Molecular Biology Today 2001. 2(3): 33-43.

Genome and Pathogenicity of *Xylella fastidiosa*

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Abstract

The complete sequencing of the *Xylella fastidiosa* genome was the first project of this kind to focus on a plant pathogen. The choice of this bacteria was tightly associated with its importance as the causal agent of citrus variegated chlorosis (CVC). Adopting a sequencing strategy based on shotgun and cosmids, the project allowed a 10 fold coverage of the genome. The specific mechanisms of pathogenicity are not yet clear while the annotation of the genome took in consideration several hypothesis. Based on the current pathogenicity hypothesis, the genes were sorted into different categories with special focus on those associated with attachment to bacterial cells and different hosts, as well as genes related to the adaptation capacity to the xylem conditions. Genes previously found only in animal pathogens were also observed in *X. fastidiosa*, suggesting that they could share some of the pathogenicity mechanisms.

Introduction

Xylella fastidiosa was the first plant pathogen to have its full genome sequenced (Simpson *et al.*, 2000). In a cooperative effort of 32 laboratories in the ONSA (Organization for Nucleotide and Sequence Analysis) network supported by FAPESP this important pathogen for citrus, grape, plum and other species was chosen to be a model for genomic studies in Brazil. After the sequencing of 23 complete bacterial genomes, this project pointed out the need for acceleration of such studies in plant pathology.

Known for its prolific growth and broad range of hosts*, X. fastidiosa* became a serious problem in Brazil when it was definitively associated with citrus variegated chlorosis (CVC), one the most destructive citrus diseases in the world (Rossetti *et al.*, 1990). As an agent of other important diseases, such as Pierce's disease specific to grape, this bacterium has been a difficult to control due to its restricted growth in the xylem vessels, its ability to survive within tissues used for vegetative propagation, and the efficient vector for dispersion plant to plant in the orchard.

This review will point out the most relevant aspects associated with its pathogenicity. Although specific mechanisms of pathogenicity are not yet clear, the annotation of the genome took in consideration several hypothesis. These hypothesis could explain why the bacteria are able to attach to surfaces, i.e, its ability to interact with surfaces and to spread within the plant, specifically in the xylem causing disease symptoms. All the genes mentioned in the text are listed in Table 1. Detailed annotation of the complete genome can be found in the *Xylella* database at NCBI or at University of Campinas (http://onsona.lbi.ic.unicamp.br/xf/). Aspects associated with disease epidemiology, interaction with vectors, hosts and other information can be found in more specific reviews (Purcell and Frazier, 1985; Hopkins, 1989; Hopkins, 1995).

Hypothesis of Pathogenicity

As a xylem-limited bacterium *X. fastidiosa* has developed survival mechanisms for living in adverse conditions including water stream turbulence at negative pressure, and low availability of nutrients,

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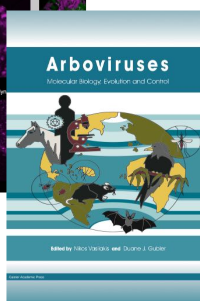

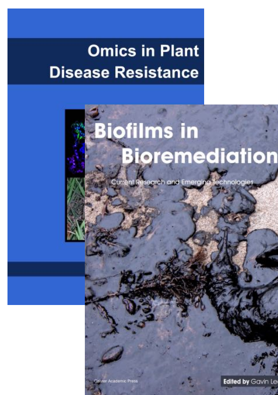

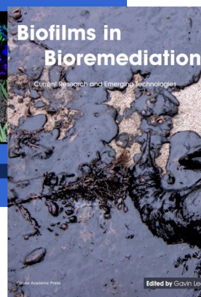

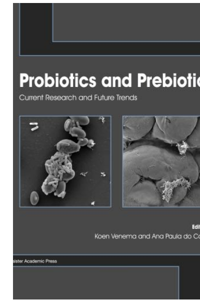

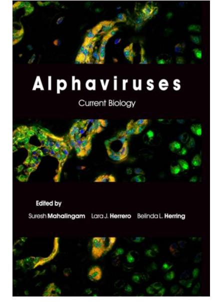

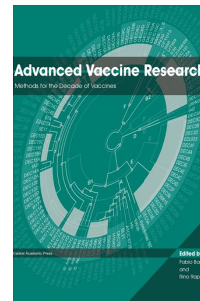

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such as nitrogen and carbon sources. These conditions, associated with the bacteria production of toxins and ability to spread within the plant, appear to be correlated with its pathogenicity (Hopkins, 1995). The bacteria seem to be able to interact with surfaces (xylem wall and other bacterium cells), uptake nutrients efficiently from the xylem sap, and produce compounds (toxins or enzymes) capable of active interaction with the plant tissues. The most accepted hypotheses of pathogenicity are based on the following mechanisms:

Occlusion of the Xylem Vessel

Scanning electron images show bacteria embedded within an amorphous extra-cellular matrix, probably consisting of extracellular polysaccharides (EPS) attached to the xylem wall or the cibarium of the vector (Brlansky *et al.*, 1983; Chagas *et al.*, 1992). The development of water stress in affected plants, specifically citrus trees, suggests the occurrence of xylem blockage (Hopkins, 1989, 1995; Goodwin *et al.*, 1988; Machado *et al.*, 1994). EPS, fimbriae, and adhesins are involved in the adhesion of bacteria-bacteria, bacteria-plant. These are essential in building up aggregates that cause occlusion in the xylem (Hopkins, 1995). The aggregates of colonies within the xylem not only promote obstructions, but also allow the colonization of the xylem up and down stream. In addition, the occlusions prohibit the free movement of nutrients in the sap and function as a filter, concentrating available nutrients for the bacteria.

Nutritional Competition

The bacterium lives in the xylem vessel obtaining all nutritional requirements from the sap, whose composition changes according to the age of the plant and the environmental conditions. This causes a competition for nutrients between the bacteria and the plant that can give rise to nutritional disturbances in the leaves, branches and fruit. It should be pointed out that the typical symptoms of iron, copper, magnesium and manganese deficiency in citrus trees are similar to those caused by *X. fastidiosa*. The bacterium efficiently uptakes carbon and nitrogen compounds and inorganic compounds essential for its metabolism from the xylem sap. Organic acids, aminoacids, amines, ammonium, nitrate, sulphate, cations (Mg, Ca), minor elements (Fe, B, Zn, Mn, etc), and plant regulators are the most prevalent compounds in the xylem sap.

Intervessel Migration

Although several species of sharpshooter leafhoper vectors (Cicadelideae) seem to transmit the bacteria efficiently, not all the vessels are uniformly infected. On the other hand, the bacteria seem to have the capacity to migrate laterally and in certain cases, such as Pierce´s disease and plum leaf scald, the uniformity required for pathogenicity may be explained by intervessel migration. Both multiplication / colonization and migration within the vessel have been related to pathogenicity (Hopkins, 1985). The production of exo-enzymes such as cellulases and pectinases, allows colonization of lateral vessels after degradation of pit membranes and may also represent an additional way of obtaining small carbohydrates molecules.

