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A systematic study of *Xylella fastidiosa* strains isolated from pecan, grapevine, oleander, and sycamore in Louisiana

Rebecca Ann Melanson

Louisiana State University and Agricultural and Mechanical College, rmelanson@agcenter.lsu.edu

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**A SYSTEMATIC STUDY OF *XYLELLA FASTIDIOSA* STRAINS ISOLATED FROM
PECAN, GRAPEVINE, OLEANDER, AND SYCAMORE IN LOUISIANA**

A Thesis

Submitted to the Graduate Faculty of the
Louisiana State University and
Agricultural and Mechanical College
In partial fulfillment of the
Requirements for the degree of
Master of Science

in

The Department of Plant Pathology & Crop Physiology

by

Rebecca Ann Melanson
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DEDICATION

I dedicate this thesis to my parents, Ulysses T. Melanson and Kay L. Melanson, who began educating me as a child and have encouraged me to continue my education ever since. They have relentlessly supported my efforts and given themselves in any means necessary to help me on my journey. I will always be grateful.

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ABSTRACT

Xylella fastidiosa causes disease in a number of economically important crops and landscape shrubs and trees including grapevine, citrus, oleander, and sycamore. In pecan, *X. fastidiosa* causes pecan bacterial leaf scorch (PBLs), which leads to defoliation and reduces nut yield. No economically effective treatments are available for PBLs. In order to improve PBLs management practices, it is necessary to determine the subspecies of *X. fastidiosa* strains that infect pecan so potential sources of inoculum can be identified. Multiprimer PCR and phylogenetic analyses using nucleotide sequence data from the 16S-23S rDNA intergenic transcribed spacer (ITS) region and *pglA* consistently identified strains of *X. fastidiosa* isolated from pecan as *X. fastidiosa* subsp. *multiplex*. Enterobacterial repetitive intergenic consensus (ERIC)-PCR and repetitive extragenic palindromic (REP)-PCR analyses were congruent with phylogenetic analyses. REP-PCR analyses indicated genetic variation within strains of *X. fastidiosa* from pecan. From these same analyses, *X. fastidiosa* strains from sycamore, grapevine and oleander from Louisiana were identified as subsp. *multiplex*, subsp. *fastidiosa* and subsp. *sandyi*, respectively. This study provides additional information about the host ranges of *X. fastidiosa* subspecies.

CHAPTER 1: INTRODUCTION

LITERATURE REVIEW

The Plant Pathogen, *Xylella fastidiosa*. *X. fastidiosa* is a xylem-limited, fastidious bacterium that causes disease in a number of economically important crops, ornamentals, and shade trees, including grapevine, peach, citrus, oleander, and sycamore (Chang *et al.*, 1993; Davis *et al.*, 1978; Purcell *et al.*, 1999; Sberald *et al.*, 1983; Wells *et al.*, 1987). The pathogen is spread from infected plant hosts to non-infected plant hosts by graft transmission and by xylem-feeding insects (Chatterjee *et al.*, 2008; Redak *et al.*, 2004; Sanderlin, 2005). Prior to 1987, some of the diseases now attributed to *X. fastidiosa* were recognized, but the causal agent was thought to be a virus or was described simply as a rickettsia-like organism or a xylem-limited bacterium (Hopkins *et al.*, 1973; Hopkins and Mollenhauser, 1973; Sberald *et al.*, 1983). It was not until the development of specialized media to culture the pathogen from infected hosts and the work of Wells *et al.* (1987) that xylem-limited bacteria producing similar diseases and showing similarity to each other but distinction from other genera were assigned to the new genus and species (Davis *et al.*, 1978; Wells *et al.*, 1987; Wells *et al.*, 1981).

X. fastidiosa are Gram-negative, straight, rod-shaped cells 0.25-0.35 x 0.9-3.5 μm in width and length (Brenner, 2005). They are aerobic and aflagellate, grow optimally from 26-28°C, and have a GC content, as determined by melting temperature, of 51.0-52.4% (Brenner, 2005). These bacteria are nutritionally fastidious, requiring specialized media for growth in the laboratory, and a number of different media have been developed for culturing of *X. fastidiosa* (Brenner, 2005; Schaad, 2001).

In 2000, a citrus variegated chlorosis (CVC) strain of *X. fastidiosa* became the first *X. fastidiosa* strain to be completely sequenced, as well as the first plant pathogenic bacterium to be completely sequenced (Simpson *et al.*, 2000). Since then, a number of other strains have been

sequenced including two strains from grapevine, Temecula1 and XF GB514, and two strains from almond, M12 and M23 (Chen *et al.*, 2010; Schreiber IV *et al.*, 2010; Van Sluys *et al.*, 2003). The genomes of these strains range in size from approximately 2.48 Mb for almond strain M12 to 2.68 Mb for CVC strain 9a5c; one or two plasmids are also present in some strains (Chen *et al.*, 2010; Schreiber IV *et al.*, 2010; Simpson *et al.*, 2000; Van Sluys *et al.*, 2003). The complete genome sequences with gene annotations for these five strains are available in the National Center for Biotechnology Information's (NCBI) GenBank (<http://www.ncbi.nlm.nih.gov/>). A gapped genome sequence of an oleander strain has also been determined (Bhattacharyya *et al.*, 2002).

Even before the designation of the new genus and species in 1987, researchers noticed differences among isolates of various hosts and proposed that different groups or pathovars existed (Kamper *et al.*, 1985). Since then, a number of subspecies have been proposed. Three subspecies of *X. fastidiosa* were proposed in 2004 based on DNA-DNA relatedness tests and intergenic transcribed spacer (ITS) sequence comparisons; the proposed subspecies were *X. fastidiosa* subsp. *piercei*, *X. fastidiosa* subsp. *multiplex*, and *X. fastidiosa* subsp. *pauca* (Schaad *et al.*, 2004b). An erratum published after the original paper correctly renamed the proposed *X. fastidiosa* subspecies *piercei* to *X. fastidiosa* subspecies *fastidiosa* after the designated type strain of the species (Schaad *et al.*, 2004a; Wells *et al.*, 1987). Subspecies *fastidiosa* includes strains causing disease in alfalfa, almond, grapevine, and maple; subspecies *multiplex* includes strains causing disease in almond, elm, peach, pigeon grape, plum, sycamore, and other shade trees; and subspecies *pauca* includes stains causing disease in citrus (Schaad *et al.*, 2004b). Two other subspecies of *X. fastidiosa* have since been proposed for strains infecting other hosts. *X. fastidiosa* subsp. *sandyi* was proposed for strains infecting oleander and is now known to infect

some other hosts (Hernandez-Martinez *et al.*, 2007; Schuenzel *et al.*, 2005). Recently, a fifth subspecies, *X. fastidiosa* subsp. *tashke*, was proposed for strains of *X. fastidiosa* infecting chitalpa in the southwestern United States (Randall *et al.*, 2009).

With the exception of a pear disease caused by *X. fastidiosa* in Taiwan (Leu and Su, 1993) and a report of *X. fastidiosa* being isolated from a grapevine in Europe (Berisha *et al.*, 1998), *X. fastidiosa* is limited to the North and South American continents (Hopkins and Purcell, 2002). Of the five described subspecies, *X. fastidiosa* subsp. *pauca* occurs only in South America, while the remaining subspecies are known to occur in North America (Randall *et al.*, 2009; Schaad *et al.*, 2004a; Schaad *et al.*, 2004b; Schuenzel *et al.*, 2005). Recent genomic studies suggest that *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *sandyi* were introduced into the United States from more tropical regions, whereas *X. fastidiosa* subsp. *multiplex* evolved in a temperate region (Nunney *et al.*, 2010). While the center of origin of *X. fastidiosa* subsp. *sandyi* is not yet known, evidence points to Central America as the center of origin of *X. fastidiosa* subsp. *fastidiosa* and North America as the source of *X. fastidiosa* subsp. *multiplex* (Nunney *et al.*, 2010).

The study of *X. fastidiosa* is becoming increasingly important as new diseases caused by this pathogen are reported and new subspecies are identified. These events are possible and new diseases and subspecies are easier to identify and report as advancements in technology continue and as information about this species increases. Among the techniques used to study *X. fastidiosa*, the polymerase chain reaction (PCR), which has gained much popularity since its development, is routinely used in laboratory investigations. Perhaps the most basic of its uses is to detect the presence of the pathogen in plant tissue or to identify a particular strain of the pathogen. In 1994, PCR with the use of *X. fastidiosa*-specific primers was developed to detect *X.*

fastidiosa in plant tissues (Minsavage *et al.*, 1994). The following year, primers specific for strains of *X. fastidiosa* causing CVC were developed (Pooler and Hartung, 1995). Further illustrating the use of PCR and the resourcefulness of published sequences, primers were developed for a multiprimer PCR that produced banding patterns unique to different *X. fastidiosa* genotypes (Almeida and Purcell, 2003; Hernandez-Martinez *et al.*, 2006).

Another application of PCR that has been used in studies of *X. fastidiosa* is repetitive sequence-based PCR (rep-PCR). This technique uses the presence of repetitive elements, such as repetitive element palindromic (REP) sequences, enterobacterial repetitive intergenic consensus (ERIC) sequences, and BOX sequences, located in various positions throughout bacterial genomes to amplify different numbers and sizes of DNA bands that are unique for different bacterial species and strains and create a DNA fingerprint for each species or strain (Versalovic *et al.*, 1991; Versalovic *et al.*, 1994). The application of rep-PCR to examine the presence of REP and ERIC elements in the genomes of strains of *X. fastidiosa* from grapevine, maple, almond, and oak showed that, with the exception of the strain from maple that had the same fingerprint as the strains from grapevine in California, strains from the same host had the same rep-PCR fingerprints, but were different from those of other hosts (Hendson *et al.*, 2001). In addition, strains of *X. fastidiosa* from grapevine in California and in the southeastern United States had the same ERIC-PCR fingerprint (Hendson *et al.*, 2001). In another study, strains of *X. fastidiosa* from citrus growing in different geographic regions in Brazil had different fingerprints and could be differentiated from *X. fastidiosa* strains from plum, coffee, and pear (Mehta *et al.*, 2001).

While a number of methods, including restriction fragment length polymorphism (RFLP) and rep-PCR, have been used to study the relationships among strains of *X. fastidiosa* isolated

from various hosts, PCR and phylogenetic analysis of nucleotide sequences are being used with increasing frequency to differentiate strains and to determine strain relatedness (Chen *et al.*, 1992; Doddapaneni *et al.*, 2007; Schaad *et al.*, 2004b). The 16S rDNA region is a highly conserved region of DNA. It has been shown to be useful in identifying *X. fastidiosa* from other bacterial species and was used in the naming of the new genus (Chen *et al.*, 2000a; Wells *et al.*, 1987). Since then, the 16S rDNA sequence has been used to compare strains of *X. fastidiosa* from a number of hosts (Chen *et al.*, 2000b; Mehta and Rosato, 2001). The less conserved 16S-23S ITS region has also been used as a means of strain comparison, often in conjunction with other tests or DNA sequences (Hendson *et al.*, 2001; Martinati *et al.*, 2005; Mehta and Rosato, 2001; Randall *et al.*, 2009). Phylogenetic analysis of the 16S-23S ITS region, for example, was used to test the patterns observed for strains in the multiprimer PCR, and indeed, corresponded favorably with the observed patterns (Hernandez-Martinez *et al.*, 2006). Sequences from both the 16S rDNA and the 16S-23S ITS regions from these studies are available in NCBI's GenBank.

Multilocus sequence typing (MLST) systems for comparison of bacterial strains are emerging as a popular technique. MLST analyses use partial DNA sequences from a set of housekeeping genes that encode necessary bacterial functions and that are unique for the particular group of bacteria being studied to characterize and group those bacteria (Maiden, 2006). Partial sequence data for a number of housekeeping genes, including *holC*, *rfbD*, *nuoL*, *nuoN*, *gltT*, *cysG*, *petC*, *pilU*, *leuA*, and *lacF* (later renamed *malF*), were obtained from *X. fastidiosa* strains and then subjected to phylogenetic analysis to study the geographic variation and evolutionary relationships among strains of *X. fastidiosa* (Schuenzel *et al.*, 2005; Yuan *et al.*, 2010). Seven of these ten genes were used in an MLST analysis that resulted in the differentiation of *X. fastidiosa* strains into clonal complexes (correlated to subspecies) and

sequence types within clonal complexes (Sally *et al.*, 2005). Since the original MLST analysis, primers to amplify portions of these seven genes were redesigned for better amplification of products or for amplification of gene products from *X. fastidiosa* subsp. *pauca*, as well as shorter products that would result in better sequence reads (Yuan *et al.*, 2010). Results from the revised MLST analysis showed that little genetic variation existed within *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *sandyi* (Yuan *et al.*, 2010). In addition to characterizing and grouping closely related bacterial strains, MLST analysis also has the ability to detect recombination (Spratt *et al.*, 2001). This is evident in the *X. fastidiosa* MLST system as both MLST systems, using the original primers and the revised primers, showed genetic recombination between *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *multiplex* in the *cysG*, *holC*, and *pilU* genes of some strains (Sally *et al.*, 2005; Yuan *et al.*, 2010). In addition to the recombination seen between *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *multiplex* (Sally *et al.*, 2005; Yuan *et al.*, 2010), MLST analyses have also shown recombination between strains of *X. fastidiosa* subsp. *pauca* infecting coffee and citrus (Almeida *et al.*, 2008). A MLST database for *X. fastidiosa* typing is available at <http://pubmlst.org/xfastidiosa/>.

