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Structural genomics of *Xanthomonas citri* subsp. *malvacearum*

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Abstract:

Cotton (*Gossypium* spp.) is a fiber cash crop extensively sown throughout the world. At the Northeast of Brazil, for example, cotton yields are highly valuable for export. However, in the last years, the producers have been challenged by the maintenance costs of the plant. Once that diseases and pests significantly reduce cotton yield, and a phytosanitary control must be implemented. The co-evolution between plants and microbes has contributed to the development of the immune system. Hence, PTI (PAMP-triggered immunity), ETS (Effector-triggered susceptibility) and ETI (Effector-triggered immunity). In plant pathogenic bacteria, type III effectors (T3Es) play a crucial role in pathogenicity, mainly against Gram-negative bacteria. Bacterial blight of cotton is incited by *Xanthomonas citri* subsp. *malvacearum*, a disease responsible for large losses of cultivars. The symptoms observed include angular leaf spot, systemic vein blight, black arm (of petioles and main stems), boll shedding, and internal boll rot. Chemicals products used to treat the disease present low efficacy and pollute the environment. Therefore, targeting the group of effectors like Xops (*Xanthomonas* outer proteins) constitutes a significant approach for the generation of more resistant plants. In this context, this study aims to identify and characterize Xops genes in genomes of *X. citri* subsp. *malvacearum*. Therefore, we selected seven genomic sequences of *X. citri* subsp. *malvacearum* in Genbank (NCBI database). Afterward, an automatic annotation was carried out using RAST (Rapid Annotation using Subsystem Technology) tool followed by manual curation. Further, we intend to obtain the structural characterization of Xops through modeling tools. During the automatic annotation (RAST), we found some plasmids and transposable elements, which explains their high genetic variability. Also, we suggested virulence genes that are implicated in plant-pathogen interaction. It will be possible to characterize genes and proteins of *X. citri* subsp. *malvacearum*, and which may subsequently be used, as targets for the control of the disease in the Brazilian Northeast.