

## **PHENOTYPIC COMPARISON OF CRISPR/CAS9 TOMATO MUTANTS TARGETING GENES RESPONSIBLE FOR THE BIOSYNTHESIS OF STRIGOLACTONES**

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*strigolactones, tomato, CRISPR/Cas9, phenotypic comparison, broomrapes*

Strigolactones (SLs) are carotenoid-derived molecules recently identified as phytohormones, which contribute in multiple ways to plant architecture and development. They intervene in the plant response to phosphorus and nitrogen starvation, inhibiting secondary branching, determining substantial modifications of the root system, and also favouring the interaction with arbuscular mycorrhizal fungi (AMF). In addition to these beneficial roles, SLs released in the rhizosphere also serve as the main germination stimulus for the seeds of parasitic plants. Four major genes – *D27*, *CCD7*, *CCD8* and *MAX1* – are involved in the biosynthesis of SLs in tomato. A phenotypic comparison programme is underway on a panel of independent CRISPR/Cas9 mutant lines with the same genetic background, for each of the four target genes.

Morphological (e.g., root and shoot architecture), reproductive (e.g., flowering time, pollen viability), productive (e.g., fruit set, fruit weight) and qualitative (e.g., shelf-life) traits were taken into account. Moreover, a biochemical analysis of root exudates and root extracts was performed together with an in vitro pathogenicity assay, to determine SL

content and susceptibility to *Phelipanche agegyptiaca* and *P. ramosa*, two of the most relevant parasitic weeds in tomato. Additionally, the interaction with AMF *Glomus intraradices* was also assessed to characterize the response of edited plants to mycorrhization.