A number of potential virulence products and their encoding genes, such as *pglA* and *vapD*, have been described in *X. fastidiosa* and are being examined to determine their presence or absence among particular strains (Marques *et al.*, 2001; Simpson *et al.*, 2000). Polygalacturonase (PglA) is required for colonization and pathogenicity in grapevine (Roper *et al.*, 2007). In *X. fastidiosa* CVC and coffee strains, *pglA*, which encodes a polygalacturonase precursor, has early termination as a result of a frameshift; this frameshift was not present in the almond, grapevine, and mulberry strains (Van Sluys *et al.*, 2003). A gene encoding a virulence-associated protein D homologue, *vapD*, was identified on the pXF51 plasmid of the CVC 9a5c

strain (Marques *et al.*, 2001). A putative *vapD* gene was also identified in the Ann-1 oleander strain (Randall *et al.*, 2009). The *vapD* sequence was cloned from strains of *X. fastidiosa* from chiltalpa and sequenced, and nucleotide and protein sequences were compared using NCBI's Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, 1990; Randall *et al.*, 2009).

Pecan Bacterial Leaf Scorch. In 2000, *X. fastidiosa* was reported as the cause of a leaf scorch disease of pecan (*Carya illinoensis*) previously attributed to fungi, and it was proposed that the disease name be changed from fungal leaf scorch to pecan bacterial leaf scorch (PBLS) (Sanderlin and Heyderich-Alger, 2000). The symptoms of PBLS are similar to those caused by the bacterium in some other plant hosts and include leaflets turning tan to brown beginning at the margin and progressing basipetally, followed by abscission of affected leaflets (Sanderlin and Heyderich-Alger, 2000). In a study on cultivar Cape Fear pecan trees, PBLS diseased trees had reduced kernel weights averaging 16% when compared to non-infected trees in the same orchard (Sanderlin and Heyderich-Alger, 2003). PBLS has been identified in over 20 pecan cultivars and in seedling trees (Sanderlin, 2005; Sanderlin and Melanson, 2007).

The majority of the studies involving *X. fastidiosa* in pecan have focused on the transmission of the pathogen in pecan. *X. fastidiosa* has been shown to survive the typical scion wood storage for pecan and can be transmitted from scions of infected trees into newly developing trees following grafting (Sanderlin, 2005). Likewise, the pathogen is also able to pass from infected pecan rootstock, through the graft union, and into scions collected from non-infected pecan (Sanderlin and Melanson, 2006). Graft transmission of the pathogen may be a major source of spread into pecan orchards (Sanderlin, 2005). A method of treating pecan scion wood with hot water successfully reduces graft transmission of the pathogen (Sanderlin and Melanson, 2008). However, the pathogen continues to spread in established orchards, apparently

by insect transmission (Li *et al.*, 2011; Sanderlin *et al.*, 2009). Insect transmission tests with the pecan spittlebug, *Clastoptera achatina*, and several leafhopper species, including *Homalodisca vitripennis* and *H. insolita*, have shown that the pathogen can also be transmitted by some insects from infected to non-infected pecan and cause disease (Melanson *et al.*, 2009; Sanderlin *et al.*, 2009).

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**CHAPTER 2: A SYSTEMATIC STUDY OF THE 16S-23S RDNA INTERGENIC
TRANSCRIBED SPACER REGION, *PGLA*, AND ERIC-PCR AND REP-PCR
FINGERPRINTS REVEALS THAT *XYLELLA FASTIDIOSA* STRAINS FROM PECAN
ARE PART OF *X. FASTIDIOSA* SUBSP. *MULTIPLEX*¹**

¹ A manuscript containing a major portion of the following chapter, the thesis abstract, and Appendix B, coauthored by R. S. Sanderlin, A. R. McTaggart, and J. H. Ham, has been submitted for publication to Plant Disease under the title, “A systematic study of the 16S-23S rRNA internal transcribed spacer region, *pglA*, and ERIC-PCR and REP-PCR fingerprints reveals that *Xylella fastidiosa* strains from pecan are part of *X. fastidiosa* subsp. *multiplex*” (Appendix A).

INTRODUCTION

Xylella fastidiosa is a Gram-negative, xylem-limited, fastidious bacterium that causes disease in a number of economically important crops, ornamental plants, and shade trees, including grapevine, peach, citrus, oleander, and sycamore (Chang *et al.*, 1993; Davis *et al.*, 1978; Purcell *et al.*, 1999; Sberald *et al.*, 1983; Wells *et al.*, 1987). Symptoms of disease in these hosts typically include scorching of leaves, reduced growth, defoliation, plant death, or chlorosis (Chen *et al.*, 2005; Hopkins and Purcell 2002; Purcell *et al.*, 1999; Sanderlin and Heyderich-Alger 2000; Sberald *et al.*, 1983; Simpson, *et al.*, 2000). Insect transmission by xylem-feeding insects in the families Cercopidae and Cicadellidae is considered the primary means of transmission of *X. fastidiosa* from infected to non-infected plant hosts (Redak *et al.*, 2004); however, other forms of transmission, including graft transmission and seed transmission, have also been reported in some hosts (Chatterjee *et al.*, 2008; Li, W. B. *et al.*, 2003; Redak *et al.*, 2004; Sanderlin, 2005).

Five subspecies of *X. fastidiosa* have been determined since the genus and species was first described by Wells, *et al.* in 1987 (Randall *et al.*, 2009; Schaad *et al.*, 2004a; Schaad *et al.*, 2004b; Schuenzel *et al.*, 2005; Wells *et al.*, 1987). These include *X. fastidiosa* subsp. *fastidiosa*, which infects and causes disease in grapevine and almond, as well as in other plant hosts (Schaad *et al.*, 2004a; Schaad *et al.*, 2004b); *X. fastidiosa* subsp. *pauca*, which infects citrus and coffee and is the only described subspecies not present in North America (Nunney *et al.*, 2010; Schaad *et al.*, 2004b); *X. fastidiosa* subsp. *multiplex*, which infects a large number of plant hosts, including almond, elm, peach, pigeon grape, plum, sycamore, and other shade trees (Schaad *et al.*, 2004b); *X. fastidiosa* subsp. *sandyi*, which was described for those strains infecting oleander and some other hosts (Schuenzel *et al.*, 2005); and the most recently described subspecies, *X.*

fastidiosa subsp. *tashke*, which contains strains infecting chitalpa in the southwestern United States (Randall *et al.*, 2009). Some degree of host specificity exists among subspecies and strains of *X. fastidiosa*; however, this specificity is not always clear and some subspecies and strains are able to infect multiple plant hosts (Hopkins, 1989). Plant hosts, including grapevine and sycamore, growing in Louisiana have been observed with their respective *X. fastidiosa*-induced diseases, and recently, *X. fastidiosa* causing oleander leaf scorch was reported in Louisiana (Singh *et al.*, 2010).

X. fastidiosa 9a5c, a strain isolated from citrus (sweet orange), was the first plant pathogenic bacterium to have its genome completely sequenced (Simpson *et al.*, 2000). Since then, additional strains of *X. fastidiosa*, including strains from almond and grapevine, have been completely sequenced; sequence information for these whole genomes as well as many DNA regions and genes of other strains is available in the National Center for Biotechnology Information's (NCBI) GenBank database (Chen *et al.*, 2010; Schreiber IV *et al.*, 2010; Van Sluys *et al.*, 2003). The availability of these complete genome sequences, as well as other sequence information from the 16S rDNA, the 16S-23S rDNA ITS region, and various genes, has enabled comparative genomic/genetic analyses among strains from different hosts and subspecies and has led to assays for the differentiation of subspecies as well as the identification of new subspecies (Hernandez-Martinez *et al.*, 2006; Huang, 2009; Schuenzel *et al.*, 2005).

In 2000, *X. fastidiosa* was reported as the causative agent of pecan (*Carya illinoensis* (Wangenheim) K. Koch) bacterial leaf scorch (PBLs) (Sanderlin and Heyderich-Alger, 2000). The symptoms of PBLs are similar to those caused by the bacterium in other plant hosts and include leaflets turning tan to brown beginning at the margin and progressing basipetally, followed by abscission of infected leaflets (Sanderlin and Heyderich-Alger, 2000). This disease

tends to occur annually and has been identified in over 20 pecan cultivars and in seedling trees (Sanderlin, 2005; Sanderlin and Melanson, 2007). *X. fastidiosa* threatens the pecan industry by causing reduced nut yields in infected trees. In pecan cv. Cape Fear trees, diseased terminals had reduced kernel weights that averaged 16% less when compared to non-infected terminals in the same orchard (Sanderlin and Heyderich-Alger, 2003). Currently, only management strategies to reduce or eliminate the introduction of this pathogen into pecan orchards exist. No resistant pecan cultivars have been identified, and there is no treatment for trees that become infected.

Compared to other diseases caused by *X. fastidiosa*, PBLS is a recently recognized disease. The majority of the studies on PBLS have been focused on the transmission of the pathogen in pecan. Because pecan cultivars are clonally propagated, graft transmission of the pathogen may be a major source of pathogen spread into orchards. *X. fastidiosa* can be transmitted from either scions or rootstocks obtained from infected pecan trees following grafting (Sanderlin, 2005; Sanderlin and Melanson, 2006). A hot-water treatment of pecan scion wood reduced graft transmission of the pathogen; however, the pathogen continues to spread in established orchards, apparently by insect transmission (Li, B. *et al.*, 2011; Sanderlin *et al.*, 2009; Sanderlin and Melanson, 2008). Most recently, insect transmission tests in pecan have shown that the pecan spittlebug, *Clastoptera achatina*, and several leafhopper species, including the glassy-winged sharpshooter (GWSS), *Homalodisca vitripennis*, and the Johnsongrass sharpshooter, *H. insolita*, are able to transmit *X. fastidiosa* from infected to non-infected pecan with subsequent PBLS development (Sanderlin and Melanson, 2010).

Thus far, pecan strains of *X. fastidiosa* have not been taxonomically grouped at the subspecies level. The taxonomic identification of the pecan strains, as well as their relationship to other strains of *X. fastidiosa* present in Louisiana and in other hosts, would aid in the

development of more effective management strategies for PBLs. These strategies should take into account other plant hosts in and around pecan orchards that may harbor the same subspecies and serve as sources of inoculum for transmission by insect vectors, such as the GWSS, which feed on and transmit the pathogen in several hosts (Adlerz and Hopkins, 1979; Almeida and Purcell, 2003b; Damsteegt *et al.*, 2006; Leininger, 2004; Purcell *et al.*, 1999).

This study determined the subspecies of *X. fastidiosa* strains isolated from pecan and other hosts in Louisiana and the phylogenetic relationship among the strains using a multiprimer PCR assay, DNA sequence analyses, and rep-PCR techniques. The information obtained through this study will contribute to a better understanding of PBLs epidemiology and *X. fastidiosa* population biology.

MATERIALS AND METHODS

Bacterial Strains, Isolation, Growth Conditions, and DNA Extraction. *X. fastidiosa* strains used in this study are listed in Table 1. Bacterial strains were previously isolated from plant tissue showing scorch-like symptoms by squeezing plant sap from pecan rachises and from grapevine and sycamore petioles directly onto a periwinkle wilt medium (Davis *et al.*, 1981) modified by D. L. Hopkins (Sanderlin, personal communication). Culture plates were subsequently incubated in the dark at 28°C and were examined periodically. Individual colonies resembling *X. fastidiosa* were propagated, transferred to tubes containing 30% glycerol, and stored at -60 to -70°C. The strain from oleander was isolated as previously described (Singh *et al.*, 2010).

Strains from pecan, grapevine, and sycamore previously tested positive for *X. fastidiosa* with a commercial *X. fastidiosa* DAS-ELISA kit (Agdia, Inc., Elkhart, IN). The oleander strain, XF Oleander, was previously verified as *X. fastidiosa* using primers specific for *X. fastidiosa*

oleander strains. (Huang, 2009; Singh *et al.*, 2010). All strains were recovered from glycerol storage and grown on modified periwinkle wilt medium at 28°C. Genomic DNA was extracted from 11-day-old cultures of all pecan, grapevine, and oleander strains, and from a one-month-old culture of the sycamore strain using the GenElute Bacterial Genomic DNA Extraction kit (Sigma, St. Louis, MO). DNA samples were stored at -20°C for long-term use or 4°C for short-term use.

Table 1. Strains of *Xylella fastidiosa* Isolated from Symptomatic Plant Tissue and Used in This Study

Strain designation	Host plant (cultivar) ^a	Location of plant host ^b	Year of isolation
XF A-05	<i>Carya illinoensis</i> Pecan (Cape Fear)	Shreveport, LA ^c	2005
XF B-05	<i>C. illinoensis</i> Pecan (Cape Fear)	Shreveport, LA ^c	2005
XF C-05	<i>C. illinoensis</i> Pecan (Cape Fear)	Shreveport, LA ^c	2005
XF A-06	<i>C. illinoensis</i> Pecan (Cape Fear)	Shreveport, LA ^c	2006
XF A-07	<i>Platanus occidentalis</i> Sycamore	Shreveport, LA	2007
XF D-07	<i>C. illinoensis</i> Pecan (Cape Fear)	Shreveport, LA ^c	2007
XF A-08	<i>Vitis vinifera</i> Grapevine	Hessmer, LA ^d	2008
XF Oleander	<i>Nerium oleander</i> Oleander	Baton Rouge, LA	2009
XF A-10	<i>C. illinoensis</i> Pecan (Oconee)	Hessmer, LA ^d	2010
XF B-10	<i>C. illinoensis</i> Pecan (Desirable)	Hessmer, LA ^d	2010

^a The scientific name, common name, and cultivar (in parentheses) for host plant are given whenever the information is known.

