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.60

A LEAKY ALLELE OF *FALSIFLORA*, THE TOMATO ORTHOLOG OF *LEAFY*, PUTATIVELY UNDERLIES THE MUTATION *PISTILLATE*

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Falsiflora, flower development, flower induction, Solanum lycopersicum

The tomato recessive mutation *pistillate* (*pi*) directly recalls the phenotype of plants disrupted in the function of class B MADS-box genes, because it shows defects on the second and third floral whorl, mainly resulting in ectopic sepal and carpel features respectively. However, after we mapped *Pi* on the distal end of chromosome 3, the hypothesis of its allelism with class B genes was discarded, because none of the latter was compatible with the position of *Pi*. Alternatively, the signs of sepalization on the three inner floral whorls that are recoverable by electron scanning microscopy, coupled with the occurrence of a 'flower within flower' phenotype, suggested that a member of the *SEPALLATA* MADS-box gene family could be responsible for the *pi* phenotype. Again, the available map position of all the tomato members of the class E clade did not coincide with the mapping of *Pi*.

Differently, inside the genetic window containing *Pi* was located the marker *FA*, which turned out to represent *Falsiflora* (*Fa*), the tomato ortholog of the *Leafy* gene in *Arabidopsis* and *Floricaula* in *Antirrhinum*. Accordingly with the function of *Leafy*/*Floricaula* in inducing flowering and conferring flower identity to the meristem, *pi* mutant plants showed delayed flowering time, an increased sympodial segment and frequently a 'leafy' phenotype of the inflorescence. The class B-like phenotype shown by *pi* mutant plants is thus an indirect consequence of the mutation in *Fa* because *Fa*, as *Leafy*, is a positive regulator of class B MADS-box genes. Sequencing of the *Fa* genomic region in a wild-type and a *pi* plant evidenced a T to C transition in the first exon causing a methionine to threonine amino acidic substitution that disrupts a strongly conserved domain. Because *fa* mutant plants, as most of those mutated in orthologous genes in different species, generally do not form complete flowers, the *pi* mutation deserve a particular interest, representing a leaky *fa* phenotype witnessing the functional linkage between flower induction and flower organ identity specification.