

FUNCTIONAL CHARACTERIZATION OF A TOMATO SYNTAXIN INVOLVED IN THE INTERACTION WITH POWDERY MILDEW FUNGI

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syntaxins, host resistance, non host resistance, powdery mildew

Syntaxins are involved in highly regulated biological functions involving dynamic membrane trafficking. Arabidopsis *PEN1* and its barley and grapevine orthologs, encoding for syntaxins of the SNARE domain superfamily, were shown to play a crucial role in host and non-host defence mechanisms against powdery mildew pathogens. In this study, an evolutionary analysis pointed out the presence of two genes (named *SIPEN1a* and *SIPEN1b*) in the tomato genome closely related with syntaxin-encoding genes involved in plant-pathogen interactions. Transgenic RNA interference technology was used for the functional characterization of *SIPEN1a* and *SIPEN1b*. We found that silenced *SIPEN1a* T₂ individuals display higher penetration of the powdery mildew fungus *Oidium neolycopersici* and impair previously effective host resistance based on the loss-of-function of the susceptibility factor *SIMLO1* (known as *mlo*-based resistance). *SIPEN1b* silenced plants also display slightly higher fungal penetration, although this difference resulted to be not significant. Histological analysis following inoculation with the non-host pathogen *Blumeria graminis* f. sp. *hordei*, causing disease on barley, also indicated increased penetration in *SIPEN1a* silenced epidermal cells, and a consequent higher rate of infection units in which the pathogen is arrested by means of post-penetrative defense mechanisms. Our findings reveal that at least one tomato syntaxin is functionally related with others previously associated with plant-pathogen interactions. Differently from Arabidopsis and similarly to barley, the impairment of a single syntaxin is sufficient to disrupt *mlo*-based resistance.