^b Shreveport, LA, is located in Caddo Parish; Hessmer, LA, is located in Avoyelles Parish; Baton Rouge, LA, is located in East Baton Rouge Parish.

^c Strains were isolated from symptomatic orchard trees or trees in pots at the Pecan Research-Extension Station in Shreveport, LA.

^d Strains were isolated from symptomatic trees or vines growing at the same location in Hessmer, LA.

***X. fastidiosa*-specific PCR.** Standard PCR was performed on all strains of *X. fastidiosa* from Louisiana with primers RST31 and RST33 (Table 2) to confirm previous ELISA and PCR results. The PCR cycling parameters and procedure and electrophoresis conditions are described in Table 3. PCR was repeated at least twice for each bacterial strain.

Multiprimer PCR Assay. A multiprimer PCR assay designed by Hernandez-Martinez, *et al.* (2006) was performed on all strains of *X. fastidiosa* from Louisiana. Primers used in the multiprimer PCR assay are listed in Table 2. The PCR cycling parameters and procedure and electrophoresis conditions are described in Table 3. PCR was repeated at least twice for each bacterial strain.

PCR and Sequence Analysis of the 16S-23S rDNA Intergenic Transcribed Spacer (ITS) Region and *pglA*. Primers G1 and L1 (Table 2) were used to amplify the 16S-23S rDNA ITS region of strains of *X. fastidiosa*. The PCR cycling parameters and procedure, modified from Henderson *et al.* (2001), are described in Table 3.

Primers XFPglA_Fw and XFPglA_Rv (Table 2) were designed to amplify the *pglA* gene of strains of *X. fastidiosa*. The PCR cycling parameters and procedure are described in Table 3.

Aliquots of the ITS and *pglA* PCR products were tested by gel electrophoresis as described in Table 3 to confirm PCR product. The remaining ITS and *pglA* PCR products were purified using the QuickClean 5M PCR Purification Kit (GenScript, Piscataway, NJ). Purified PCR products were sequenced by the Louisiana State University School of Veterinary Medicine's GeneLab, Baton Rouge, LA, or by Macrogen Inc., Seoul, Korea. Products from at least two independent PCR reactions for ITS and *pglA* were sequenced for each strain to ensure correct base identification with the exception of strains XF A-10 and XF B-10 from pecan whose ITS sequence was not obtained or was determined from a single PCR product, respectively

Table 2. Primers^a Used in This Study

Primer name	Primer sequence (5' → 3')	Test	Reference
RST31	GCGTTAATTTTCGAAGTGATTTCGATTGC	species ID	(Minsavage <i>et al.</i> , 1994)
RST33	CACCATTCGTATCCCGGTG	species ID	(Minsavage <i>et al.</i> , 1994)
XF1968-L	GGAGGTTTACCGAAGACAGAT	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
XF1968-R	ATCCACAGTAAAACCACATGC	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
XF2542-L	TTGATCGAGCTGATGATCG	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
XF2542-R	CAGTACAGCCTGCTGGAGTTA	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
ALM1	CTGCAGAAATTGGAAACTTCAG	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
ALM2	GCCACACGTGATCTATGAA	multiprimer PCR	(Hernandez-Martinez <i>et al.</i> , 2006)
G1	GAAGTCGTAACAAGG	ITS amplification	(Jensen <i>et al.</i> , 1993)
L1	CAAGGCATCCACCGT	ITS amplification	(Jensen <i>et al.</i> , 1993)
XFPglA_Fw	GCCTCCGGTGCGACTGCTTC	<i>pglA</i> amplification ^b	This study
XFPglA_Rv	GCTGCGATTGGACACACATTG	<i>pglA</i> amplification	This study
ERIC1R	ATGTAAGCTCCTGGGGATTAC	ERIC-PCR ^c	(Versalovic <i>et al.</i> , 1991)
ERIC2	AAGTAAGTGATGGGGTGAGCG	ERIC-PCR	(Versalovic <i>et al.</i> , 1991)
REP1R-I	IIICGICGICATCIGGC	REP-PCR ^d	(Versalovic <i>et al.</i> , 1991)
REP2-I	ICGICTTATCIGGCCTAC	REP-PCR	(Versalovic <i>et al.</i> , 1991)

^a Primers were synthesized by Bioneer, Inc (Alameda, CA).

^b Primers were designed within homologous regions surrounding the designated *pglA* gene in the complete genome sequences of *X. fastidiosa* strains 9a5c, Temecula1, M12, and M23 available in NCBI's GenBank.

^c ERIC-PCR: enterobacterial repetitive intergenic consensus PCR

^d REP-PCR: repetitive extragenic palindromic PCR

ITS and *pglA* sequences were analyzed with Geneious Pro 5.4 (Biomatters LTD, Auckland, New Zealand) (Drummond *et al.*, 2011). Alignment of sequences was performed with ClustalW2 (European Molecular Biology Laboratory's European Bioinformatics Institute, available at www.ebi.ac.uk) (Chenna *et al.*, 2003). *pglA* sequences were translated into protein sequences using ExPASy Translate (Swiss Institute of Bioinformatics, <http://expasy.org/>) (Gasteiger *et al.*, 2003).

Table 3. PCR and Electrophoresis Conditions for Tests Conducted in This Study

^a PCR reagents and DNA template solutions were used at the following concentrations: GeneAmp® 10X PCR Buffer I containing 15 mM MgCl₂ (Applied Biosystems, Calsbad, CA); 10X EasyA® reaction buffer (Agilent Technologies, Santa Clara, CA); EasyA® high fidelity PCR cloning enzyme (5 U/μl) (Agilent Technologies, Santa Clara, CA); homemade *Taq* polymerase, ~ 1.0 U/μl; primers, 10 μM; MgCl₂, 50mM; dNTP mix, 10 mM; DNA template, 1 ng/μl. Sterile ddH₂O was used to bring the volume up to the desired reaction volume. Primer sequences are listed in Table 2.

^b PCR was performed in a DNA Engine Peltier Thermal Cycler (Bio-Rad, Hercules, CA).

^c Agarose gels contained ethidium bromide for visualization of PCR products under UV light. PCR products were visualized and photographed with a KODAK Gel Logic 1500 Imaging System (Eastman Kodak Company, Rochester, New York). Unless specified, gels were run under standard conditions in 1X Tris-borate EDTA (TBE) buffer (Sambrook and Russell, 2001).

Test	PCR reaction components ^a	PCR program ^b	Gel electrophoresis ^c
Species ID	25 µL volume: 2 µl of template DNA, 2.5 µl of GeneAmp® 10X PCR Buffer I, 1.0 µl each of primers RST31 and RST33, 0.5 µl of dNTP mix, 1 µl of <i>Taq</i> polymerase	95°C for 1 min; 40 cycles: 95°C for 30 s, 55°C for 30 s, 72°C for 45 s; 72°C for 5 min (Minsavage <i>et al.</i> , 1994)	0.7 to 1.0% agarose gel
Multiprimer PCR assay	25 µL volume: 2 µl template DNA, 2.5 µl of GeneAmp® 10X PCR Buffer I, 1.0 µl each of primers XF1968-L, XF1968-R, XF2542-L, XF2542-R, ALM1, and ALM2, 0.5 µl of dNTP mix, 1.0 µl of <i>Taq</i> polymerase	94°C for 5 min; 40 cycles: 94°C for 1 min, 55°C for 1 min, 72°C for 1 min; 72°C for 10 min (Hernandez-Martinez <i>et al.</i> , 2006)	1.5 % agarose gel
ITS amplification	50 µL volume: 15 µl of template DNA, 5.0 µl of GeneAmp® 10X PCR Buffer I, 2 µl each of primers G1 and L1, 1.0 µl of dNTP mix, 1.5 µl of <i>Taq</i> polymerase	94°C for 5 min; 21 cycles: 94°C for 40 s, 55°C for 1 min, 72°C for 2 min; 72°C for 10 min (Hendson <i>et al.</i> , 2001)	0.7 to 1.0% agarose gel
<i>pglA</i> amplification	50 µL volume: 1.0 µl template DNA, 5.0 µl of 10X EasyA® reaction buffer, 2 µl each of primers XFPglA_Fw and XFPglA_Rv, 1.5 µl of MgCl ₂ , 1.0 µl of dNTP mix, 0.2 µl of EasyA® high fidelity PCR cloning enzyme	95°C for 5 min; 21 cycles: 94°C for 40 s, 60°C for 30 s, 72°C for 2 min; 72°C for 7 min	0.7 to 1.0% agarose gel
ERIC-PCR	25 µL volume: 2 µl of template DNA, 2.5 µl of GeneAmp® 10X PCR Buffer I, 5.0 µl each of primers ERIC1R and ERIC2, 0.8 µl of dNTP mix, 1.0 µl of <i>Taq</i> polymerase	95°C for 7 min; 30 cycles: 94°C for 1 min, 52°C for 1 min, 65°C for 8 min; 65°C for 16 min (Mehta <i>et al.</i> , 2001)	1.8% agarose gel; 60 V for 14 hours at 4 to 6°C
REP-PCR	25 µL volume: 2 µl of template DNA, 2.5 µl of GeneAmp® 10X PCR Buffer I, 5.0 µl each of primers REP1R-I and REP2-I, 0.8 µl of dNTP mix, 1.0 µl of <i>Taq</i> polymerase	95°C for 6 min; 30 cycles: 94°C for 1 min, 40°C for 1 min, 65°C for 4 min; 72°C for 16 min (Mehta <i>et al.</i> , 2001)	1.8% agarose gel; 60 V for 14 hours at 4 to 6°C

Rep-PCR Fingerprinting. Rep-PCRs were performed on the basis of two repetitive elements: enterobacterial repetitive intergenic consensus PCR (ERIC-PCR) and repetitive extragenic palindromic PCR (REP-PCR) (Versalovic *et al.*, 1991). Primers used for ERIC-PCR and REP-PCR are listed in Table 2. The PCR cycling parameters and procedures and electrophoresis conditions for ERIC-PCR and REP-PCR are described in Table 3. Each rep-PCR was repeated at least twice. The presence or absence of bands between 100 bp and 1,650 bp for ERIC-PCR and between 400 bp and 2,000 bp for REP-PCR was recorded. A consensus dataset for distinguishable bands that regularly appeared within these ranges in rep-PCR fingerprints was used for phylogenetic reconstruction.

Phylogenetic Analyses. DNA sequences of *X. fastidiosa* strains used for comparative analyses in this study were obtained from NCBI's GenBank (Appendix B).

ITS sequences from 49 strains of *X. fastidiosa* and one strain of *Xanthomonas campestris* pv. *campestris* were aligned with MUSCLE and cured in Gblocks (Méthodes *et algorithmes* pour la Bio-informatique LIRMM, http://www.phylogeny.fr/version2_cgi/index.cgi) (Dereeper *et al.*, 2008). A maximum likelihood (ML) search for the best-scoring ML tree of the cured ITS sequences was performed in RAxML using the rapid bootstrapping algorithm and the GTRMIX model of evolution (Appendix C) (Stamatakis, 2006; Stamatakis *et al.*, 2008). Analyses were run with 1000 bootstrap replicates. A Markov Chain Monte Carlo (MCMC) search for the cured ITS sequences was performed in MrBayes 3.1 (Appendix D) (Huelsenbeck and Ronquist, 2001; Larget and Simon, 1999; Ronquist and Huelsenbeck, 2003). Four runs each with four chains were tested until the standard deviation of the split frequencies reached 0.01. A starting tree obtained from the ML analysis was used for Bayesian analysis.

The aligned *pglA* and *pglA*-homologous sequences from 13 strains of *X. fastidiosa* were analyzed in RAxML and MrBayes, as previously described, except that MCMC search runs were tested until the standard deviation of the split frequencies reached 0.02 and no starting tree was used (Appendices C and D).

Phylogenetic reconstruction using the unweighted pair group method with arithmetic mean (UPGMA) was performed in MEGA5 for the individual and combined datasets of binary data for ERIC-PCR and REP-PCR (Tamura *et al.*, 2011). Analyses were run with 1000 bootstrap replicates. A MCMC search for the individual and combined datasets for ERIC-PCR and REP-PCR was performed in MrBayes 3.1 (Appendix D). Four runs each with four chains were tested until the standard deviation of the split frequencies reached 0.01.

A MCMC search for the total combined data set of 49 strains of *X. fastidiosa* and one strain of *X. campestris* pv. *campestris* including the aligned and cured ITS sequences, the aligned *pglA* sequences, and the binary data from ERIC-PCR and REP-PCR was performed in MrBayes 3.1 (Appendix D). Four runs each with four chains were tested until the standard deviation of the split frequencies reached 0.02. A starting tree obtained from the ML analysis for the aligned and cured ITS sequences was used for the MCMC search. Since *pglA* sequences were only available for strains whose complete genomes have been published, these sequences were included with the ITS sequences in the combined dataset so that a *pglA* sequence from a particular subspecies and host was included with the ITS sequence of a strain from the same subspecies and host. These sequences were included as follows: 9a5c *pglA* sequence included with strain CI.X0; Temecula1 *pglA* sequence included with strain PD 95-2; XF GB514 *pglA* sequence included with strain PD 95-4; M12 *pglA* sequence included with strain Dixon; and M23 *pglA* sequence included with strain ALS1.