Production of Toxins

Symptoms resembling disturbances caused by exogenous toxins or disruption in plant regulators are visible in the leaves and fruits of several species infected with *X. fastidiosa*. EPS, such as xanthan gum and toxins such as bacteriocins and RTX are produced by several Gram negative bacteria. These may disrupt cells and organelles inducing the development of symptoms such as chlorosis, or affecting growth and development of the tree. It is reasonable to suppose that such toxins especially those from bacteria living within xylem vessel could affect tissues and organs above the colonization area.

Interactions with Surfaces

Adhesion and persistence of the pathogen, in spite of host defense factors, could be the key to pathogenicity during development of the disease (Costerton *et al.*, 1981). Extracellular polysaccharides (EPSs) and adhesins (pili and non-pili formation) in plant bacteria have been related to their survival, colonization and adhesion to host tissues.

Besides electrostatic forces generated by the charged surfaces of the bacteria and the plant cell wall, the habitats of *X. fastidiosa* (the xylem vessel and the foregut system of the vectors) are characterized by high turbulence and low nutrient concentration. Thus, the colonization of such specific habitats is probably mediated by an efficient mechanism of attachment to other bacteria and to the surfaces of the hosts. According to Hopkins (1989; 1995), extracellular strands such as fibrous microfibrils, fimbriae, and EPS, are considered to be the major component of the dense matrix of *X. fastidiosa* within the vessels (Brlansky *et al.*, 1983). This matrix was also verified in xylem vessels of citrus trees with CVC symptoms (Chagas *et al.*, 1992).

EPS

Extracellular polysaccharides are normally produced by species of *Erwinia*, *Pseudomonas* and *Xanthomonas* (Denny, 1995), causing plant diseases such as wilt by blocking xylem vessels. This polymer is also required for colonization and enhances the pathogen survival within host tissues by acting as a protection mechanism against environmental stress (Király *et al.,* 1997).

Gum gene cluster similar to the xantham gum of *Xanthomonas campestris* pv campestris (Xcc) (Becker *et al*., 1998) was identified in the *X. fastidiosa* genome, but lacking the genes *gum*I, *gum*L and *gum*G (Figure 1). The absence of *gum*I (glycosyltransferase V) should not allow the incorporation of a terminal mannose to the polymer. Consequently, the addition of pyruvate by the ketal-pyruvate transferase enzyme (*gum*L) and acetyl group (*gum*G - acetyl transferase II enzyme) should also not occur. Mutations in *gum*I produce a less viscous polytetrameric gum (Leigh and Coplin, 1992).

Pili and Non-pili Structures

Bacterial adhesion to host tissues is usually mediated by adhesins occurring on the cell surface. These adhesins can either be assembled in structures like pili or fimbriae, or directly associated with the microbial cell surface, so called non-pili adhesins (Soto and Hultgreen, 1999). The genes responsible for the assembly of such structures and their importance in human and animal pathosystems are well-characterized (Soto and Hultgreen, 1999). In contrast, the importance of fimbrial structures to the plant pathogenic process is not yet well determined (Romantschuk, 1992). The functions of type-4 pili structures that are more related to pathogenicity are adhesion to host cell surface, adhesion bacteria-bacteria and twitching motility, a form of surface translocation of bacteria (Hahn, 1997; Kirov *et al.*, 1999).

X. fastidiosa contains ORFs encoding pili and non-pili adhesins. Out of more than 30 genes involved in the type-4 fimbriae synthesis, 26 were detected in its genome (Table 1). Among them are *pil*E, which encodes the pilin-like protein, and the *pil*S and *pil*R genes that control the transcription of fimbrial subunits (Hobbs *et al*., 1993). Moreover, genes that act in response to some environmental signal regulating pilus biosynthesis and movement of bacteria (*pil*G, H, I, and J) (Alm and Mattick, 1997) are also present.

Alginate, an exopolysaccharide that causes cells to become mucoid, is another determinant virulence factor in *P. aeruginosa* (Schurr *et al*., 1994), and *P. seringae* pv seringae (Yu *et al*., 1999). The alginate gene *alg*R encodes a non-pili adhesin similar to both the *hsf* gene product *of H. influenzae* (St Geme, 1996), and to the *usp*A1 gene product of *Moraxella catarrhalis* (Cope *et al*., 1999). Homologues to these genes are present in *X. fastidiosa* and encode adhesins, non-pili structures that are directly associated with the bacterial cell surface. Filamentous hemagglutinins, structures related to bacterial adhesion, were identified in the *X. fastidiosa* genome. Three genes (*psp*A) with homology to hemagglutinin-like structures from *Neisseria meningitidis* were observed. This was the first time that a hemagglutinin was identified in a phytopathogenic bacteria.

Plant Cell Wall Degradation

Like many plant pathogens, *X. fastidiosa* seems to produce an array of enzymes capable of hydrolyzing components of plant cell wall. The importance of such enzymes in pathogenicity has been reported (Hopkins 1985, 1995). The extracellular enzymes are not only important for nutrition but they also play an essential role in lateral vessel to vessel movement since they are responsible for degradation of

pit membranes. The ability of the bacteria to move through the vessels has been pointed out as a key element in pathogenicity. Some avirulent strains of Pierce´s Disease (PD) grow well in culture, but are not able to move through the xylem (Hopkins, 1985). In the genome of *X. fastidiosa* several genes coding for cell wall degradation enzymes were identified.

Cellulases

Microbial cellulose degradation usually involves enzymes of two major types: ENGs (endo-1,4-b-glucanases) and EXGs (cellobiohydrolases). ENGs cleave internal b-1,4-glucosidic bonds, whereas EXGs cut the dissaccharide cellobiose from the non-reducing end of the cellulose polymer chain. These enzymes show different types of synergy when hydrolyzing crystalline cellulose (Henrissat *et al.*, 1985; Meinke *et al.*, 1994). *X. fastidiosa* has three ORFs similar to ENGs and one to EXG.

Endo-1,4-b-Glucanase

Two ORFs with strong similarity to genes encoding extracellular endoglucanases (*eng*XCA) of Xcc were found in *X. fastidiosa*. However, the *X. fastidiosa* protein shows a Glu/Ser rich region instead of Thr/Pro (Knowles *et al.*, 1987), which could be a potential site for proteolysis. A third ORF encoding ENG is similar to *egl* of *Ralstonia solanacearum*. The *egl* mutant produced at least 200-fold less endoglucanase than the wild-type strain suggesting that other glucanases are produced at very low levels. This EGL-deficient strain was significantly less virulent than the wild-type strain on tomato plants (Roberts *et al.*, 1988).

Cellobiohydrolases

A similar ORF of exocellobiohydrolase A (*cbh*A) of *Cellulomonas fimi* was found. The structure and activity of the *cbh*A catalytic domain are closely related to those of CBH II, an exocellobiohydrolase from the fungus *Thichoderma reesei* a key enzyme in the hydrolysis of crystaline cellulose. CbhA was the first enzyme of this kind to be characterized in bacteria (Meinke *et al.*, 1994; Wood and Garcia-Campayo, 1990).

Pectinases

A wide range of fungal and bacterial plant pathogens produce pectolytic enzymes (pectate lyase, pectin lyase, and exopolygalacturonate lyase) that cleave by b-elimination. On the other hand, polygalacturonase and exo-poly-a-D-galacturonosidase cleave by hydrolysis (Collmer and Kenn, 1986). In the genome of *X. fastidiosa*, an ORF similar to the polygalacturonase genes of different organisms was found. The greatest similarity was found with the gene *pgl*A (polygalacturonase) *of R. solaneacearum* (Huang and Shell, 1990). However, in this ORF of *X. fastidiosa* there is a frameshift suggesting it is nonfunctional.

