarity with other five GCN-5 related N-acetyltransferase in Ath.

The homozygote for the dominant mutation confirmed the reduced fertility with siliques carrying few seeds, and it exhibited an early flowering and a terminal height less than wild type.

Cytological analysis of flower buds in the mutant indicates a role of *TERTIA* in meiosis. In microsporogenesis, 2-4 unpaired chromosomes and nonhomologous synapsis involving two chromosome pairs occurred at diakinesis/metaphase I. A premature segregation of sister kinetochores of unpaired chromosomes, and absence of segregation of the two associated chromosome pairs were observed at anaphase I evidencing a mixture of reductional and equational division. Abnormalities in chromosome segregation and in migration towards the poles characterized meiosis II, as well. A high number of triads (38%), tetrads showing degeneration of one microspore (9%), and dyads (9%) were observed at the end of meiosis. Similar abnormalities were observed in female meiosis. Ovary histology revealed that about half of megaspore mother cells arrested their development before embryo sac formation.

The *TERTIA* gene was found to be expressed mainly in flower buds, and a much lower expression was detected in mature leaves. By the semiquantitative RT-PCR method and by Real-Time RT-PCR, *TERTIA* mRNA levels were found to be higher (3x in flower buds and 0.25x in leaf) in the mutant as compared to wild type.

Screening of publically available mutants identified four Salk lines carrying a T-DNA insertion in different exons and introns of *TERTIA* gene. Preliminary investigations on these lines have shown a decrease in seed production as compared to wild type. Construct *CaMV35S::TERTIA* will be used to transform Ath wild type.