Convergence of all Bayesian analyses was tested using the cumulative and compare functions in AWTY (http://king2.scs.fsu.edu/CEBProjects/awty/awty_start.php) (Nylander *et al.*, 2008). Phylogenetic trees were obtained from RAxML for ITS sequence, *pglA* sequence, and total combined analyses and from MEGA5 for ERIC-PCR and REP-PCR data analyses. Bootstrap values from ML analyses or UPGMA analyses greater than 70% and posterior probabilities from MCMC analyses greater than 0.95 were included on phylogenetic trees. *X. fastidiosa* strain XF A-10 was not included in the ML searches or in the MCMC analysis of the total combined dataset due to a lack of sequence data.

RESULTS

Genetic Verification of *X. fastidiosa* Strains Isolated from Pecan and Other Plant Hosts in Louisiana. A DNA band approximately 733 bp in size, the expected product size for *X. fastidiosa* when using *X. fastidiosa*-specific primers RST31 and RST33, was produced from all bacterial strains isolated from pecan and other hosts (grapevine, oleander, and sycamore) from Louisiana and used in this study (Fig. 1; data not shown for XF A-10 and XF B-10).

Multiprimer PCR Assay of *X. fastidiosa* from Louisiana. Three DNA bands approximately 412 bp, 521 bp, and 638 bp in size, the expected sizes of the products amplified from the multiprimer PCR assay for the *X. fastidiosa* subsp. *multiplex* Almond Leaf Scorch (ALS) II genotype, were amplified from each of the pecan and sycamore strains from Louisiana (Fig. 2; data not shown for XF A-10 and XF B-10) (Hernandez-Martinez *et al.*, 2006). A single band approximately 412 bp in size, the expected size of the product amplified from the multiprimer PCR assay for the *X. fastidiosa* subsp. *fastidiosa* Pierce's disease (PD) genotype, was amplified from the Louisiana grapevine strain, XF A-08 (Fig. 2) (Hernandez-Martinez *et al.*, 2006). A single band approximately 638 bp in size, the expected size of the product amplified



Figure 1. Agarose gel showing the expected 733-bp PCR product using primers RST31 and RST33, specific for *Xylella fastidiosa*, for bacterial strains isolated from diseased grapevine, oleander, pecan, and sycamore from Louisiana. A strain of *Burkholderia glumae* and sterile distilled deionized water (ddH₂O) were used as negative controls. Samples were arranged as follows: lane 1: 1 kb plus ladder (Invitrogen); lane 2: XF A-05 (pecan); lane 3: XF B-05 (pecan); lane 4: XF C-05 (pecan); lane 5: XF A-06 (pecan); lane 6: XF D-07 (pecan); lane 7: XF A-08 (grapevine); lane 8: XF Oleander (oleander); lane 9: XF A-07 (sycamore); lane 10: *B. glumae* 336gr-1; and lane 11: sterile ddH₂O. Strains XF A-10 and XF B-10 from pecan (not pictured) also produced the expected PCR products from primers RST31 and RST33.

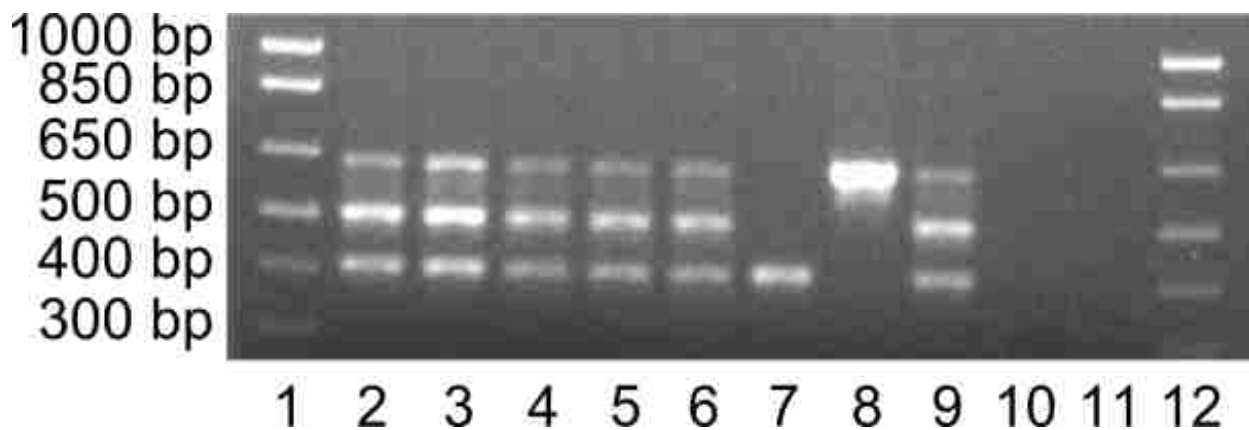


Figure 2. Agarose gel (1.5%) showing multiprimer PCR products of strains of *Xylella fastidiosa* isolated from diseased grapevine, oleander, pecan, and sycamore from Louisiana. A strain of *Burkholderia glumae* and sterile distilled deionized water (ddH₂O) were used as negative controls. Samples were arranged as follows: lane 1: 1 kb plus ladder (Invitrogen); lane 2: XF A-05 (pecan); lane 3: XF B-05 (pecan); lane 4: XF C-05 (pecan); lane 5: XF A-06 (pecan); lane 6: XF D-07 (pecan); lane 7: XF A-08 (grapevine); lane 8: XF Oleander (oleander); lane 9: XF A-07 (sycamore); lane 10: *B. glumae* 336gr-1; lane 11: sterile ddH₂O; and lane 12: 1 kb plus ladder. Strains XF A-10 and XF B-10 from pecan (not pictured) produced all three possible PCR products from the multiprimer PCR.

from the multiprimer PCR assay for the *X. fastidiosa* subsp. *sandyi* Oleander Leaf Scorch (OLS) genotype, was amplified from the Louisiana oleander strain, XF Oleander (Fig. 2) (Hernandez-Martinez *et al.*, 2006).

Sequence Analyses of the 16S-23S rDNA ITS Region of *X. fastidiosa* Strains from Louisiana. ITS sequences were obtained from nine strains of *X. fastidiosa* used in this study (Appendix E). ClustalW2 alignment of the ITS sequences trimmed to the same starting and ending points (Appendix F) showed that the ITS sequences from all strains of *X. fastidiosa* from pecan and sycamore from Louisiana were identical. These strains had a sequence identity of 98% when compared to the grapevine (XF A-08) and oleander (XF Oleander) strains from Louisiana (Appendix F). A basic local alignment search tool (BLAST) (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) search of the pecan and sycamore ITS sequence against the complete genomes of *X. fastidiosa* showed the highest sequence identity to *X. fastidiosa* subsp. *multiplex* strain M12 from almond (100%), followed by *X. fastidiosa* subsp. *pauca* strain 9a5c from citrus (99%), and *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond (98%) (Appendix G) (Altschul *et al.*, 1990). A BLAST search of the ITS sequence from grapevine strain XF A-08 showed the highest sequence identity (100%) to *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond (Appendix G). A BLAST search of the ITS sequence from oleander strain XF Oleander showed the highest sequence identity (99%) to *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond (Appendix G).

ITS sequences obtained for strains of *X. fastidiosa* in this study were deposited in GenBank under accession numbers JN092378 through JN092385 (Appendix B).

Sequence Analyses of *pglA* of *X. fastidiosa* Strains from Louisiana. DNA sequences of *pglA* encoding a polygalacturonase, a major virulence factor of *X. fastidiosa* (Roper *et al.*, 2007), were obtained from eight strains of *X. fastidiosa* used in this study (Appendix H). ClustalW2 alignment of the *pglA* sequences (Appendix I) showed that the *pglA* sequences from all *X. fastidiosa* strains from pecan and sycamore from Louisiana were identical. These strains had a sequence identity of 98% when compared to the grapevine (XF A-08) and oleander (XF Oleander) strains from Louisiana (Appendix I). A BLAST search of the pecan and sycamore *pglA* sequence against the complete genome sequences of *X. fastidiosa* showed the highest sequence identity (99%) to *X. fastidiosa* subsp. *multiplex* strain M12 from almond, followed by *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond (98%), and *X. fastidiosa* subsp. *pauca* strain 9a5c from citrus (97%) (Appendix J). A BLAST search of the *pglA* sequence from grapevine strain XF A-08 showed the highest sequence identity (100%) to *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond (Appendix J). A BLAST search of the *pglA* sequence from oleander strain XF Oleander showed the highest sequence identity (98%) to *X. fastidiosa* subsp. *fastidiosa* strains Temecula1 and GB514 from grapevine and M23 from almond and to *X. fastidiosa* subsp. *multiplex* strain M12 from almond (Appendix J).

Early termination, which is present in the *pglA* gene of strain 9a5c from citrus (Van Sluys *et al.*, 2003), was not found in any of the *pglA* sequences from strains of *X. fastidiosa* from Louisiana (Appendix K).

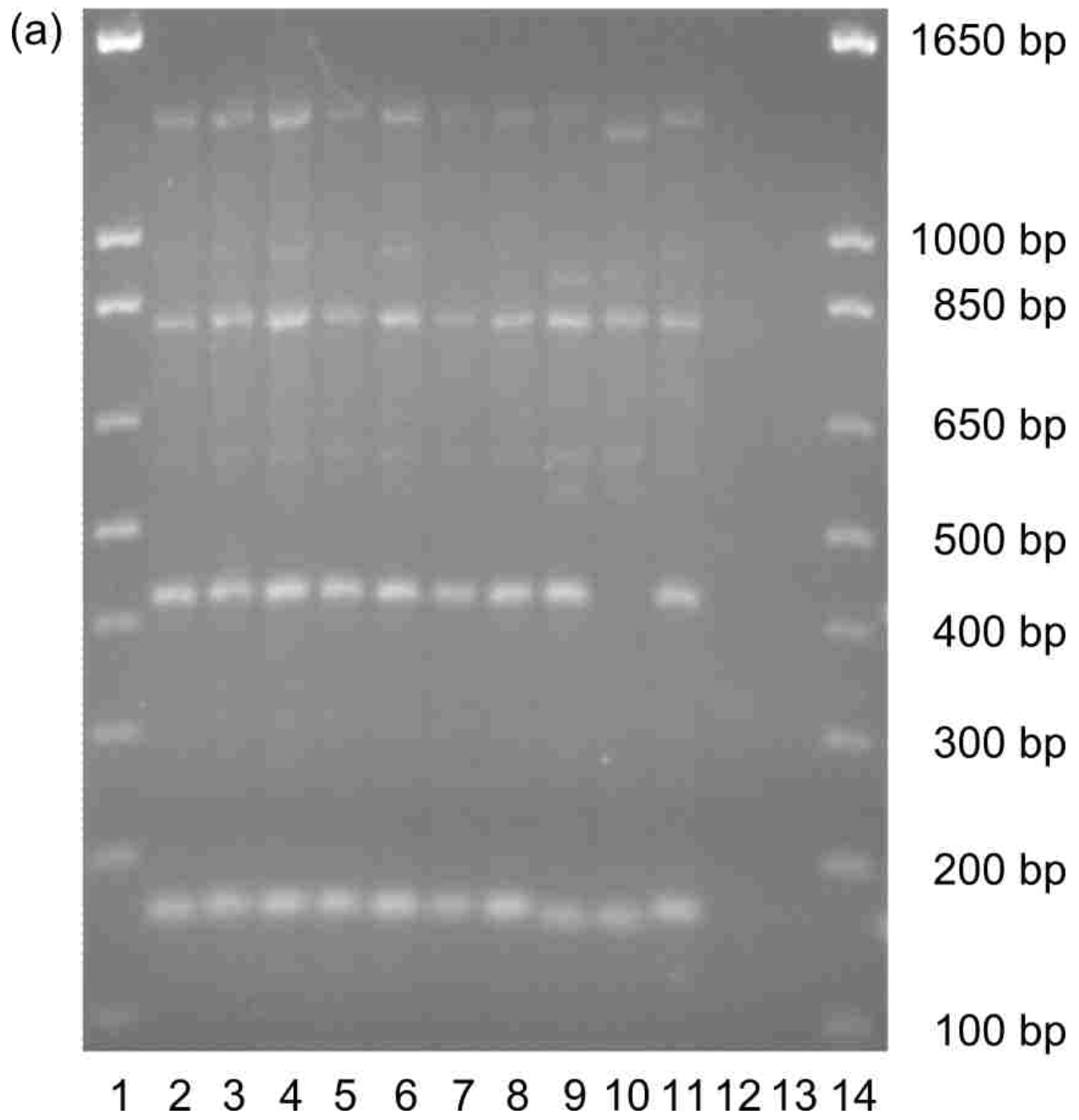
pglA sequences obtained from strains of *X. fastidiosa* in this study were deposited in GenBank under accession numbers JN092387 through JN092394 (Appendix B).

Rep-PCR Analyses of *X. fastidiosa* Strains from Louisiana. Bands in ten band classes between 100 bp and 1,650 bp for ERIC-PCR and in nine band classes between 400 bp and 2,000 bp for REP-PCR were scored as being present or absent for each *X. fastidiosa* strain tested (Appendix L).