Glycoside Hydrolase

An ORF showing partial homology with the *xylA* gene of *Ruminococcus flavefaciens* is also present in the *X. fastidiosa* genome. It codes for the family 3 glycosyl hydrolase (Henrissat *et al.*, 1989). BLASTp searches using this protein resulted in partial hits with several b-xylosidases and b-glucosidases from different organisms including bacteria and fungi (La Grange *et al.*, 1997; Goyal and Eveleigh, 1996).

Regulator of EPS and Extracellular Enzymes

The synthesis of extracellular enzymes and EPS in Xcc is subject to co-ordinated regulation by a cluster of genes called *rpf* (regulator of pathogenicity factors) (Dow *et al.*, 2000). The biosynthetic regulation of extracellular enzymes and EPS in *X. fastidiosa* may occur in a way similar to Xcc, since several of these genes were detected. ORFs similar to *rpf*A and *rpf*B are found in close proximity to one another in the *X. fastidiosa* genome, but they are not arranged in cluster as in the Xcc genome. The *rpf*A gene codes for a bifuncional protein which acts as an aconitase at high iron levels and at low iron concentration works as a regulatory protein (Wilson *et al.*, 1998). The *rpf*B and *rpf*F genes are required for a small molecule-mediated pathway, these genes represent a mechanism for regulating virulence factor synthesis in response to physiological or environmental changes (Barber *et al.*, 1997). An ORF

similar to *rpf*F is present in *X. fastidiosa*, and as in Xcc, it is adjacent to *rpf*C and other genes present in the cluster (Figure 2). The *rpf*C, *rpfG* and *rpfH* genes encode components of a "two-component" phosphorelay system (Barber *et al.*, 1997) which is involved in regulating gene expression in response to environmental stimuli (Tang *et al.*, 1991). The *rpf*G gene was detected in the *X. fastidiosa* genome downstream of *rpf*C but there is no ORF similar to *rpf*H. More recently eight other genes belonging to the *rpf* cluster of Xcc were identified (Dow *et al.*, 2000). Two of these genes, *rec*J and *gre*A, have functions in recombination and transcriptional elongation, respectively. Mutation in *rpf*D had minor effects on the production of extracellular enzymes and EPS. Mutation of *rpf*E leads to a reduction in the levels of endoglucanase, protease, and EPS, but there is an increase in polygalacturonate lyase. Mutation in *orf*4 had no effect on polygalacturonate lyase, but reduced the levels of protease and endoglucanase. However, *orf*1, 2, and 3 mutations did not affect the synthesis of extracellular enzymes or EPS. In the genome of *X. fastidiosa*, ORFs similar to *rpf*D, *orf*1, 2, 3, and 4 were not found. Nevertheless, ORFs highly similar to *rec*J, *rpf*E, and *gre*A were detected in cluster. The absence of some genes may be related to absence of some extracellular enzymes or components of the EPS biosynthesis machinery of *Xylella.*

Biosynthesis of Toxins and Antibiotics

Although the production of toxins and/or antibiotics can not always be associated with pathogenicity, their presence increases virulence and severity of symptoms. Toxins can be important in the development of plant diseases, mainly for the establishment of the pathogen within the plant and development of symptoms, like chlorosis and necrosis.

Hemolysin

Hemolysin, a toxic protein produced and secreted by *E. coli* is among the cytolytic, structurally homologous proteic bacterial toxins known as RTX (repeats in toxin) toxins (Trent *et al.*, 1998). RTX cytolysins are a family of calcium-dependent, pore-forming, secreted toxins found in a variety of gram-negative bacteria encoded in the gene cluster *hly*CABD. *X. fastidiosa* may also synthesize hemolysin-like toxins that can act against other endophytic microorganisms in the xylem. In its genome there is one ORF homologous to the gene that codes for the hemolysin III protein of *Bacillus cereus*. Three other ORFs show homology to different hemolysin-type calcium binding proteins (128.4 kDa -25 gly-rich repeats, 138.9 kDa and 173.0 kDa -43 Gly-rich repeats) of the *Neisseria meningitidis* iron-regulated protein FRPC (also known as cytotoxin RTX homolog FrpC). *Xylella* also has homologous ORFs to *hly*C, *hly*D and *hly*A of *E. coli*. However the homologue of *hly*B, the gene responsible for the toxin secretion was not found suggesting that *hly*D may have this function. As in *E. coli*, only the ORFs homologous to *hly*C and *hly*D are in a cluster.

Bacteriocin

X. fastidiosa also synthesizes a bacteriocin-like protein. In general, bacteriocins are ribosomally synthesized antimicrobial polypeptides (Schripsema *et al.*, 1996), whose production involves several genes (Nes *et al.*, 1996). The bacteriocin found in *X. fastidiosa* is similar to the one found in *Rizobium leguminosarum*, a RTX protein similar to hemolysin and leukotoxin (Oresnik *et al.*, 1999).

Two copies of *cva*C encoding a colicin-like precursor similar to the *E. coli* colicin V precursor were found in a cluster. Colicin V belongs to a family of small peptide bacteriocins produced by *E.coli* and other closely related bacteria (Havarstein *et al.*, 1994). The secretion of colicin V in *E. coli* requires the products of two linked genes *cva*A (a secretion protein) and *cva*B (for peptide tranport) both have homologous in *X. fastidiosa. X. fastidiosa* also has a similar ORF to *tol*C encoding for an outer membrane protein, which is probably involved in the transport of a hemolysin-like protein that is similar to the ABC-transporter dependent secretion of *E. coli*.

Polyketides constitute a huge family of structurally diverse natural products including those with antibiotic and antiparasitic activities. The biosynthesis of polyketides is similar to the assembly of fatty acids but unlike a fatty acid, a polyketide synthase (PKS) can make additional choices in the starting and extending groups. *X. fastidiosa* appears to have a polyketide synthase, a key enzyme involved in the production of antibiotics. Two ORFs were found similar to peptide synthase which is involved in the

biosynthesis of peptide antibiotics.

Adaptation to the Strees Conditions

Proteolytic Enzymes

Several ORFs related to protein degradation were found in the *X. fastidiosa* genome. However, the analysis of the sequences does not give a hint as to whether or not the proteases are involved in pathogenesis. There is only one ORF, *htr*A (high temperature resistance) whose product is highly similar to proteins found in pathogenic organisms. *htrA* is a periplasmic serine protease essential for cell survival at high temperatures (Lipinska *et al.* 1989, 1990). A proposed function for this protein is to remove denatured protein that could be toxic for the cells (Lipinska *et al*., 1990). Skórko-Glonek *et al.* (1999) showed this protein importance for defense against oxidative stress. It should be pointed out that one the most efficient mechanisms of defense in plant is the production of reactive oxygen species (ROS) (Wojtaszek, 1997; Dat *et al*., 2000). *htrA* is also a protein induced by ferrous sulfate and cumene hydroperoxide. *X. fastidiosa* has two genes (*htr*A and *muc*D (mucilage) that belong to this family which is not an uncommon feature since some other organisms like *E. coli*, *P. aeruginosa,* and *B. abortus* have at least two of such elements in their genomes. Interestingly, *alg*W (another homologue of *htr*A) and *muc*D were shown to affect the expression of the mucoid phenotype in *P. aeruginosa* (Boucher *et al*., 1996). Alginate is responsible for this phenotype and has been related to persistence of the pathogen in patients. It acts leading to resistance to free radical released by macrophages (Simpson *et al*., 1989). These genes may be important factors for adapting to such an environment.

