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. 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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