All pecan strains, regardless of the cultivar from which they were isolated, and the sycamore strain produced the same ERIC-PCR fingerprint (Fig. 3a). Obvious band differences were present in the ERIC-PCR fingerprints between the grapevine and oleander strains and between these strains and those from pecan and sycamore (Fig. 3a). Namely, bands approximately 155 bp, 550 bp, and 880 bp in size were present only in grapevine strain XF A-08 and oleander strain XF Oleander but not in any of the other strains; bands approximately 160 bp and 950 bp in size were present in all pecan strains and in sycamore strain XF A-07 but not in grapevine strain XF A-08 or oleander strain XF Oleander; bands approximately 300 bp and 420 bp in size were present in all strains except oleander strain XF Oleander; and a band approximately 1,275 bp in size was present in oleander strain XF Oleander but not in any of the other strains (Fig. 3a)

REP-PCR fingerprints of pecan strains, however, showed variation among some pecan strains (Fig. 4a). Pecan cv. Cape Fear strain XF A-06 and sycamore strain XF A-07 produced a band approximately 900 bp in size that was not present in any of the other strains tested (Fig. 4a). Pecan cv. Oconee strain XF A-10 failed to produce a band approximately 1,900 bp in size that was present in all of the other pecan strains and in sycamore strain XF A-07, but produced a slightly larger band, approximately 1,950 bp in size, that was not present in any of the other strains tested.

Figure 3. (a) Agarose gel (1.8%) showing ERIC-PCR product fingerprints from 10 strains of *Xylella fastidiosa* isolated from diseased grapevine, oleander, pecan, and sycamore from Louisiana. Sterile distilled deionized water (ddH₂O) was used as a negative control. Samples were arranged as follows: lane 1: 1 kb plus ladder (Invitrogen); lane 2: XF A-05 (pecan – CF); lane 3: XF B-05 (pecan – CF); lane 4: XF C-05 (pecan – CF); lane 5: XF A-06 (pecan – CF); lane 6: XF D-07 (pecan – CF); lane 7: XF A-10 (pecan – O); lane 8: XF B-10 (pecan – D); lane 9: XF A-08 (grapevine); lane 10: XF Oleander (oleander); lane 11: XF A-07 (sycamore); lane 12: *Burkholderia glumae* 336gr-1; lane 13: sterile ddH₂O; and lane 14: 1 kb Plus ladder. Pecan cultivar designations: CF = Cape Fear; D = Desirable; O = Oconee. (b) Phylogram constructed from the ERIC-PCR fingerprints shown in (a). Branch tip labels include the plant host and cultivar, when applicable, from which the strain of *X. fastidiosa* was obtained and the strain name (parentheses). Phylogram was obtained from a UPGMA analysis (1000 bootstrap replicates) using MEGA5. Bootstrap values (>70%) are shown above branch nodes; posterior probabilities (>0.95) obtained from Bayesian inference in MrBayes 3.1 are shown below branch nodes.



(Figure 3 continued)

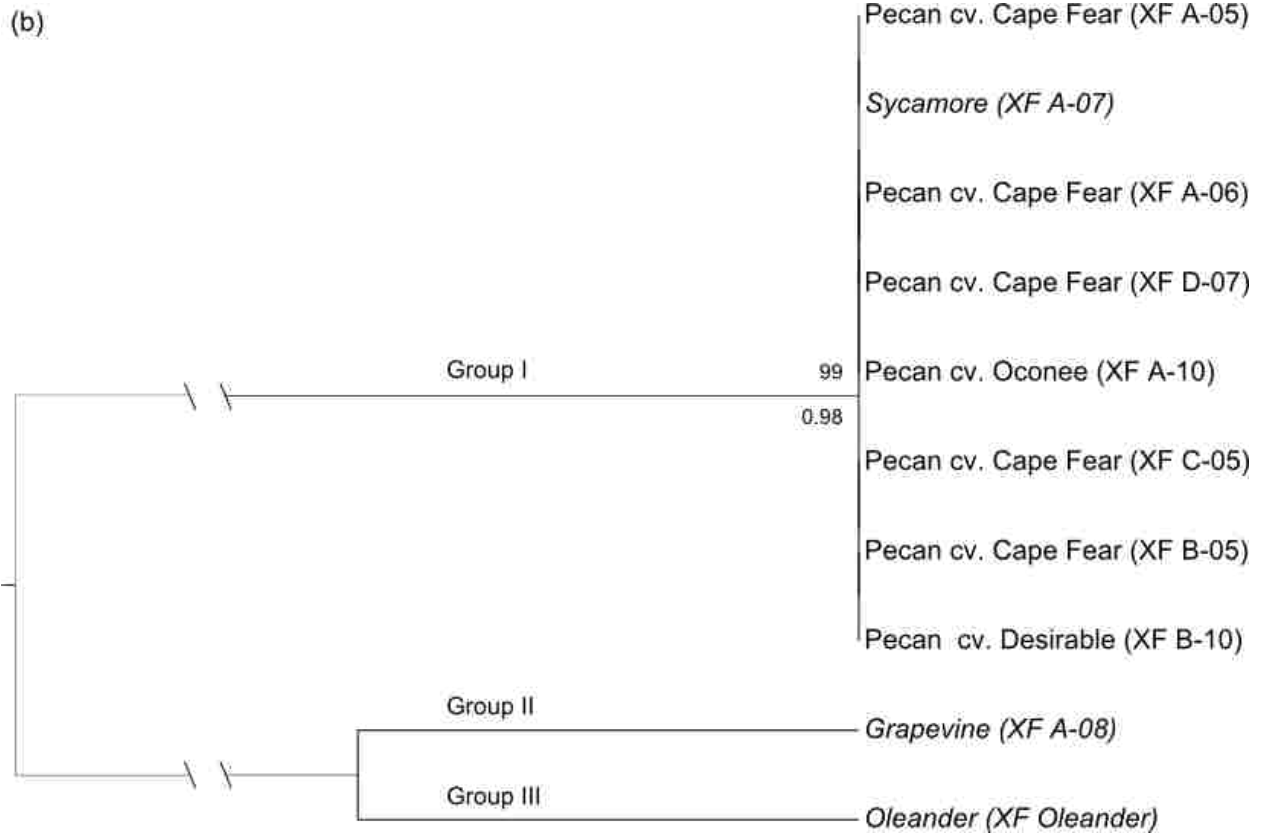
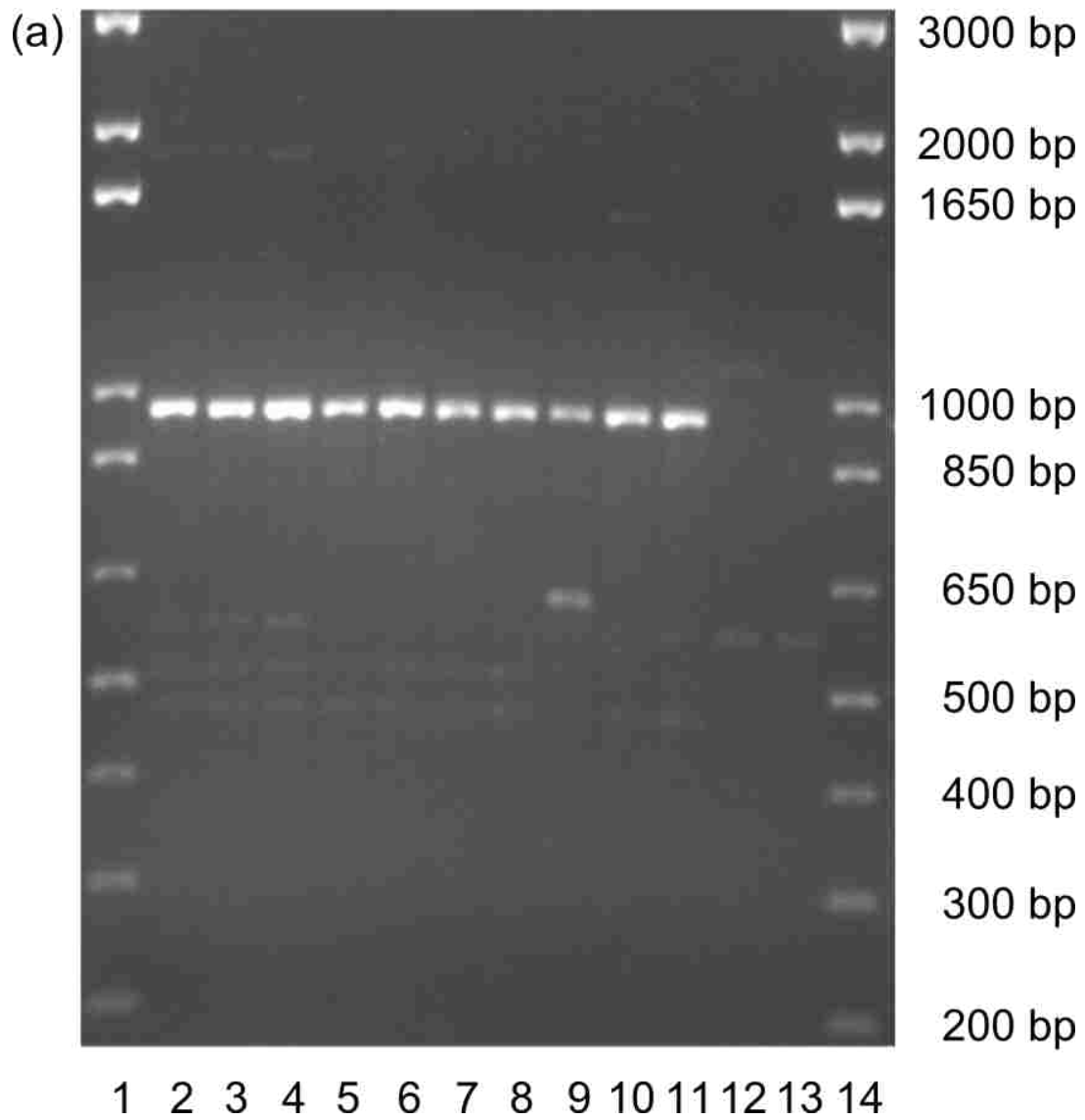
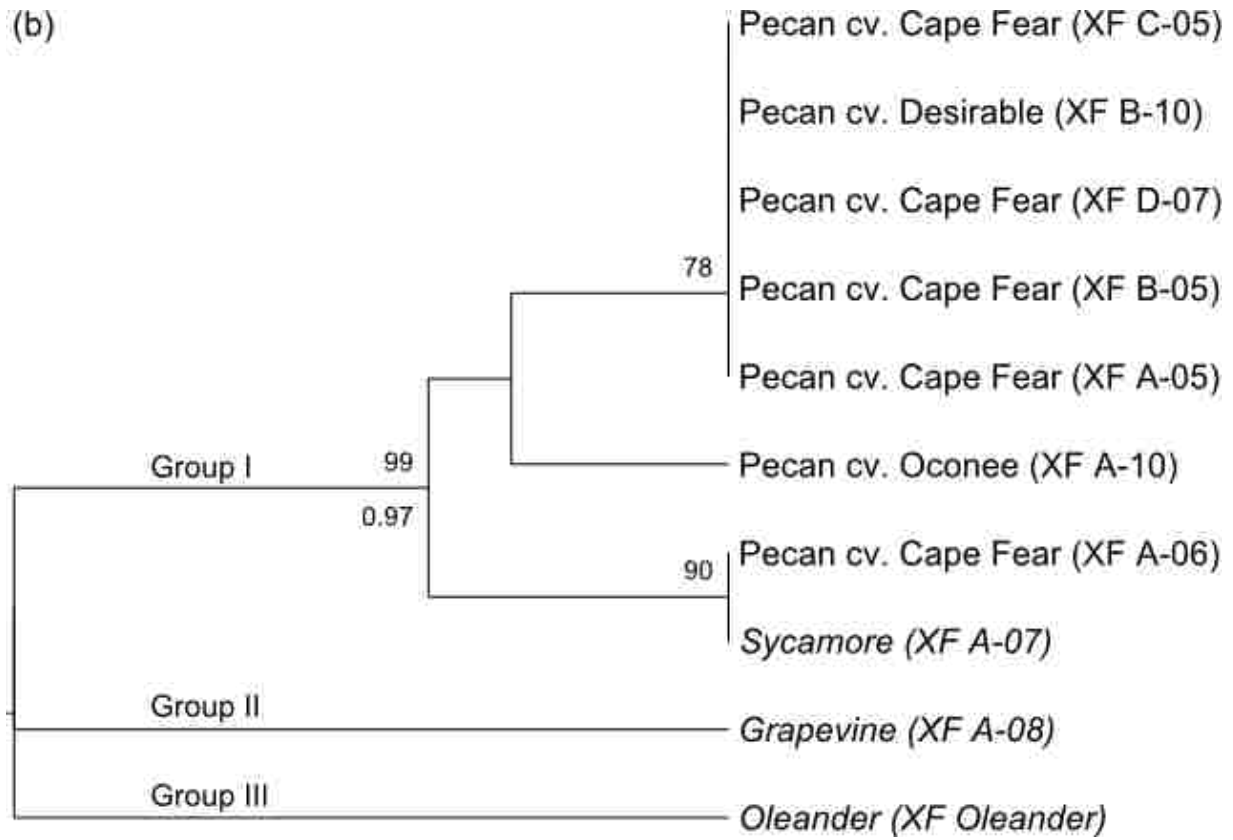


Figure 4. (a) Agarose gel (1.8%) showing REP-PCR product fingerprints from 10 strains of *Xylella fastidiosa* isolated from diseased grapevine, oleander, pecan, and sycamore from Louisiana. Sterile distilled deionized water (ddH₂O) was used as a negative control. Samples were arranged as follows: lane 1: 1 kb plus ladder (Invitrogen); lane 2: XF A-05 (pecan – CF); lane 3: XF B-05 (pecan – CF); lane 4: XF C-05 (pecan – CF); lane 5: XF A-06 (pecan – CF); lane 6: XF D-07 (pecan – CF); lane 7: XF A-10 (pecan – O); lane 8: XF B-10 (pecan – D); lane 9: XF A-08 (grapevine); lane 10: XF Oleander (oleander); lane 11: XF A-07 (sycamore); lane 12: *Burkholderia glumae* 336gr-1; lane 13: sterile ddH₂O; and lane 14: 1 kb plus ladder. Pecan cultivar designations: CF = Cape Fear; D = Desirable; O = Oconee. (b) Phylogram constructed from the REP-PCR fingerprints shown in (a). Branch tip labels include the plant host and cultivar, when applicable, from which the strain of *X. fastidiosa* was obtained and the strain name (parentheses). Phylogram was obtained from a UPGMA analysis (1000 bootstrap replicates) using MEGA5. Bootstrap values (>70%) are shown above branch nodes; posterior probabilities (>0.95) obtained from Bayesian inference in MrBayes 3.1 are shown below branch nodes.



