

## COMPARATIVE GENOMICS OF *XYLELLA FASTIDIOSA* SOUTH AMERICAN STRAINS

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**Reporting Period:** The results reported here are from work conducted August 2009 to October 2010.

### ABSTRACT

Using DNA microarray hybridization we have previously identified significant differences in gene composition between *Xylella fastidiosa* (*Xf*) CVC (Citrus Variegated Chlorosis) strains 9a5c and J1a12<sup>1</sup>. Strain 9a5c exhibit virulent phenotype both in citrus and in hosts used as models of infection while strain J1a12 displays less virulent phenotype in citrus and tobacco. The genomic differences identified include the absence or high divergence of 14 coding sequences in the genome of J1a12, which correlates with its less virulent phenotype. To deepen the comparison between virulent and less virulent CVC strains, as well as between strains isolated from infected plants in South America, we are conducting a project aiming the complete genome sequencing and comparison of several *Xf* strains. Through the comparison of these new genomic sequences with known genomes of other *Xf* strains as well as other phytopathogens we hope to enlarge the knowledge of the repertoire of genes potentially associated with evolution, adaptation to hosts, pathogenicity and virulence. Currently, we have sequenced the genomes of four strains (J1a12, U24d, Fb7 and 3124). Strains U24d and Fb7 were isolated from citrus plants with symptoms of CVC, respectively in the State of São Paulo (Brazil) and Argentina. Strain 3124 was isolated from a coffee plant with leaf scald symptoms. Initial analysis of these four new genomes confirm the previously observed differences between the genomes of J1a12 and 9a5c and allowed identification of additional differences between the genomes of J1a12 and 9a5c, including sequences that are apparently unique J1a12. Among these differences is the presence of an additional 27,258 bp plasmid that has not been described in other citrus isolates and shows extensive identity with the recently described plasmid from *Xf* mulberry-infecting strains<sup>2</sup>. Moreover phylogenetic trees based on multiple loci, separate, as expected, the strains from North and South America into distinct groups and suggest the occurrence of a higher frequency of genetic recombination between South American strains.

### REFERENCES CITED

- 1 Koide, T. *et al.* DNA microarray-based genome comparison of a pathogenic and a nonpathogenic strain of *Xylella fastidiosa* delineates genes important for bacterial virulence. *J Bacteriol* 186, 5442-5449 (2004).
- 2 Stenger, D. C., Lee, M. W., Rogers, E. E. & Chen, J. Plasmids of *Xylella fastidiosa* mulberry-infecting strains share extensive sequence identity and gene complement with pVEIS01 from the earthworm symbiont *Verminephrobacter eiseniae*. *Physiological and Molecular Plant Pathology* 74, 238-245 (2010).

### FUNDING AGENCIES

Funding for this project was provided by Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), and Financiadora de Estudos e Projetos (FINEP)