

MALE-STERILE TOMATO MUTANTS FOR POSSIBLE USE IN HYBRID SEED PRODUCTION

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Notwithstanding the autogamous pollination system, hybrid varieties are presently the most widely adopted commercial seed stocks for tomato (*Solanum lycopersicum* L.). While a number of male-sterile mutants have been described, genic male sterility (GMS) has not been the choice material of plant breeders because GMS lines retain the major disadvantage that male-fertile segregants must be rogued out of hybrid seed fields. Therefore, the production of tomato hybrid seed still relies on manual emasculation. One workable solution to harness GMS is the selection of conditional sterility sources, where sterile anthers could be restored to fertility by permissive growth conditions or by the application of appropriate growth regulators. To this end, mutant alleles must be characterized that ensure maximum expressivity in the prohibitive conditions and a good fertility in permissive environments. The molecular characterization of mutants candidate to be used as conditional male-steriles will be extremely advantageous, for developing tools for assisted backcrossing, for discovering new alleles by screening saturated mutagenized populations and for understanding the molecular basis of 'conditionality' in order to modulate it with conventional or biotechnological approaches.

In this research, five tomato mutants showing staminal [*pistillate (pi)*, *stamenless-2 (sl-2)*, *7B-1*, *variable male sterile (vms)*] or functional [*positional sterile-2 (ps-2)*] sterility have been studied at the phenotypic and molecular levels. The expressivity of these mutations in spring conditions has been high, because very scarce or no seed was produced under open pollination. Differently, all the mutants except *pi* produced seed when pollinated with wild-type pollen. For this reason, *pi* was discarded as a possible source of male sterility for hybrid seed production. Mapping studies on the five genes integrated all the loci into the tomato molecular map. Comparison with the map location of the sequences corresponding to tomato class B MADS-box genes indicated *vms* as a candidate for being involved in the *SIGLO* locus, whereas *Sl-2* and *7B-1* were candidate to correspond to the *SIDEF* gene. These results provide the basis for unraveling the genetic and molecular mechanisms controlling male sterility/fertility in the studied genotypes and to pursue their exploitation in hybrid seed production.