Oxidative Stress

The xylem-limited bacteria *X. fastidiosa* can be exposed to active oxygen produced both by the plant and by other endophytic microorganisms living in the xylem vessels. To overcome detoxification and prevent damage caused by reactive oxygen the bacteria might require an efficient protection mechanism. Enzymes involved in the detoxification or protection of oxidative stress include superoxide dismutases, catalases, enzymes involved in DNA and protein repair, and transcription factors involved in the transduction and regulation of genes (Loprasert *et al*., 1996; Farr and Kogoma, 1991; Bauer *et al*., 1999). Exposure to peroxide stimulus activates OxyR which drives the expression of several genes including heat-shock proteins, catalase, alkyl hydroperoxidase reductase, and glutathione reductase a protein associated with H_2O_2 cellular resistance. The signal for induction of the SoxR regulon is not known but the most regulated genes are *sod*A (superoxide dismutase), *nfo* (Endonuclease IV) and *zwf* (glicose-6-P dehydrogenase) all of them with roles in the antioxidant defense. The SoxR system can also affect the expression of porins in the outer membrane (*ompF*) these are associated with multiple antibiotic resistance.

Genes of the *oxyR* (H_2O_2) and *soxR* (superoxide response) regulons are present in the genome of *X. fastidiosa* these are involved directly in cell detoxification and adaptation to adverse conditions. Genes were found that code for catalase, superoxide dismutase, alkyl hydroperoxide reductase, glutathione reductase, and an organic hydroperoxide resistance protein which is similar to several other bacteria. Genes coding for enzymes involved in the repair of DNA, membrane and proteins against damage caused by oxygen radicals were also detected. O*xy*R, a transcriptional regulator factor that controls the expression of H_2O_2 inducible proteins was found with greater similarity to Xcc than *E. coli* or *S. typhimurium* (Farr and Kogoma, 1991). *sox*R, as known in *E. coli* and *S. typhimurium* was not found.

Osmotic Stress

Within the xylem *X. fastidiosa* survives in a highly diluted solution which includes organic (aminoacids, amines, plant regulators, organic acids, etc.) and inorganic compounds (macro and micronutrients) uptaken by roots. Since the composition and flux in the xylem are strictly associated to environmental factors (water potential in the system air-leaves-roots, composition of the soil solution) and uptake capacity of the roots, representative changes occur in the sap composition during the day. The bacteria should have osmosensing adaptive mechanisms to respond both passively and actively to these changes. As pointed out by Wood (1999), more than specific sensors, osmoregulars are devices that

implement the response of an organism to a changing environmental osmolarity.

Among genes related to osmoregulars (Wood, 1999) the *X. fastidiosa* genome contains *mdo*H, *mdo*G (membrane derived oligosacharide), porin (*opr*O), and an outer membrane protein (*mop*B) all of which well evaluated in several bacteria. Although many genes of several bacteria have been associated with osmoresponse, this adaptation capacity certainly should involve complex processes typical to each microorganism and its habitat. Therefore, more functional studies should be done with *X. fastidiosa* for a better characterization of such genes.

Iron Metabolism

In the *X. fastidiosa* genome there are at least 67 ORFs involved in iron metabolism. The mechanism of iron acquisition in plant pathogens seems to be based mainly on the production of siderophores. When there is low internal iron level the cytosolic ferric uptake regulatory protein (Fur) product of the *fur* gene (Hantke, 1984) acts as an iron responsive transcriptional repressor (Crosa, 1997; Neilands, 1995). At low iron levels in the cell, Fur has lower affinity for the operator of the sequences in the promoters of siderophore biosynthesis or transport genes. As the iron concentration raises more ferrous ion binds to Fur protein enhancing Fur binding to the operator (De Lorenzo *et al.*, 1988; De Lorenzo *et al.*, 1987). Thus, there is a decrease in transcription of Fur-regulated genes and consequently a lower production of siderophores. Less iron is chelated and the rate of iron assimilation decreases.

X. fastidiosa appears to have a Fur similar to *X. campestris* pv *vesicatoria* ferric uptake regulator but the production of siderophores in *X. fastidiosa* is not yet clear. The only ORF related to siderophores synthesis found in *X. fastidiosa* encodes a protein similar to factors involved in the secretion of pyroverdine, a siderophore *of P. aeruginosa*. Another mechanism for iron uptake in bacteria is through the TonB, ExbB, ExbD1 system. *X. fastidiosa* has ORFs homologous to *ton*B, *exb*B, *exb*D1, *exb*D2 in a cluster that are highly similar to the genes of *Xcc* (Wiggerich *et al.*, 1997).

Detoxification and Drug Efflux

X. fastidiosa seems to have at least two different mechanisms for drug inactivation: Multidrug Resistance (MDR) and Specific Drug Resistance (SDR), both of which are well known in bacteria and can afford protection against toxic compounds. The bacteria may also have drug efflux mechanisms to release and transport those compounds. The secondary drug transporters comprise the largest group of known drug extrusion systems in bacteria, some of which are involved in multidrug resistance, whereas others mediate efflux with a high specificity. The secondary drug transporters can be subdivided into three groups: the Major Facilitator Superfamily (MFS) of transporters; the Resistance, Nodulation and cell Division (RND) family of membrane proteins; and the family of Small Multidrug Resistance (SMR) transporters. In *Xylella fastidiosa* there are at least two of these groups, MFS and RND.

Other detoxification proteins were found in the *Xylella fastidiosa* genome. ORFs encoding proteins specific for toluene and tetracycline resistance, penicillin tolerance and inactivation of b-lactam antibiotics are also present in the genome. This arsenal makes this bacterium a strong competitor in a very harsh environment.

Not Detected Genes

Common sense would predict phytopathogenic bacteria to have a limited range of hosts. In general, the hosts are limited to members of a single species or genus. Avirulence (*avr*) genes present in the pathogen encode factors which interact with matching resistance (R) proteins in the host (for recent reviews see Bonas and Van den Ackerveken, 1999 and Martin, 1999). Bacterial avirulence genes that have been characterized fall into two groups: those that resemble *avrBs3* of *Xanthomonas campestris* pv. vesicatoria, and those that resemble *avr* gene of *Pseudomonas syringae*, together with some gene of *X. campestris* (*other* pathovars) and *Pseudomonas solanacearum*. This subdivision involves differences in both structural and functional characteristics (Vivian and Gibbon, 1997). There are growing evidences that Avr proteins have a primary function in virulence, even though the HR

(hypersensitive)-triggering effects of the Avr-R interactions are epistatic over these virulence functions. It is still unknown how Avr proteins promote parasitism but support for such a primary role comes from observations that their place of action is within host cells (Alfano and Collmer, 1997). The Type III secretion system is responsible for delivering these proteins to the interior of the host cells. Its components are encoded by genes called *hrp* (hypersensitive response and pathogenicity) or *hrc* (*hrp* conserved) that are present both in plant and animal pathogens. In the *Xylella fastidiosa* genome no homology with known *avr*, *hrp* or *hrc* was found. The absence of such genes suggests that the pathogenicity of *Xylella fastidiosa* is not related to the presence of Avr proteins and therefore, it does not depend on a type III secretion machinery for the transport of such proteins. As mentioned earlier in this review, Xylella does not penetrate the plant actively, the cells are rather inoculated by the vector straight into the xylem of the plant so it does not need the structures that are important in the first interactions with the host.

