

Exploring TAL effectors diversity in common bacterial blight causative agents as a tool to identify targets for improving resistance in common bean

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Common bacterial blight (CBB), caused by *Xanthomonas* spp., is responsible of significant yield losses in common bean (*Phaseolus vulgaris*). Transcription Activator-Like (TAL) effectors produced by these pathogens are pivotal in disease development by modulating host plant gene expression. This study explores the diversity of TAL effectors in *Xanthomonas* spp. strains responsible for CBB, aiming at identifying potential targets for developing resistant common bean cultivars. We sequenced a strain isolated in Italy using Nanopore platform and predicted its TAL effector genes. Moreover, we predicted TAL effector genes using all NCBI available genome assemblies that were obtained through long-read sequencing technologies. Our preliminary results led to the discovery of several new TAL classes in *X. phaseoli* pv. *phaseoli*, indicating a high diversity of TAL effectors among the strains. These new TAL classes are putatively targeting key genes involved in plant defence responses. Future validation of the targets identified in this study will provide crucial insights for breeding varieties with enhanced resistance. Target host genes will be explored in the future for their function in a mutagenized population recently developed on a commercial variety.