

Analysis of genomic islands of virulence and pathogenicity in *Xanthomonas campestris*

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Abstract

Brazilian viticulture activity has remarkably increased in the northeastern region of the country over the last years. However, significant losses have occurred due to the local climate rough conditions that raise susceptibility of grape vine species such as *Vitis vinifera* to bacterial infections. In this context, *Xanthomonas campestris* pv. *viticola*, a Gram negative aerobic pathogenic bacteria, is associated with bacterial canker and many other phytopathologies, due to factors such as xanthomonadin and xantham gum production. Since it was first isolated from an Indian viticulture in the 70's, extensive studies have tried to elucidate how to control *X. campestris* pv. *viticola* infections in grape vine. Nevertheless, there is still a shortage of information regarding the molecular mechanisms and the acquisition of virulence genes in this organism. Therefore, we believe that identifying and exploring genomic content from *Xanthomonas campestris* strains would improve knowledge concerning its pathogenicity and help develop future approaches to control the disease. Pathogenicity islands (PAI) are described as a set of virulent genes which have been horizontally transferred among Eubacteria, providing the organism with the ability to cause pathologies. In this sense, we aimed to identify genes that are present in PAIs from *X. campestris* pv. *viticola*. For automatic annotation process, seven complete genome of *X. campestris* pv. *campestris* strains obtained from National Center for Biotechnology Information (NCBI) genome database were submitted on Rapid Annotation using Subsystem Technology (RAST). Afterwards, the annotated genomes were analyzed on Seed viewer and Artemis. Finally, Genomic Island Prediction Software (GIPSy) and Islandviewer4 were used to provide a better prediction view and analysis of PAIs. We show that almost 45% of genome can be annotated using subsystems and that 77 genes are directly related to virulence, defense mechanisms and disease activity. The proteins encoded by these 77 genes were divided in two basic subcategories: antibacterial peptides and resistance to toxic compounds and antibiotics related to copper homeostasis. In summary, we reveal that the genomes of all seven *Xanthomonas* strains are very similar to each other but do possess relevant differences in terms of genes encoding pathogenicity factors. Moreover, there are high expectations for finding a resembling pattern on *X. campestris* pv. *viticola*, making possible the development of genetic improvements of plants, without the use of chemical agents.

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