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

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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 guality trait because it leads to seedlessness and is often associated with further positive qualitative aspects. Among the sources of genetic parthenocarpy described the *parthenocarpic fruit* (*pat*) in tomato, 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 ( SlHB15) was identified as the best candidate. Functional validation of the involvement of SlHB15 in the pat mutation was obtained by detecting phenotypes of Arabidopsis orthologous mutants, of co-suppressed plants and of lines edited in SlHB15 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 involved in several developmental processes such has been as vasculature development and hormone homeostasis.