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Xylella fastidiosa comparative genomics

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Summary

Comparison of the genome sequences of *Xylella fastidiosa* strains reveals new drug targets

Significance and context

The Gram-negative plant pathogenic bacterium *Xylella fastidiosa* is responsible for economically important diseases in grapevine and citrus. These include, for instance, citrus variegated chlorosis, which affects all commercial sweet orange varieties. Symptoms include variegations on older leaves with chlorotic zones and brownish lesions with gum-like material. Affected fruit has no commercial value. In grapevines, *X. fastidiosa* may cause the so-called Pierce disease. *X. fastidiosa* is transmitted by sharpshooter leafhopper, and treatment of the disease is currently based mainly on the use of insecticides and the removal of infected shoots. *X. fastidiosa* also causes leaf scorch on oleander and almond. Bhattacharyya *et al*. compared the draft genome sequences of the *X. fastidiosa* strain XFY (*X. fastidiosa* pv. oleander) and XFX (*X. fastidiosa* pv. almond) with the previously published genome sequence of XFA (*X. fastidiosa* pv. citrus).

Key results

The genome sequences contained 2,731,748 (XFA), 2,625,581 (XFY) and 2,434,849 (XFX) base-pairs (bp). The G+C content was about equal for the three genomes at 52%. The genomes contain 2,985 (XFA), 2,870 (XFY) and 2,681 (XFX) open reading frames (ORFs), 58%, 62% and 62% of which were assigned functions. The XFY and XFX genomes contain a plasmid, of 30,270 and 51,158 bp, respectively, with a slightly lower G+C content of about 49%. The XFY plasmid carries genes encoding a type IV secretion system, a putative transcription regulator and a nickase. Pathway analysis revealed that the genomes contain 958 (XFA), 965 (XFY) and 938 (XFX) pathways. Compared to the genome of XFA, some functions were missing in the other two genomes. These include functions involving ribosomal SSU (1 missing in XFY, 10 missing in XFX), ribosomal LSU (4 missing in XFY, 17 missing in XFX), and aminoacyl-tRNA (1 missing in XFY, 2 missing in XFX). In addition, it was suggested that all *X. fastidiosa* strains possess a simple aerobic respiratory complex, enabling aerobic respiration only under high oxygen concentrations. No indications of the presence of a cytochrome *c* oxidase or other type of quinol oxidase as terminal oxidases were noticed. Thus, because cytochrome *o* (*bo*) ubiquinone is the only terminal oxidase present in these bacteria, it would be a suitable candidate drug target.

Functional reconstruction using data revealed by the genome sequence, enabled growth media to be developed on which *X. fastidiosa* strains were more easily cultivated.

Links

The website of the *Xylella%20fastidiosa*%20genome%20project provides updates of the project, and the complete proteome is available from EMBL-EBI%20databases:%20proteome%20analysis.

Reporter's comments

Bhattacharyya *et al*. compared the genome sequences of three plant pathogenic *X. fastidiosa* strains and performed a functional reconstruction to deduce new growth medium compositions that may facilitate the cultivation of those bacteria. New functions were revealed that might be involved in host-range determination and in plant pathogenicity. Extensive mutant screening, and phenotypic and biochemical analyses will be required to pinpoint pivotal functions for survival of *X. fastidiosa* strains in soil and infection of agronomically important crops. This may uncover bacterium-specific drug targets that can be used to protect crops against these severe plant pathogens.

Table of links

Genome%20Research

Xylella%20fastidiosa%20genome%20project

EMBL-EBI%20databases:%20proteome%20analysis

References

1. Bhattacharyya A, Stilwagen S, Reznik G, Feil H, Feil WS, Anderson I, Bernal A, D'Souza M, Ivanova N, Kapatral V, et al: Draft sequencing and comparative genomics of *Xylella fastidiosa* strains reveal novel biological insights. Genome Res. 2002, 12: 1556-1563.