(Figure 4 continued)



Phylogenetic Analyses of *X. fastidiosa* Strains from Louisiana. Three main groups were recovered from Bayesian inference and UPGMA using the ERIC-PCR dataset (Fig. 3b). Group I, which was well supported by Bayesian posterior probability (0.98) and UPGMA bootstrap (99%), was monophyletic and included all strains of *X. fastidiosa* from pecan and sycamore (Fig. 3b). Group II included only the grapevine strain and was separate from all other strains of *X. fastidiosa* from Louisiana. Group III included only the oleander strain and was also separate from all other strains of *X. fastidiosa* from Louisiana.

Three main groups were recovered from Bayesian inference and UPGMA using the REP-PCR dataset (Fig. 4b). Group I, which was well supported by Bayesian posterior probability (0.97) and UPGMA bootstrap (99%), was monophyletic and included all strains of *X. fastidiosa* from pecan and sycamore (Fig. 4b). Three subgroups, however, were present within Group I: one subgroup included strain XF A-06 from the pecan cultivar Cape Fear and strain XF A-07 from sycamore (UPGMA bootstrap = 90%); the second subgroup included only strain XF A-10 from the pecan cultivar Oconee; and the third subgroup included four strains from the cultivar Cape Fear (XF A-05, XF B-05, XF C-05, and XF D-07) and strain XF B-10 from the pecan cultivar Desirable (UPGMA bootstrap = 78%) (Fig. 4b). Group II and Group III included only the grapevine strain and the oleander strain, respectively, separating each of them from all other strains.

A UPGMA phylogram recovered from the combined ERIC-PCR and REP-PCR datasets was similar to the REP-PCR UPGMA phylogram with similar support from bootstrap values and posterior probabilities except that it showed the pecan-sycamore subgroup to be more closely related to the larger pecan subgroup (Fig. 5).

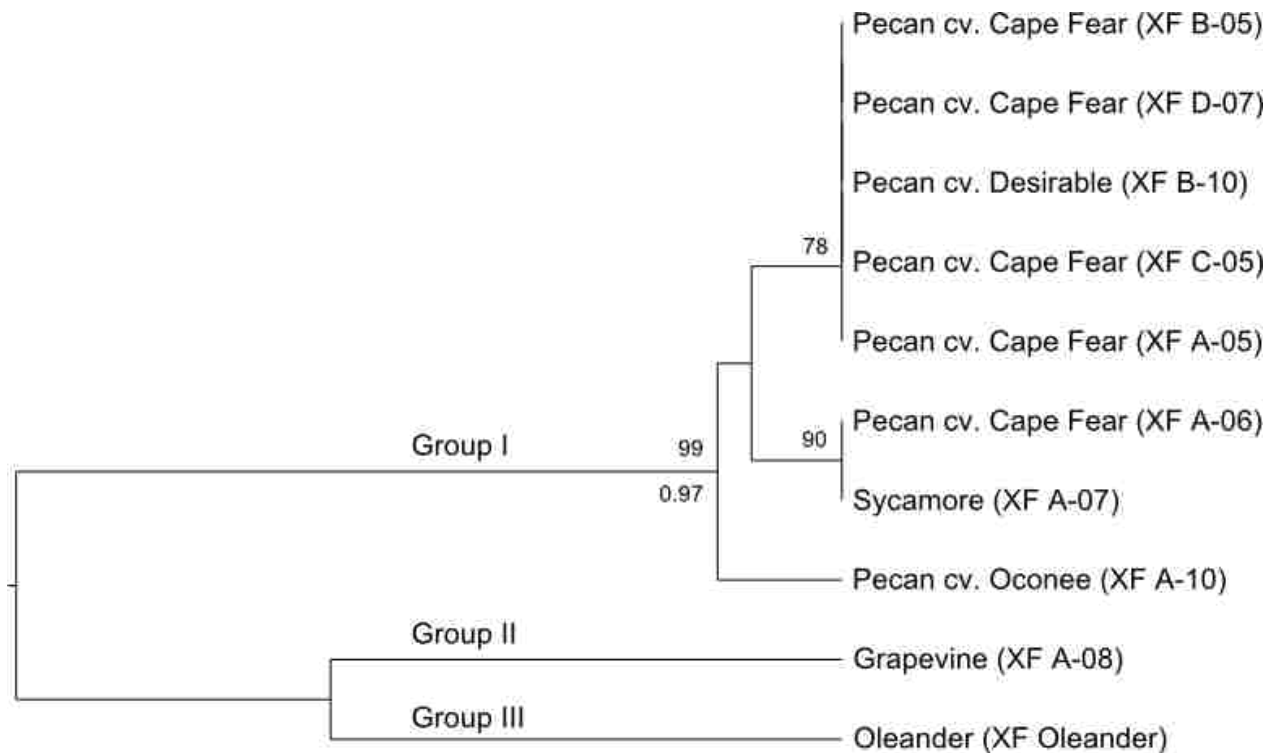


Figure 5. Phylogram constructed from the combined ERIC-PCR and REP-PCR product fingerprints. Branch tip descriptions include the plant host and cultivar, when applicable, from which the strain of *X. fastidiosa* was obtained and the strain name (parentheses). Phylogram was obtained from a UPGMA analysis (1000 bootstrap replicates) using MEGA5. Bootstrap values (>70%) are shown above branch nodes; posterior probabilities (>0.95) obtained from Bayesian analysis in MrBayes 3.1 are shown below branch nodes.

The ML phylogram of aligned and cured 16S-23S ITS regions from 49 strains of *X. fastidiosa* and from one strain of *X. campestris* pv. *campestris* included as an outgroup placed the majority of the *X. fastidiosa* strains into six major monophyletic or paraphyletic groups with bootstrap values greater than 84% (Fig. 6). The majority of these groups were also strongly supported by posterior probabilities greater than 0.95. Group I was monophyletic and included strains from citrus and coffee. Group II was paraphyletic with unresolved relationships among strains from a variety of hosts, including the pecan and sycamore strains from Louisiana and strains from almond and peach. Group III was a monophyletic group within Group II, and included strains of *X. fastidiosa* from chitalpa (Randall *et al.*, 2009). Group IV was a

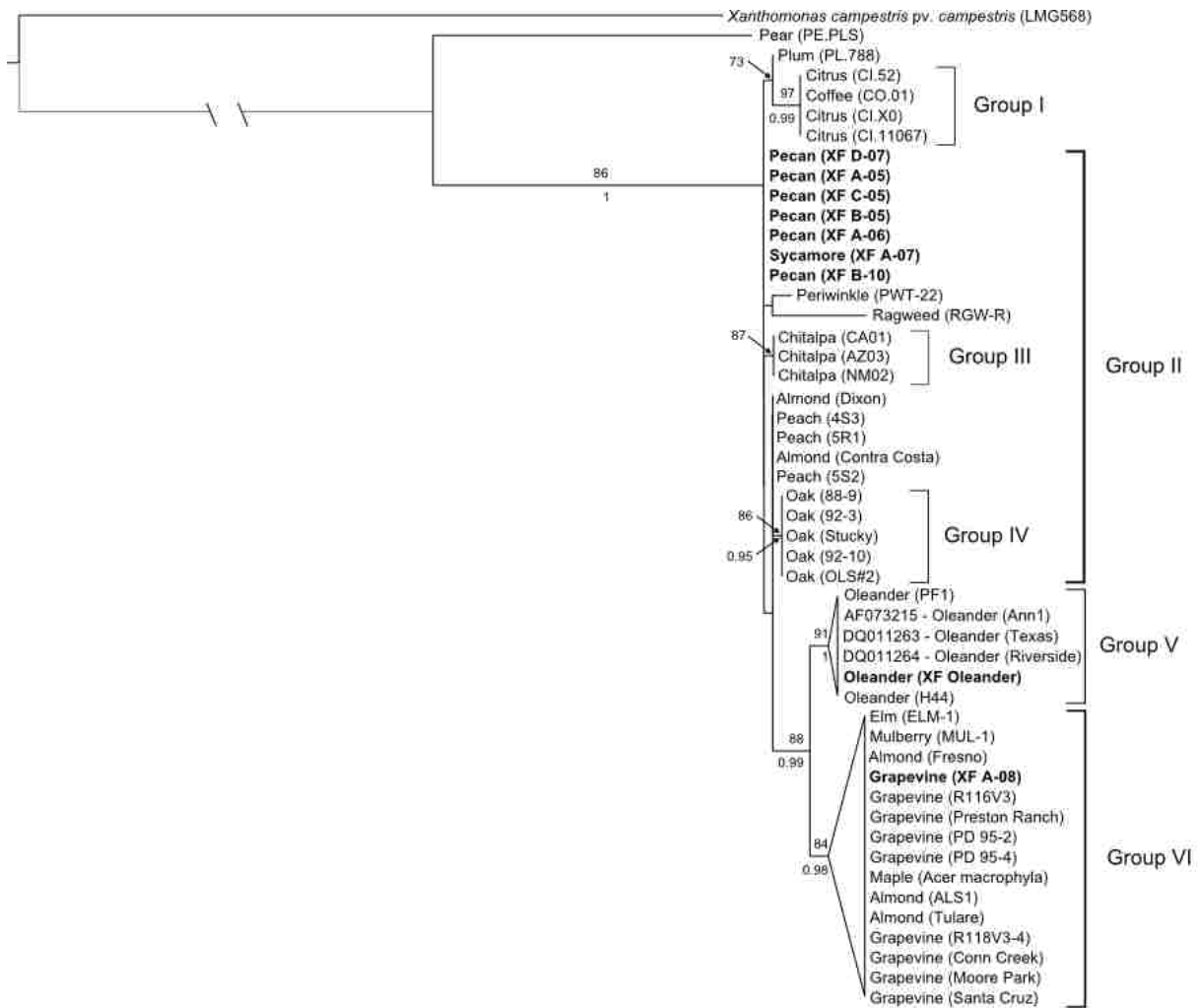


Figure 6. Phylogram of the 16S-23S rDNA intergenic transcribed spacer (ITS) sequence dataset from 49 strains of *Xylella fastidiosa* and one strain of *Xanthomonas campestris* pv. *campestris* included as an outgroup. Branch tip labels include the host and strain name (parentheses) of *X. fastidiosa*. ITS sequences obtained from this study are indicated in bold. Sequences from all other strains were obtained from NCBI's GenBank (accession numbers in Appendix B). Phylogram was obtained from a maximum likelihood (ML) search using RAxML. Bootstrap values (>70%) from 1000 bootstrap replicates from the ML search are shown above branch nodes; posterior probabilities (>0.95) obtained from Bayesian inference in MrBayes 3.1 are shown below branch nodes.

monophyletic group also recovered within Group II that included strains of *X. fastidiosa* from oak. Group V was monophyletic and included strains of *X. fastidiosa* from oleander, including the Louisiana oleander strain. Group VI was monophyletic and included strains of *X. fastidiosa* from almond and grapevine, including the Louisiana grapevine strain.

The ML phylogram of the aligned *pglA* sequences from 13 strains of *X. fastidiosa*, including citrus strain 9a5c used as an outgroup, separated the strains into four groups (Fig. 7). The pecan and sycamore strains formed a monophyletic group with *X. fastidiosa* subsp. *multiplex* strain M12 from almond. The Louisiana grapevine strain formed a monophyletic group with strains of *X. fastidiosa* subsp. *fastidiosa* from grapevine and almond. The Louisiana oleander strain did not group with other strains of *X. fastidiosa*. *X. fastidiosa* subsp. *pauca* strain 9a5c from citrus also did not group with other strains of *X. fastidiosa*. Most of the major groups were strongly supported with bootstrap values greater than 85% and posterior probabilities of 0.99 (Fig. 7).

The MCMC phylogram of the total combined dataset of 49 strains of *X. fastidiosa* and one strain of *X. campestris* pv. *campestris* including the aligned and cured ITS sequences, the aligned *pglA* sequences, and the binary data from ERIC-PCR and REP-PCR placed the majority of the *X. fastidiosa* strains into six major monophyletic or paraphyletic groups with bootstrap values greater than 84% (Fig. 8). Though the location of groups on the phylogram differed in comparison to the phylogram recovered from the cured ITS sequences (Fig. 6), the different monophyletic and paraphyletic groups in this analysis were comprised of the same strains of *X. fastidiosa* as the previous analysis. The pecan and sycamore strains were still part of a large paraphyletic group that included other strains of *X. fastidiosa* from almond and peach. This analysis showed increased posterior probability support for a number of groups (Fig. 8).

