Hormonal regulation of floral organ development in the tomato (*Solanum lycopersicum* L.) mutant *stamenless*

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Extensive genetic and molecular studies have led to the broadly accepted ABCE model of flower development. Floral homeotic genes encoding transcription factors combinatorially specify organ identity in each floral whorl. However, less is known regarding how these genes control changes at the cellular level during floral organ formation. Phytohormones have been suggested to play a role as transducers of genetic information during floral development in model species. We investigated the hormonal regulation of floral organ development in a tomato (*Solanum lycopersicum* cv. Primabel) B class mutant - *stamenless* (*sl-Pr*) - that exhibits homeotic conversion of petals into sepals and stamens into carpels. This phenotype results from mutations in the coding sequence of one of the four tomato B class genes, namely *Tomato APETALA3* (*TAP3*). Expression analyses showed that the *sl-Pr* mutation does not affect the other B gene expression in the tomato flower. Treatments with phytohormones revealed that gibberellins could partly revert the *sl-Pr* phenotype but affected neither the *SL* (*TAP3*) nor the other ABCE gene expression. Quantification of endogenous polyamines and phytohormones content in the Primabel cv. and *sl-Pr* mutant tomato flowers along their development showed that the *sl-Pr* mutation reduced gibberellins, auxins, cytokinins, salicylic acid, spermine and tyramine concentrations and increased jasmonic acid and abscisic acid in tomato flowers. To further investigate the hormonal control of the tomato floral organs, we compared the expression of genes coding for enzymes involved in the metabolism of the different class of phytohormones in the four floral organ whorls of Primabel cv. and *sl-Pr* mutant flowers. Together, our results revealed a role of phytohormones in flower development downstream of the *SL* (*TAP3*) gene in tomato.