Other Genes Potentially Associated with Pathogenicity

Genes associated with virulence were also identified in the Xylella genome. Copies of *xrv*A (Xanthomonas regulator of virulence) and *vap* (virulence associated proteins) genes of *Dichelobacter nodosus*. *vap*A encodes an antitoxin similar to HigA (host inhibition of growth) from the killer plasmid Rts1 (Tian *et al.*, 1996). An ORF upstream of *vap*A codes for a toxin similar to HigB from the same plasmid, it was then termed *tox*A (toxin) (Bloomfield *et al.*, 1997). In this system, only cells carrying *vap*A survive in presence of ToxA. There is also a homologue of *hig*B upstream of *vap*A in *Xylella fastidiosa*, suggesting the same functionality. It is interesting to note that these genes are located in one of the phages present in this *Xylella* genome.

Conclusions

The genome project of *X. fastidiosa* was a milestone in the plant pathology. The choice for this bacteria as the first plant pathogen to be sequenced, was tightly associated to its importance as the causal agent of citrus variegated chlorosis which became a real threat for the world´s citrus industry. Unlike other completely sequenced bacteria, very little is known about the biology of *X. fastidiosa*. Studies on physiology and pathogenicity of the bacteria were challenged by its fastidious growth, and its specificity to xylem tissues of woody plants, probably associated to the vector specificity. Therefore, an open question is how the knowledge of the genome could help us better understand the biology of this microorganism, specially its pathogenicity.

As a fastidious bacteria living exclusively within xylem vessels, and surviving well in the foregut system of the vectors, *X. fastidiosa* seems to have no mechanism of interaction cell to cell involving specific virulence or pathogenicity genes, like many other pathogens. Its fastidious growth that can not be changed even by cultivation in rich medium, may reflect adaptation to the xylem conditions of low nutrient concentration, negative pressure, and high turbulence. On the other hand, this bacterium has a wide range of hosts, suggesting either that it also has a general mechanism of pathogenicity, or that these mechanisms can not be identified among those already known.

The capacity of the insects to transmit the bacteria plant to plant together with the survival aptitude of the bacteria within the insect, suggest that the bacteria should also have more interaction mechanisms with the vector than supposed before. This bacterium interacts efficiently with both plants and insects. Its capability to interact with surfaces building biofilms and aggregates makes it similar to animal pathogens.

Although the size of a genome can not be correlated with the specialization of an organism, it should be pointed out that *X. fastidiosa* has a small genome compared to phylogenetically related bacteria, like *E. coli* and *Xanthomonas* spp. and even though around 53% of its genes still do not have a known function. In the future, the information generated by completely sequencing other genomes together with the functional genome projects will provide a better understanding of the complex functioning of these organisms.

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Table 1. Genes related to pathogenesis predicted by sequence analysis of the *Xylella fastidiosa* (strain 9a5c) genome