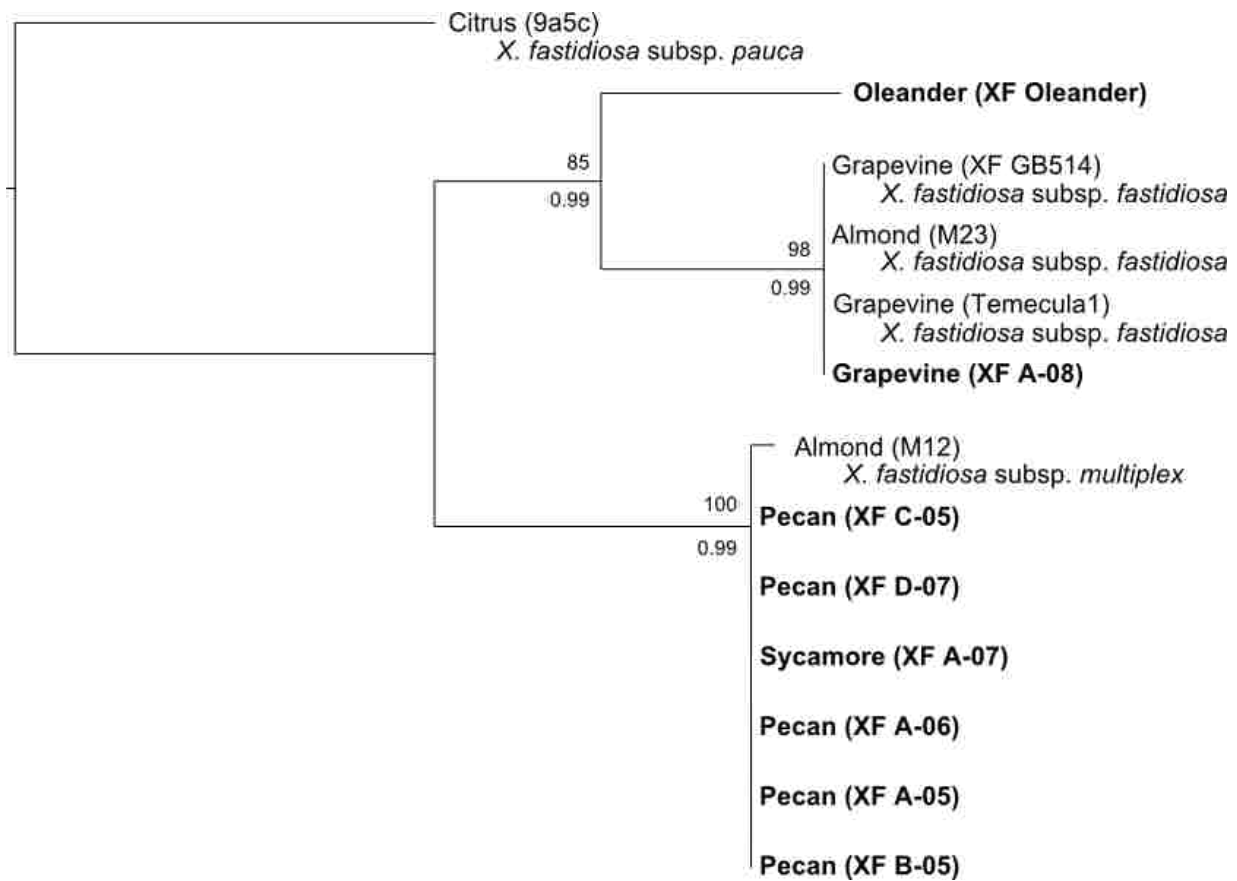
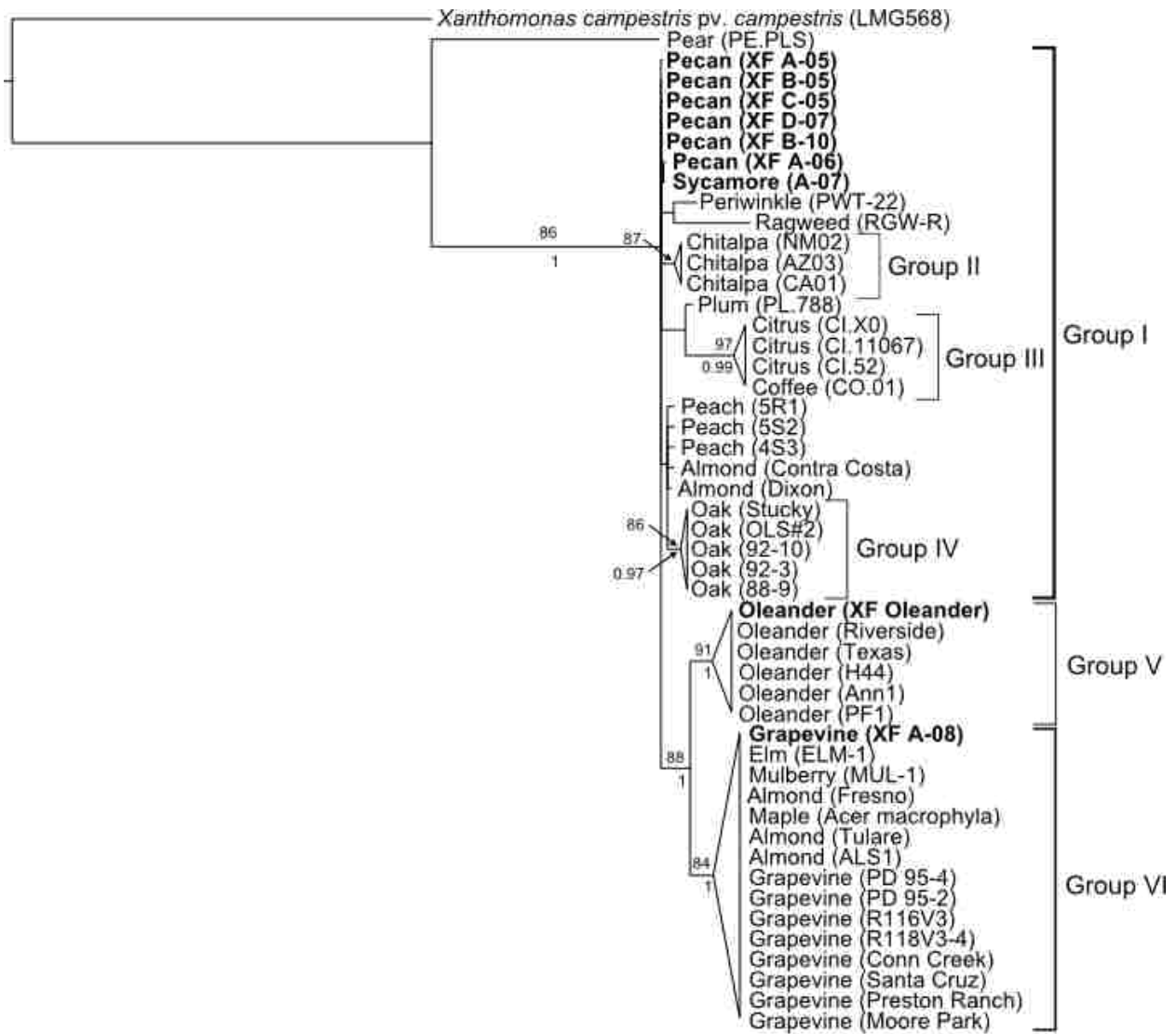


Figure 7. Phylogram of *pglA* sequences from 13 strains of *Xylella fastidiosa* with the citrus strain 9a5c used as an outgroup. Branch tip labels include the host strain name (parentheses) of *X. fastidiosa*; the known subspecies of *X. fastidiosa* are indicated below each branch tip label. *pglA* sequences obtained from this study are indicated in bold. Sequences from all other strains were obtained from NCBI's GenBank. Phylogram was obtained from a maximum likelihood (ML) search using RAxML. Bootstrap values (>70%) from 1000 bootstrap replicates from the ML search in RAxML are shown above branch nodes; posterior probabilities (>0.95) obtained from Bayesian inference in MrBayes 3.1 are shown below branch nodes.

Figure 8. Phylogram of the combined dataset constructed from available 16S-23S rDNA intergenic transcribed spacer (ITS) sequences, *pglA* sequences, and ERIC-PCR and REP-PCR product fingerprints from 49 strains of *Xylella fastidiosa* and one strain of *Xanthomonas campestris* pv. *campestris* included as an outgroup. Pecan strain XF A-10 was not included in the analysis due to a lack of sequence data. Since *pglA* sequences were only available for strains whose complete genomes have been published, these sequences were included with the ITS sequences in the combined dataset as follows: 9a5c *pglA* sequence included with strain CI.X0; Temecula1 *pglA* sequence included with strain PD 95-2; XF GB514 *pglA* sequence included with strain PD 95-4; M12 *pglA* sequence included with strain Dixon; and M23 *pglA* sequence included with strain ALS1. Branch tip labels include the plant host from which the strain of *X. fastidiosa* was obtained and the strain name (parentheses). ITS sequences, ERIC-PCR and REP-PCR data obtained from this study are indicated in bold. Sequences from all other strains were obtained from GenBank (accession numbers in Appendix B). Phylogram was obtained from Bayesian analysis in MrBayes 3.1. Bootstrap values (>70%) from 1000 bootstrap replicates obtained from the maximum likelihood search in RAxML of the 16S-23S ITS sequences cured in Gblocks and shown in Fig. 6 are shown above branch nodes; posterior probabilities (>0.95) obtained from the Bayesian inference of the combined data set in MrBayes 3.1 are shown below branch nodes.



Convergence of all Bayesian analyses was verified using the cumulative and compare functions in AWTY (Appendix M).

DISCUSSION

X. fastidiosa is a complex plant pathogen that infects and causes disease in a wide range of hosts (Purcell and Hopkins, 1996). Subspecies classifications have been based largely on molecular techniques and host plant infectivity. However, genetic differences within subspecies and even within strains from the same host have also been observed (Almeida *et al.*, 2008; Mehta *et al.*, 2001; Scally *et al.*, 2005). Recombination has also been shown to occur between subspecies and between strains from different hosts (Almeida *et al.*, 2008; Scally *et al.*, 2005; Schuenzel *et al.*, 2005). The presence of multiple subspecies and strains of *X. fastidiosa* in the same geographic region with common insect vectors may increase the opportunity for continuing diversification within this species and the possibility of the occurrence of new diseases in hosts that have yet to be infected by *X. fastidiosa* (Nunney *et al.*, 2010).

Pecan, the only native nut grown commercially in the United States (Perez and Pollack, 2003), is produced in 15 states (Agricultural Statistics 2010, USDA-NASS), including California, New Mexico, Texas, Louisiana, Georgia, and Florida, where diseases caused by *X. fastidiosa* have been reported and are known to occur. Despite this and the fact that *X. fastidiosa* causes disease in pecan, pecan strains of *X. fastidiosa* have rarely been studied. Consequently, genetic and taxonomic information regarding pecan strains of *X. fastidiosa* is very limited. In this investigation, various molecular techniques and phylogenetic methods were used to study the taxonomy of *X. fastidiosa* strains isolated from pecan and other hosts in Louisiana at a sub-specific level and to determine the *X. fastidiosa* subspecies grouping of the strains from pecan. Three strains of *X. fastidiosa* isolated from grapevine, oleander, and sycamore growing in

Louisiana were included for comparative analysis in experiments as strains from these host plants typically identify as *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *sandyi*, and *X. fastidiosa* subsp. *multiplex*, respectively. To the best of our knowledge, this is the first phylogenetic study of *X. fastidiosa* strains from pecan and from Louisiana.

The multiprimer PCR assay identified strains of *X. fastidiosa* from Louisiana by genotype and subspecies (Fig. 2). The amplification of three products from the multiprimer PCR assay indicated that strains of *X. fastidiosa* from pecan and sycamore from Louisiana are of the ALSII genotype that belongs to *X. fastidiosa* subsp. *multiplex* and includes strains that caused mild PD symptoms in grapevine (Fig. 2) (Almeida and Purcell, 2003a; Hernandez-Martinez *et al.*, 2006). A limitation of the multiprimer PCR assay is that it was designed using strains of *X. fastidiosa* from a limited number of hosts, specifically almond, grapevine, and oleander. It is uncertain if strains from different hosts will produce the same results. Host-plant inoculations that should determine the relevance of the pecan strains as an ALSII genotype and their ability to cause disease symptoms in grapevine are currently being conducted. The multiprimer PCR assay identified the grapevine strain from Louisiana as the PD genotype of *X. fastidiosa* subsp. *fastidiosa* and the oleander strain from Louisiana as the OLS genotype of *X. fastidiosa* subsp. *sandyi* (Fig. 2).

Sequence analysis of the 16S-23S rDNA ITS region, which has been used in previous studies to identify strains of *X. fastidiosa* below the species level, indicated that the pecan and sycamore ITS sequences were identical and most similar to other *X. fastidiosa* subsp. *multiplex* strains (Jensen *et al.*, 1993; Martinati *et al.*, 2005; Mehta and Rosato, 2001). Our findings that the ITS sequences of the pecan strains from Louisiana were identical to each other and that the ITS sequence of the grapevine strain from Louisiana was identical to those of the completely

sequenced grapevine strains were not surprising since a previous study showed that, with the exception of almond strains, all strains from the same host had the same ITS sequence (Hendson *et al.*, 2001). Phylogenetic analysis of the ITS region supported the subspecies groupings determined from the multiprimer PCR assay (Figs. 2 and 6). In addition, the major groups of *X. fastidiosa* strains identified in this study were consistent with groups from previous phylogenetic analyses based on ITS sequences, with the exception that the strains from chitalpa formed a monophyletic group within the unresolved subspecies *multiplex* group (Fig. 6) (Hendson *et al.*, 2001; Martinati *et al.*, 2005; Mehta and Rosato, 2001).

