Xylella fastidiosa comparative genome analyses provide insights into pathogen-plant interaction

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Xylella fastidiosa infects a wide range of plant hosts and causes severe plant diseases such as Citrus Variegated Chlorosis (CVC) and Pierce's Disease (PD) of grapevine. This Gram-negative bacterium is transmitted to new host plants during xylem sap feeding by sharpshooter vectors and once inside the xylem vessel, *X. fastidiosa* proliferates as a biofilm along the xylem wall. In susceptible plants, leaf scorching, chlorotic leaf spots, shoot dwarfing, fruit dehydration and plant stunting are among the disease symptoms. Conversely, *X. fastidiosa* is capable of colonizing a large number of host plants asymptomatically. Several determinants have been implicated in the *X. fastidiosa* pathogenicity and virulence such as fimbrial and afimbrial adhesins, cell-wall degrading enzymes, type-4 pilus-dependent motility and signaling mediated by small diffusible molecules, most of these revealed through the genome sequences of 9a5c and Temecula-1 strains, causal agents of CVC and PD, respectively. Genomes of other *X. fastidiosa* strains isolated from distinct plant hosts in South and North America (grapevine, citrus, almond tree, oleander, elderberry, coffee, plum, hibiscus) have been recently sequenced. In this presentation I will review the differences in these genomes that correlate with the distinct phenotypes displayed by these strains *in vitro* and *in planta*, such as virulence, adhesiveness and motility of bacterial cells[1,2]. I will also discuss differences among *X. fastidiosa* genomes that can potentially impact host specificity. Our pan-genome studies showed that *X. fastidiosa* has an open genome and that most of mobile genetic elements (MGE)-encoded genes correspond to accessory genes. The comparative genome analyses we have performed revealed the diversity of MGE-related regions, which appear in larger numbers in South American strains. Particularly noteworthy, is the lack of a complete CRISPR-cas system in *X. fastidiosa* genome, which might explain the large number of prophage regions in relation to other *Xanthomonadacea* members. Finally, the phylogenetic comparisons by both phylogenomic and MLSA methods show that strains from North and South America are divided in two well-defined clades.

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References: [1]Pierry, P. M. 2012. Pirossequenciamento e análise comparativa de genomas do fitopatógeno *Xylella fastidiosa*. Dissertação de Mestrado; [2]de Santana, W. O. 2012. Genômica comparativa de *Xylella fastidiosa*: diversidade do pangenoma e análise de genes de patogenicidade. Tese de Doutorado.