Gene	Size of gene product (aa)	Amino acid sequence relatedness with BLASTp score	Accession no. of *Xylella* database*	Accession no. of homologue**	Size of homo-logue	Percentage identical (I) and (aa)similar (S) amino acids	No. of position compared
Interactions with surfaces							
*gum*B	117	GumB protein from *X. campestris*	XF2370	gil2120724	213	67% (I) 82 % (S)	212
*gum*C	467	GumC protein from *X. campestris*	XF2369	gil2120725	449	56% (I) 73 % (S)	441
*gum*D	484	GumD protein from *X. campestris*	XF2367	gil2120726	484	69% (I) 78 % (S)	338
*gum*E	424	GumE protein from *X. campestris*	XF2366	gil2120727	432	61% (I) 75 % (S)	407
*gum*F	363	GumF protein from *X. campestris*	XF2365	gil2120728	364	37% (I) 50 % (S)	334
*gum*H	380	GumH protein from *X. campestris*	XF2364	gil2120730	380	62% (I) 73% (S)	380
*gum*J	510	GumJ protein from *X. campestris*	XF2362	gil2120732	498	60% (I) 74% (S)	466
*gum*K	281	GumK protein from *X. campestris*	XF2361	gil2120733	295	60% (I) 74% (S)	278
*gum*M	265	GumM protein from *X. campestris*	XF2360	gil2120735	263	69% (I) 76% (S)	231
*fim*T	187	Pre-pilin like leader involved in type 4 fimbrial biogenesis from *P. aeruginosa*.	XF0028	gil1161220	169	36%(I) 50 % (S)	69
*pil*V	158	Pre-pilin leader sequence from *P. aeruginosa*	XF0029	gil643582	185	33%(I) 70%(S)	56
*pil*X	195	PilX protein from *P. aeruginosa*.	XF0031	gil1246301	172	24%(I) 39%(S)	120
*pil*Y1	1230	PilY gene product of *P. aeruginosa*	XF0032	gil1246302	1161	31%(I) 45%(S)	629
*pil*E	139	Type IV pilin protein from *P. aeruginosa*	XF0033	gil2120639	141	29%(I) 39%(S)	137
*fim*A	320	FimA protein from *E. coli*	XF0080	gil1816487	184	31%(I) 47%(S)	163
*fim*D	901	Fim D protein involved in the export and assembly of FimA fimbrial across the outer membrane from *E.coli*.	XF0081	gil1232060	882	38%(I) 56%(S)	810
*pil*M	392	Fimbrial assembly membrane protein from *P. siryngae*	XF0369	gil895925	354	58%(I) 74%(S)	349
*pil*N	220	Fimbrial assembly membrane protein from *P. aeruginosa*	XF0370	gil530857	198	44%(I) 65%(S)	168
*pil*O	222	Fimbrial assembly membrane protein from *Pseudomonas syringae*	XF0371	gil530858	207	41%(I) 56%(S)	200
*pil*P	176	Fimbrial assembly membrane protein from *P. aeruginosa*	XF0372	gil530859	174	40%(I) 61%(S)	151
*pil*Q	637	Fimbrial assembly membrane protein from *P. aeruginosa*	XF0373	gil459551	727	34%(I) 52%(S)	589
*pil*H	132	PilH protein from *P. aeruginosa*	XF0450	gil1172507	121	50%(I) 72%(S)	120
*pil*Y1	1472	Fimbrial assembly protein from *P. aeruginosa*	XF0478	gil1246302	1161	33%(I) 47%(S)	600
*pil*E	125	Type IV pilin from Legionella pneumophila	XF0479	gil3002996	149	36%(I) 50%(S)	112
*pil*Z	118	Type 4 fimbriae assembly protein from *P. aeruginosa*	XF0677	gil972779	118	62%(I) 76%(S)	111
*pil*Y1	1217	PilY1 gene product from *P. aeruginosa*	XF1224	gil1246302	1161	30%(I) 44%(S)	711
*pil*U	376	Twitching motility protein from *P. aeruginosa*	XF1632	gil2120641	382	60%(I) 78%(S)	369
*pil*T	344	Twitching motility pilT protein from *P. aeruginosa*	XF1633	gil130214	344	74%(I) 86%(S)	344
*xps*O	287	A type IV pre-pilin leader peptidase from *X. campestris*	XF2537	gil529683	344	74%(I) 86%(S)	344
*pil*C	490	*P. aeruginosa* fimbrial assembly protein PilC	XF2538	gil130213	406	49%(I) 66%(S)	397
*pil*B	577	*P. aeruginosa* fimbrial assembly protein PilB	XF2544	gil130212	566	54%(I) 72%(S)	569
*pil*R	497	*P. aeruginosa* transcriptional activator PilR	XF2545	gil281546	445	58%(I) 69%(S)	469
*pil*S	629	*P. aeruginosa* sensor protein PilS	XF2546	gil464393	530	36%(I) 52%(S)	521
*pil*J	693	Pilus biogenesis and twitching motility protein PILJ from *P. aeruginosa*.	XF1953	gil1172509	682	42%(I) 56%(S)	675
*pil*I	176	Pilus biogenesis and twitching motility protein PILI from *P. aeruginosa*.	XF1954	gil1172508	178	33%(I) 53%(S)	172
*pil*G	145	Pilus biogenesis and twitching motility protein PIG from *P. aeruginosa*.	XF1955	gil1172506	135	82%(I) 92%(S)	119
*alg*Z	346	Sensor protein AlgZ involved in the alginate production from *P. aeruginosa*.	XF1625	gil1542971	358	36%(I) 48%(S)	323
*alg*R	252	Alginate biosynthesis regulatory protein AlgR1 from *P. syringae*.	XF1626	gil4884829	248	45%(I) 56%(S)	238
hsf	2059	Hsf protein related to type B surface fibrils from *Haemophilus influenzae*.	XF1529	gil1666683	2353	21%(I) 34%(S)	1944
hsf	1190	Hsf protein related to surface fibrils and adhesin Hia from *H. influenzae*.	XF1981	gil1666683	2353	29%(I) 45%(S)	313
*psp*A	3455	Hemagglutinin-like secreted protein from *Neisseria meningitidis*.	XF2775	gil2623258	2273	31%(I) 46%(S)	905
*psp*A	3442	Hemagglutinin-like secreted protein from *Neisseria meningitidis*.	XF2196	gil2623258	2273	31%(I) 46%(S)	905
*psp*A	3282	Hemagglutinin-like secreted protein from *Neisseria meningitidis*.	XF0889	gil2623258	2273	27%(I) 42%(S)	915
Plant cell wall degradation							
*eng*XCA	565	Extracellular endoglucanase precursor from *X. campestris*	XF0810	spIP19487	493	33% (I) 47 % (S)	279
*eng*XCA	592	Extracellular endoglucanase precursor from *X. campestris*	XF0818	spIP19487	493	62% (I) 75 % (S)	370
egl	356	Endo-1,4-beta-glucanase from *Ralstonia solancearum*	XF2708	spIP17974	426	45% (I) 62 % (S)	316
*cbh*A	683	Exocellobiohydrolase A from *Cellulomonas fimi*	XF1267	spIP50401	872	56% (I) 69 % (S)	438
*pgl*A	Frame shift gene	Polygalacturonase precursor from *Ralstonia solancearum*	XF2466	spIP20041	529	63% (I) 71 % (S)	128
*xyl*A	882	Family 3 glycoside hydrolase from *Ruminococcus flavefaciens*	XF0845	gil5690010	690	42% (I) 54% (S)	405
Regulator of EPS and extracellular enzyme							
*rpf*A	908	Aconitase from *X. campestris*	XF0290	gil2661438	922	77% (I) 84% (S)	916
*rpf*B	569	Regulator of pathogenicity factors from *X. campestris*.	XF0287	gil1922920	560	70% (I) 83% (S)	560
*rpf*F	290	Regulator of pathogenicity factors from *X. campestris*.	XF1114	gil1922922	289	67% (I) 78% (S)	280
*rpf*C	662	Sensory/regulatory protein from *X. campestris*.	XF1115	spIP49246	677	58% (I) 73% (S)	660
*rpf*G	386	Response regulator from *X. campestris*.	XF1113	gil7688439	378	74% (I) 83% (S)	378
*lys*U	506	Lysyl-tRNA synthetase from *E. coli*.	XF1112	spIP14825	505	56% (I) 72% (S)	477
*prf*B	338	Peptide chain release factor 2 from *Haemophilus influenzae*.	XF1111	spIP43918	365	66% (I) 82% (S)	326
*Rec*J	581	Single-stranded DNA exonuclease from *E. coli*	XF1110	spIP21893	577	42% (I) 59% (S)	563
*Rpf*E	293	Regulatory protein from *X. campestris*.	XF1109	gil7228157	306	64% (I) 74% (S)	267
GreA	154	Transcriptional elongation factor from *E. coli*.	XF1108	spIP21346	153	62% (I) 81% (S)	153
Biosynthesis of toxins and antibiotics							
*cvp*A	233	Colicin V production protein from *Haemophilus influenzae*	XF1948	spIP45108	163	29% (I) 47%(S)	144
*cva*B	707	Colicin V secretion protein cvaB from *E. coli*	XF1220	spIP22520	698	36%(I) 54%(S)	675
*cva*A	420	Colicin V secretion protein from *E. coli*	XF1216	spIP22519	413	24%(I) 44%(S)	408
none	2064	Bacteriocin from Rhizobium leguminosarum	XF2407	gil2961326	958	24%(I) 38%(S)	1133
*hly*B	720	Toxin secretion ABC transporter ATP-binding protein *E. coli*	XF2397	spIP10089	707	71%(I) 66(S)	700
*hly*D	473	Hemolysin secretion protein D	XF2398	spIP06739	478	37%(I) 57%(S)	478
*frp*C	1208	Hemolysin-type calcium binding protein from *Neisseria meningitidis*	XF0668	spIP55127	1829	30%(I) 43%(S)	486
*frp*C	1636	hemolysin-type calcium binding protein from *Neisseria meningitidis*	XF1011	spIP55127	1829	25%(I) 39%(S)	1274
*frp*C	1296	Hemolysin-type calcium binding protein from *Neisseria meningitidis*	XF2759	spIP55127	1829	30%(I) 44%(S)	1211
*frn*E	256	Polyketide synthase (PKS) from *Streptomyces roseofulvus*	XF2135	gil3170570	252	34%(I) 50%(S)	228
*dnr*U	294	Daunorubicin C-13 ketoreductase from *Streptomyces peucetius*	XF1741	gil3778997	287	31%(I) 44%(S)	255
*non*F	229	NonF protein from *Streptomyces griseus* subsp. *Griseus*	XF1137	gil5002553	234	34%(I) 46%(S)	211
*het*I	197	Putative HetI protein from *Anabaena* sp.	XF1934	spIP37695	237	33%(I) 42%(S)	184
St3F7.11	503	Peptide synthase from *Streptomyces coelicolor*	XF1038	gil2808752	532	22%(I) 34%(S)	519
St3F7.11	563	Peptide synthase from *Streptomyces coelicolor*	XF2276	gil2808752	532	25%(I) 36%(S)	569

