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A TOMATO HOMEOTIC MUTANT PUTATIVELY INVOLVED IN THE FUNCTION OF *SEPALLATA* MADS-BOX GENES

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Despite the importance of tomato as a model and crop species, studies on its reproductive biology have lagged behind those that have elucidated the molecular control of flower development in other taxa. Indeed, many floral phenotypes have been described in decades of tomato genetics, but for very few of them the underlying genes have been identified so far. Because the increasing availability of genome sequence data will greatly facilitate forward genetics in tomato, novel descriptive and mapping information will help the attribution of genes to phenotypes. In this contribution, we present our work on *pistillate* (*pi*), a mutant forgotten after the first description of C.M. Rick and J. Robinson in the middle of the last century, that directly recalls mutations affecting B class MADS-box genes.

Plants homozygous for the *pi* allele appear with Mendelian proportions in segregating populations. Compared to wild-type (WT), mutant plants show higher frequency of compound inflorescences, reversion of inflorescence meristem to vegetative identity and frequently a modified sympodial segment. The most striking aberration in *pi* mutant flowers is the homeotic transformation of stamens into carpels. More rarely, homeotic conversions are reported also in the second floral whorl, with staminoid and carpelloid petals. Ultrastructural analysis reveals more or less subtle sepaloid features in the three inner floral whorls, mainly based on the presence, distribution and amount of glandular and non glandular trichomes. In the ovary, a 'flower within flower' phenotype was seldom observed; in one instance such phenotype was coupled with the setting of a parthenocarpic fruit, that contained a new flower inside. Mapping information indicated that none of the tomato class B MADS-box genes can be candidate for the *Pi* locus. Conversely, the complex *pi* phenotype parallels those described in natural or engineered mutants affected in the function of *SEPALLATA* (class E) genes.