Proceedings of the 51st Italian Society of Agricultural Genetics Annual Congress
Riva del Garda, Italy – 23/26 September, 2007
ISBN **978-88-900622-7-8**

Poster Abstract – D.65

PROGRESSES TOWARDS THE CLONING OF THE TOMATO *PARTHENOCARPIC FRUIT* (*PAT*) GENE

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COS markers, fruit set, parthenocarpy, positional cloning, tomato

Our aim is to understand the molecular genetic mechanisms underlying the *parthenocarpic fruit* (*pat*) mutation of tomato, a recessive mutation conferring parthenocarpy in tomato (*Solanum lycopersicum* L.) and pleiotropic effects affecting the anthers and the ovules. Expression analysis of genes encoding key enzymes involved in GA biosynthesis showed that in normal tomato ovaries the transcript of *GA20ox1* is in low copy number before anthesis and only pollination and fertilization increase its transcription levels and, thus, GA biosynthesis. In the unpollinated ovaries of the *pat* mutant, this mechanism is de-regulated and *GA20ox1* is constitutively expressed, indicating that a high GA concentration could play a part in the parthenocarpic phenotype. The levels of endogenous GAs measured in the floral organs of the *pat* mutant support such a hypothesis. As genes involved in the control of GA synthesis (*LeT6*, *LeT12* and *LeCUC2*) and response (*SPY*) are also altered in the *pat* ovary, it is suggested that the mutation affects a regulatory gene located upstream of the control of fruit set exerted by GAs.

In addition, we have pursued the positional cloning of the *Pat* gene, by Bulk Segregant Analysis using a set of segregating populations. Former results located the *Pat* locus to the long arm of chromosome 3 between the COS markers T0796 and T1143, previously anchored on the genetic tomato map (EXPEN 2000, www.sgn.cornell.edu). By pursuing the microsynteny between tomato and Arabidopsis, novel PCR-derived COS markers have been developed and mapped inside the target window. T0796 and T1143 display a clear hit with a number of BACs belonging to two plausible unlinked contigs of the tomato *Hind*III physical map. Hence we have both verified their occurrence and carried out a matching test of the new markers on the two contigs. Moreover, a CAPS marker derived from a BAC end sequence pertaining one of the two contigs was integrated into the target window. The whole data obtained so far allowed us to refine with new anchor-points the genetic region spanning 1.2 cM between T0796 and T1143, and to restrict the *Pat*-containing interval to about 0.2 cM.