Adaptation to the stress conditions							
*htr*A	481	Periplasmic serine protease (HtrA) from *E. coli*	XF0285	spIP09376	474	43% (I) 60% (S)	468
*muc*D	514	Periplasmic serine protease (MucD) from *Pseudomonas aeruginosa*	XF2241	giI1184684	474	46% (I) 61% (S)	469
*cpe*B	781	Catalase from *Streptomyces reticuli*	XF2232	giI2120724	740	64% (I) 75 % (S)	733
*sod*A	242	Superoxide dismutase [MN] precursor from *Acinetobacter calcoaceticus*	XF1921	giI6685985	228	60% (I) 74 % (S)	207
*ahp*C	206	Subunit C of alkyl hydroperoxide reductase from *Salmonella typhimurium*	XF1530	spIP19479	187	70% (I) 83 % (S)	187
*ahp*F	571	Subunit F of alkyl hydroperoxide reductase from *X. campestris*	XF1531	spIo06465	530	73% (I) 83 % (S)	531
ohr	143	Organic hydroperoxide resistance protein from *X. campestris.*	XF1827	giI3098342	142	66% (I) 77 % (S)	141
gpo	190	Glutathione peroxidase-like protein from *Lactococcus lactis*	XF1890	spIo32770	157	50% (I) 72% (S)	157
gst	205	Glutathione S-transferase from *Haemophilus influenzae*	XF1210	spIP44521	209	38% (I) 58% (S)	209
*mut*X	168	8-oxo-dgtpase from *Streptococcus pneumoniae*	XF1262	spIP41354	154	38% (I) 57% (S)	136
*mut*M	271	Formamidopyrimidine DNA glycosylase from *E. coli*	XF0071	spIP05523	269	49% (I) 65% (S)	270
*mut*M	271	Formamidopyrimidine DNA glycosylase from *E. coli*	XF0170	spIP05523	269	49% (I) 65% (S)	270
*mut*Y	357	A/G-specific adenine glycosylase from *Salmonella typhimurium*	XF1909	spIQ05869	350	43% (I) 59% (S)	346
nth	218	Endonuclease III from *E. coli*	XF0647	spIP20625	211	67% (I) 79% (S)	208
*xth*A	264	Exodeoxyribonuclease III from *Synechocystis* sp.	XF1933	giI1653682	275	45% (I) 58% (S)	265
*oxy*R	325	Oxidative stress transcriptional regulator from *X. campestris.*	XF1532	giI2098748	313	74% (I) 83% (S)	303
*mdo*G	537	Periplasmic glucan biosynthesis protein from *E. coli.*	XF2682	spIP33136	511	36% (I) 55% (S)	493
*mdo*H	615	Periplasmic glucan biosynthesis protein from *E. coli.*	XF1623	spIP33137	847	36% (I) 52% (S)	615
*opr*O	398	Porin O precursor from *Pseudomonas aeruginosa.*	XF0321	spIP32977	438	23% (I) 39% (S)	409
*mop*B	389	Outer membrane protein from *Methylococcus capsulatus.*	XF0343	giI4104020	348	27% (I) 40% (S)	384
*msc*L	134	Large-conductance mechanosensitive channel from *E. coli.*	XF0039	spIP23867	136	43% (I) 61% (S)	136
*Sur*E	262	Survival protein from *Legionella pneumophila.*	XF0858	giI5771428	251	60% (I) 74% (S)	248
fur	164	Ferric uptake regulator Fur from *Xanthomonas campestris* pv. vesicatoria	XF2344	giI5532520	136	75%(I) 80%(S)	136
*ybi*L	776	TonB-dependent receptor from *E. coli*	XF0599	spIP75780	760	46%(I) 63%(S)	738
*ync*D	683	Probable tonB-dependent receptor YNCD precursor from *E. coli*	XF1496	spIP76115	700	23%(I) 37%(S)	529
*ton*B	221	TonB protein from *Xanthomonas campestris* pv. campestris	XF0009	spIO34261	223	82%(I) 92%(S)	87
*exb*B	254	Biopolymer transport ExbB protein from *Xanthomonas campestris* pv. campestris	XF0010	spIO34260	253	77%(I) 81%(S)	254
*exb*D1	140	Biopolymer transport ExbD1 protein from *Xanthomonas campestris* pv. campestris	XF0011	spIO34259	140	76%(I) 85%(S)	140
*exb*D2	136	Biopolymer transport ExbD2 protein from *Xanthomonas campestris* pv. campestris.	XF0012	spIO34258	136	76%(I) 84%(S)	134
*lin*C	255	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase from *Sphingomonas paucimobilis*	XF1726	spIP50197	250	41% (I) 56%(S)	189
*lyt*B	316	Drug tolerance protein from *Acinetobacter* sp.	XF2416	giI5915671	316	64%(I) 79%(S)	314
*thd*F or *trm*E	451	Thiophene and furan oxidation protein from *Coxiella burnetii*	XF2778	spIP25522	452	42%(I) 57%(S)	423
*amp*G	509	Beta-lactamase induction signal transducer protein from *E. coli*	XF0165	spIP36670	491	45%(I) 63% (S)	168
pbp	455	Beta-lactamase-like protein from *Pyrococcus abyssi*	XF1621	giI5457571	477	24%(I) 46%(S)	366
*tet*V	418	Tetracycline-resistance from *Mycobacterium smegmatis*	XF0993	giI2613096	419	21%(I) 34%(S)	382
*acr*F or *env*D	1055	Acriflavine resistance protein from *E. coli*	XF2094	spIP24181	1034	47%(I) 64%(S)	1038
*yer*P	1027	Acriflavin resistance protein from *Bacillus subtilis*	XF0243	giI2632985	1065	22%(I) 42%(S)	1059
*yeg*N	1034	Acriflavin resistance protein F (EnvD protein) from *E. coli*	XF2386	spIP76398	753	39%(I) 55% (S)	758
*yeg*N	1077	Acriflavin resistance protein F (EnvD protein) from *E. coli*	XF2385	spIP76398	753	44% (I) 62%(S)	760
*mex*C	369	Membrane fusion protein MexC from *Pseudomonas aeruginosa.*	XF0244	giI1399757	387	20%(I) 38%(S)	362
*mex*E	368	MexE protein from *Pseudomonas aeruginosa*	XF2084	giI1707644	414	24%(I) 36%(S)	358
*mtr*C	411	Membrane fusion protein MtrC precursor from *E. coli.*	XF2384	giI1736780	455	35%(I) 52%(S)	389
*mm*R	472	Methylenomycin A resistance protein from *Streptomyces coelicolor.*	XF1765	spIP11545	475	33%(I) 49(S)	390
*ydh*E	469	Multidrug efflux protein from *E. coli.*	XF2686	spIP37340	457	29%(I) 46%(S)	442
*tol*C	452	Outer membrane protein TOLC precursor from *E. coli.*	XF2586	spIP02930	445	32%(I) 52%(S)	493
*ttg2*D	218	Toluene tolerance protein Ttg2D from *Pseudomonas putida.*	XF0418	giI4336801	215	24%(I) 48%(S)	185
*ttg2*C	178	Toluene tolerance protein Ttg2D from *Pseudomonas putida.*	XF0419	giI4336800	161	37%(I) 53%(S)	148
*ttg2*B	249	Toluene tolerance protein Ttg2B from *Pseudomonas putida.*	XF0420	giI4336799	260	44%(I) 64%(S)	245
*ttg2*A	264	Toluene tolerance protein Ttg2A from *Pseudomonas putida.*	XF0421	giI4336798	269	44%(I) 63%(S)	249

