

ADVANCES IN THE CHARACTERIZATION OF TOMATO MUTANTS PUTATIVELY AFFECTED IN CLASS B MADS-BOX TRANSCRIPTION FACTORS

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The interested towards male sterile mutants in tomato dates back long time ago due to the perspective of using male sterility (MS) in hybrid seed production. In order to exploit genic MS, the selection of conditional sources, where sterile anthers are be restored to fertility by permissive growth conditions or by the application of appropriate growth regulators, has been regarded as useful strategy. Therefore, mutants with conditional expression, such as *stamenless (sl)*, *stamenless-2 (sl-2)*, *7B-1* and *variable male sterile (vms)*, have been deeply studied in the past. To identify the genes underlying these mutations would be very important in order to pursue the discovery of new alleles by the screening of large mutagenized populations. In this research we describe our recent advances towards this goal. Literature data and examination of the phenotype indicated as candidates for these mutations members of the class B MADS-box transcription factors family, that specify the identity of the second (petals) and third (stamens) floral whorl. In *Arabidopsis thaliana* and *Antirrhinum majus*, this class of genes is composed of only two members that, referring to the *A. majus* nomenclature, are known as *DEFICIENS (DEF)* and *GLOBOSA (GLO)*. In tomato, as in most solanaceae and in other families, these transcription factors both underwent a duplication event followed by subfunctionalization, leading to two *DEF*-like members (*SIDEF* and *SITM6*) and to two *GLO*-like members (*SIGLO1* and *SIGLO2*). Through genetic analysis, we confirmed that the *sl* and *sl-2* mutations are allelic and demonstrated that *7B-1* is also traceable to the same locus. Surprisingly, analysis of two independent mapping populations, one segregating *sl-2* and one segregating *7B-1*, excluded the involvement of these mutants in the *SIDEF* locus on the long arm of chromosome 4, as was earlier reported in the literature. The flower phenotype of the two mutants, similar in that they show nearly normal petals and heavy carpellization of the anther cone, indicates *SITM6*, the paralog of *SIDEF*, as a better candidate for the *Sl/7B-1* locus. Experiments with new mapping populations to confirm this hypothesis are under way. For the *vms* mutant, mapping experiments indicated that it co-localizes with the *SIGLO1* locus on the long arm of chromosome 8. Sequencing of *SIGLO1* in the mutant and in its nearly isogenic wild-type revealed that the mutant carries a transition leading to an E123K residue substitution in the K-domain, a region under strong purifying selection that is involved in protein–protein interaction.