

## **A POINT MUTATION IN THE HD-ZIP III TRANSCRIPTION FACTOR SLCORONA/SLHB15 UNDERLIES THE PHENOTYPE OF THE PARTHENO-CARPIC FRUIT (PAT) TOMATO MUTANT**

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*fruit development, parthenocarpy, tomato, HD-Zip transcription factors, ovule development*

Parthenocarpy entails fruit set independently of pollination and fertilization, allowing fruit production under pollen-limiting environments and in sterile genotypes. It also represents a fruit quality trait because it leads to seedlessness and is often associated with further positive qualitative aspects. Among the sources of genetic parthenocarpy described in tomato, the *parthenocarpic fruit (pat)* mutation showed strong expressivity, high fruit set and enhanced fruit quality. The complexity of the *pat* “syndrome” associates to parthenocarpy pleiotropic effects in the vegetative and floral phenotype, involving stamen and ovule developmental deviations. Fine mapping located the *Pat* locus within a 0.19 cM window on the long arm of Chr3, comprising nine annotated genes. By comparative analysis, a class-III HD-Zip gene ortholog to *CORONA/HB15* in Arabidopsis (*SIHB15*) was identified as the best candidate. Functional validation of the involvement of *SIHB15* in the *pat* mutation was obtained by detecting phenotypes of Arabidopsis orthologous mutants, of co-suppressed plants and of lines edited in *SIHB15* with CRISPR/Cas9 technology. In knock-out lines, parthenocarpy was extremely strong and further research is ongoing to assess permissive seed production conditions. This research set a link between parthenocarpy and the class-III HD-Zip transcription factor family, which has been involved in several developmental processes such as vasculature development and hormone homeostasis.