Other genes potentially associated with pathogenicity							
*xrv*A	134	Virulence regulator from *X. oryzae*	XF0749	giI1360644	133	47% (I) 60% (S)	126
*xrv*A	138	Virulence regulator from *X. oryzae*	XF1493	giI1360644	133	40% (I) 55% (S)	133
*hig*A	105	Proteic killer suppression protein hig A from plasmid Rts1	XF0721	giI2144255	92	40% (I) 66% (S)	93
*hig*B	91	Proteic killer suppression protein hig B from plasmid Rts1	XF0720	giI2144254	104	33% (I) 58% (S)	75
*vap*D	151	Virulence-associated protein D (vapD) from *Actinobacillus actinomycetencomitans*	Xfa0052	giI1651211	143	64% (I) 83% (S)	129
*vap*E	488	Virulence-associated protein E (vapE) from *Dichelobacter nodosus*	XF0506	giI563258	437	29% (I) 42% (S)	424
*vap*E	501	Virulence-associated protein E (vapE) from *Dichelobacter nodosus*	XF2121	giI563258	437	31% (I) 43% (S)	404

* http://onsona.lbi.ic.unicamp.br/xf
** http://www.ncbi.nlm.nih.gov

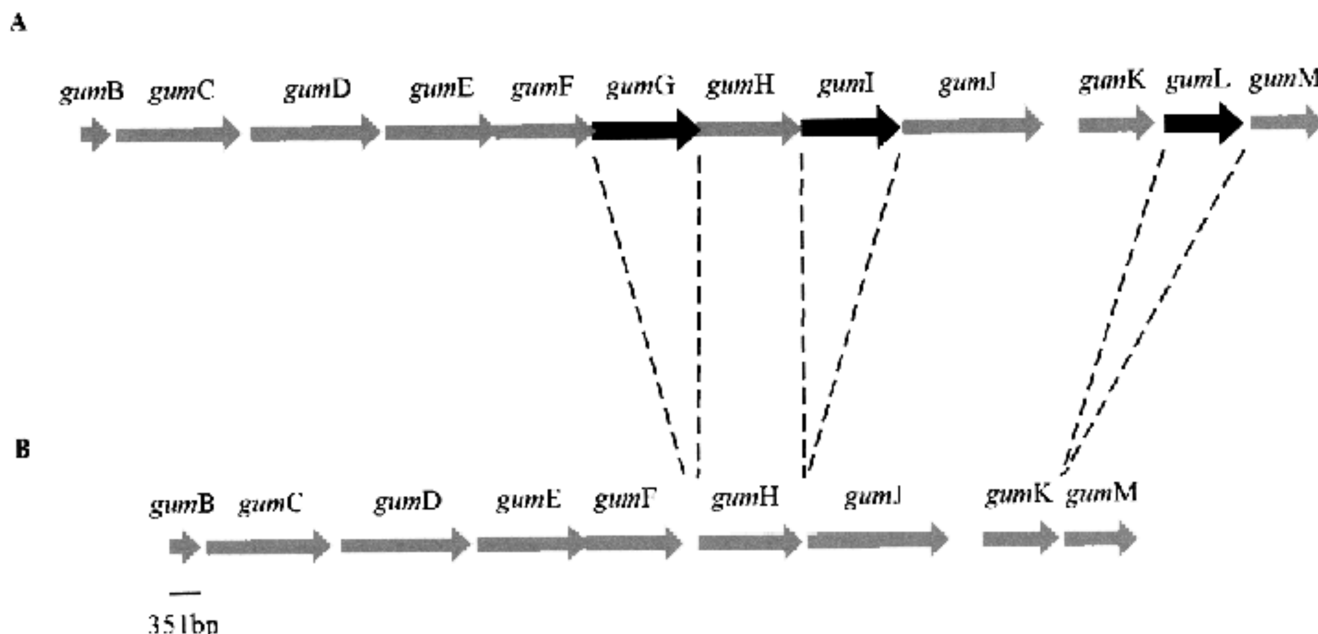

Figure 1. Gene cluster coding for xantham gum in *Xanthomonas campestris* pv campestris (A), and *Xylella fastidiosa* (B), in which *gum*G, I and L are not present. Genes above are transcribed from left to right; those below are transcribed from right to left. Grey arrows represent the genes present both in *Xanthomonas campestris* and *Xylella fastidiosa*. Black arrows mark the genes absent in the *Xylella fastidiosa* genome.

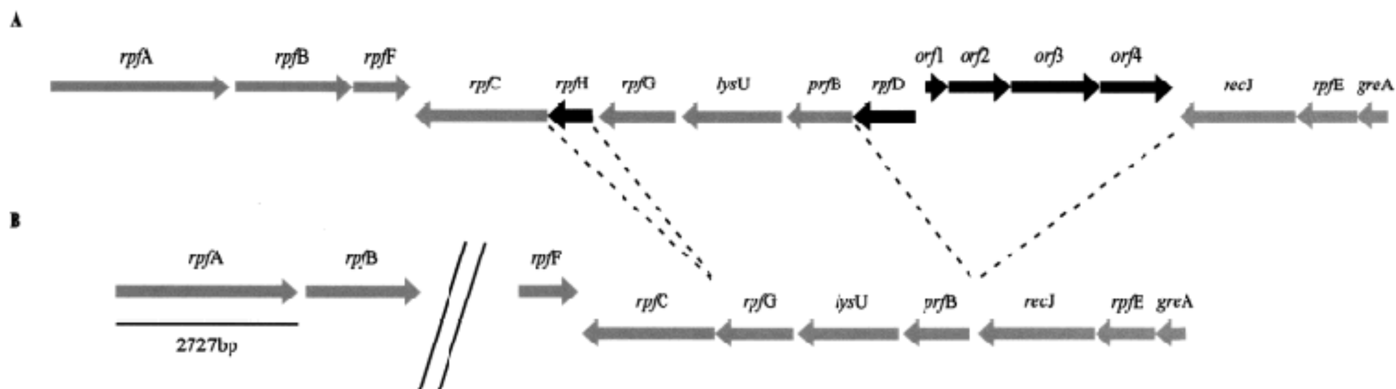

Figure 2. *Xanthomonas campestris* pv. campestris *rpf* gene cluster based on Barber *et al.*, (1997) and Dow *et al.*, (2000); B – Putative *rpf* gene cluster of *Xylella fastidiosa*. Genes above are transcribed from left to right; those below are transcribed from right to left. Grey arrows represent the genes present both in *Xanthomonas campestris* and *Xylella fastidiosa*. Black arrows mark the genes absent in the *Xylella fastidiosa* genome.