A frameshift causing early termination in the polygalacturonase precursor gene, *pglA*, was found in citrus and coffee strains but not in almond, grapevine, mulberry, or oleander strains of *X. fastidiosa* (Van Sluys *et al.*, 2003). A frameshift was not found in this study in *pglA* of pecan, grapevine, oleander, or sycamore strains from Louisiana. It was suggested that this frameshift possibly made *pglA* nonfunctional and accounted for the less aggressive nature of citrus variegated chlorosis strains compared to Pierce's disease strains of *X. fastidiosa* (Almeida *et al.*, 2001; Van Sluys *et al.*, 2003). Polygalacturonase is required for colonization and pathogenicity in grapevine but is not necessary for the development of disease in citrus (Roper *et al.*, 2007; Van Sluys *et al.*, 2003). Despite the absence of a frameshift in *pglA* of *X. fastidiosa* pecan, oleander and sycamore strains, it is unknown if this gene is required for colonization and pathogenicity of these strains. As with the ITS sequences, all *pglA* sequences from pecan and sycamore were identical. These sequences were more closely related to the *X. fastidiosa* subsp. *multiplex* strain than to any other subspecies. The *pglA* sequence from grapevine in Louisiana was not identical to other grapevine or subsp. *fastidiosa* strains, but was more closely related to these strains than to other strains. Sequence analysis of *pglA* separated strains of *X. fastidiosa*

into the same subspecies groups as the multiprimer PCR assay, providing further support for these groups (Figs. 2 and 7).

ERIC-PCR and REP-PCR separated the Louisiana pecan and sycamore strains from the Louisiana grapevine strain and the Louisiana oleander strain (Figs. 3 and 4). REP-PCR revealed genetic differences within the strains of *X. fastidiosa* from pecan while ERIC-PCR failed to detect any differences (Figs. 3 and 4). Similar results were reported for *X. fastidiosa* strains from citrus in which REP-PCR banding patterns were more discriminative than the ERIC-PCR banding patterns (Mehta *et al.*, 2001). While the differences in the citrus strain REP-PCR profiles corresponded to differences in geographic location (Mehta *et al.*, 2001), differences in the strains of *X. fastidiosa* from pecan were observed within the same geographic location and the same cultivar in this study (Table 1, Fig. 4). In the REP-PCR, one of the five pecan strains from the cultivar Cape Fear, XF A-06, clustered with and was more closely related to the sycamore strain, XF A-07, than to the other pecan strains (Fig. 4). This subgroup was more related to the pecan strain from the cultivar Oconee, XF A-10, than to the subgroup containing four other pecan strains from the cultivar Cape Fear (XF A-05, XF B-05, XF C-05, and XF D-07) and the pecan strain from the cultivar Desirable, XF B-10 (Fig. 4). The significance of the genetic variation observed among pecan strains in the REP-PCR is not currently known.

The phylogenetic analysis of the combined dataset of the ITS sequences, *pglA* sequences, and ERIC-PCR and REP-PCR data strengthened support for a number of groups identified in this study but did not place the pecan strains in a separate monophyletic group within the *X. fastidiosa* subsp. *multiplex* group (Fig. 8). Additional strains from pecan and other hosts and additional genetic information may be necessary to distinguish the pecan strains as a separate monophyletic group. A multilocus sequence typing (MLST) analysis, which identified different

clonal complexes within *X. fastidiosa* subsp. *multiplex* (Sally *et al.*, 2005), may be able to identify a new clonal complex for pecan strains or may group pecan strains with other similar strains, possibly sycamore strains, based on this study. Amplification and sequencing of part of these genes using primers designed for the original MLST system analysis for *X. fastidiosa* were attempted (Appendix N); however, because returned sequences were not always readable, this sequence data was not included in phylogenetic analyses (Appendix O). Further attempts to obtain sequences with the newly designed MLST primers (Yuan *et al.*, 2010) should be pursued.

Results from the various experiments conducted in this study consistently grouped the strains of *X. fastidiosa* from pecan together with each other and with the strain of *X. fastidiosa* from sycamore from Louisiana and as part of a larger group that included strains of *X. fastidiosa* subsp. *multiplex* from other host plants. For this reason, strains of *X. fastidiosa* from pecan should be considered a part of *X. fastidiosa* subsp. *multiplex*. In addition, the analyses conducted in this study placed the Louisiana grapevine strain with other grapevine strains from *X. fastidiosa* subsp. *fastidiosa* and the Louisiana oleander strain with other oleander strains from *X. fastidiosa* subsp. *sandyi*.

Studies on PBLB incidence in the research orchards at the Pecan Research-Extension Station have shown consistent disease spread within some cultivars (Sanderlin *et al.*, 2009). Disease severity and rate of spread also differ between pecan cultivars. Even though the majority of the pecan strains utilized in this study came from a single location and from a single cultivar, genetic variation was detected within these strains. The genetic differences observed between strains of *X. fastidiosa* from pecan from the same location and from the same cultivar in the REP-PCR test suggest that these strains may not be clones originating from a single source of infection. However, it cannot be ruled out that some mutation occurred to cause the genetic

variation seen in the REP-PCR while a single strain spread throughout the orchards. To determine the biological meaning of these observed genetic variations within the pecan strains of *X. fastidiosa*, additional studies including host specificity tests with different plant hosts and pecan cultivars are needed.

One of the difficulties in working with *X. fastidiosa* is that it is very fastidious and slow growing. Isolation attempts from pecan over several years have had low success rates and yielded few strains. Conscious efforts should be made to build a collection of *X. fastidiosa* pecan strains suitable for future studies. This collection should include strains from various cultivars as well as from various geographic locations.

This work provides a foundation for studies with additional strains of *X. fastidiosa* from Louisiana to determine variation that exists in this wide-spread pathogen within Louisiana and other southeastern U.S. states. Future studies that examine new diseases and the systematics of *X. fastidiosa*, and that continue to investigate the diversification of the species, will help to provide a better understanding of the population dynamics of this pathogen and to highlight research focus areas for effective management of plant diseases caused by this pathogen.

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CHAPTER 3: CONCLUSIONS

X. fastidiosa threatens the pecan industry by causing reduced nut yields in infected trees. Currently, management strategies are limited to reducing or eliminating the introduction of this pathogen into pecan orchards. No resistant cultivars have been identified. Furthermore, there is no treatment or cure once trees become infected, and disease tends to occur annually. This situation amounts to decreased income for growers with infected trees in their production orchards. Many studies are being conducted in other hosts infected by *X. fastidiosa*, and several subspecies with some apparent host specificity have been identified. A considerable amount of information about pathogen transmission has been determined for *X. fastidiosa* in pecan, but there is little information, particularly at the molecular level, on strains infecting pecan. Thus far, pecan pathogenic strains of *X. fastidiosa* have not been grouped to subspecies. This information is needed to develop more effective pecan bacterial leaf scorch (PBLs) management strategies, particularly to make it possible to clearly identify alternative hosts that could serve as reservoirs of inoculum for *X. fastidiosa* diseases in Louisiana.

Multiprimer PCR and phylogenetic analyses using nucleotide sequence data from the 16S-23S rDNA ITS region and *pglA* consistently identified strains of *X. fastidiosa* from pecan as *X. fastidiosa* subsp. *multiplex*. ERIC-PCR and REP-PCR analyses supported phylogenetic analyses. Based on these data, strains of *X. fastidiosa* from pecan should be considered a part of *X. fastidiosa* subsp. *multiplex*. Results from these experiments also identified the Louisiana grapevine strain as *X. fastidiosa* subsp. *fastidiosa*, the Louisiana oleander strain as *X. fastidiosa* subsp. *sandyi*, and the Louisiana sycamore strain as *X. fastidiosa* subsp. *multiplex*. In addition, REP-PCR showed that genetic variation exists among strains of *X. fastidiosa* from pecan. This genetic variation has not yet been explored, but warrants further study, particularly since the same genetic variant was observed in the strain of *X. fastidiosa* from sycamore.

Despite the presence of multiple subspecies of *X. fastidiosa* present in Louisiana, this investigation only identified *X. fastidiosa* subsp. *multiplex* in pecan. It is possible that pecan can only be infected by *X. fastidiosa* subsp. *multiplex* strains or by particular strains of *X. fastidiosa* subsp. *multiplex*. Host range inoculation tests with strains of *X. fastidiosa* from other subspecies and from other hosts within *X. fastidiosa* subsp. *multiplex* should be conducted to determine infectivity of pecan by different subspecies and strains. The knowledge from these tests would further aid in PBLIS management methods by determining which plant species may harbor pecan-infecting strains of *X. fastidiosa* and how these species should be managed when adjacent to pecan orchards. As of now, a possible threat only exists when host plants infected with *X. fastidiosa* subsp. *multiplex* are growing in and around pecan orchards. Even if plant hosts do not harbor strains of *X. fastidiosa* known to infect pecan, genetic recombination, which has been reported within and between subspecies, could yield novel strains able to infect pecan. Further studies on this pathogenic bacterial species, on its mechanisms of pathogenicity, and on the factors that determine host specificity will provide additional information that may aid in the understanding of this species as a whole.

APPENDIX A: SUBMISSION TO PLANT DISEASE

A manuscript containing a major portion of Chapter 2, the thesis abstract, and Appendix B, coauthored by R. S. Sanderlin, A. R. McTaggart, and J. H. Ham, has been submitted for publication to Plant Disease under the title, “A systematic study of the 16S-23S rRNA internal transcribed spacer region, *pglA*, and ERIC-PCR and REP-PCR fingerprints reveals that *Xylella fastidiosa* strains from pecan are part of *X. fastidiosa* subsp. *multiplex*”.

Manuscript ID	Manuscript Title	Date Created	Date Submitted	Status
PDIS-09-11-0730-RE	A systematic study of the 16S-23S rRNA internal transcribed spacer region, <i>pglA</i> , and ERIC-PCR and REP-PCR fingerprints reveals that <i>Xylella fastidiosa</i> strains from pecan are part of <i>X. fastidiosa</i> subsp. <i>multiplex</i>	01-Sep-2011	02-Sep-2011	SE: Charkowski, Amy EIC: Davis, R. Michael NE: Not Assigned ADM: Gold, Linda PROD: Not Assigned ■ Awaiting SE Decision

Email correspondence between Dr. Jong Hyun Ham, advisor, and Dr. Amy Charkowski, Plant Disease senior editor assigned to my manuscript:

jham@agcenter.lsu.edu wrote:
20-Sep-2011

PDIS-09-11-0730-RE - A systematic study of the 16S-23S rRNA internal transcribed spacer region, *pglA*, and ERIC-PCR and REP-PCR fingerprints reveals that *Xylella fastidiosa* strains from pecan are part of *X. fastidiosa* subsp. *multiplex*

Dear Amy:

My student, Rebecca Melanson, plans to defend her master's thesis on November. I want to ask your permission to include the submitted manuscript (PDIS-09-11-0730-RE) into her master's thesis as a chapter. Submission status of the manuscript will be indicated on the front page of the chapter and the manuscript will be edited appropriately for the thesis.

By the way, would you also let me know when reviewers will be assigned for our manuscript?

Thank you for processing our manuscript and I will look forward to hearing from you soon.

Best regards,

Jong

From: Amy Charkowski
Sent: Friday, September 23, 2011 11:28 AM
To: Ham, Jong
Subject: Re: Plant Disease

(APPENDIX A continued)

Hi Jong Hyun,

Yes it is fine to include her chapter. I will have time to catch up on plant disease things this weekend, so can provide an update then.

Best wishes -

Amy

Amy Charkowski
Dept. Plant Pathology
Univ. Wisconsin - Madison

Email correspondence between Dr. Jong Hyun Ham, advisor, and Dr. R. Michael Davis, Plant Disease senior editor-in-chief:

On Behalf Of jham@agcenter.lsu.edu
Sent: Wednesday, September 21, 2011 11:44 AM
To: R. Michael Davis
Subject: Plant Disease

9-21-2011

PDIS-09-11-0730-RE - A systematic study of the 16S-23S rRNA internal transcribed spacer region, pglA, and ERIC-PCR and REP-PCR fingerprints reveals that *Xylella fastidiosa* strains from pecan are part of *X. fastidiosa* subsp. *multiplex*

Dear Dr. Davis:

Rebecca Melanson, the senior author of this manuscript and my graduate student, will defend her master's thesis in November. We ask you a permit to include a major portion of this manuscript into her thesis as a chapter. Submission of this manuscript to Plant Disease will be clearly indicated on the front page of the chapter and appropriate editing will be implemented to the manuscript for fitting into the thesis.

We will be looking forward to hearing from you soon on this matter.

Sincerely,
Dr. Jong Hyun Ham

From: Mike Davis
Sent: Thursday, September 22, 2011 1:33 PM
To: Ham, Jong
Subject: RE: Plant Disease

Dr. Ham: Plant Disease allows and encourages this. Mike

**APPENDIX B: BACTERIAL STRAINS AND GENBANK ACCESSION NUMBERS
USED IN THIS STUDY FOR PHYLOGENETIC ANALYSES**

Strain designation	Plant host	Geographical origin	GenBank accession no	Accession no description	Reference
<i>Xylella fastidiosa</i>					
M12	Almond	California	CP000941	Complete genome ^a	(Chen <i>et al.</i> , 2010)
M23	Almond	California	CP001011	Complete genome	(Chen <i>et al.</i> , 2010)
ALS1	Almond	California	AF073240	Partial ITS ^b	(Hendson <i>et al.</i> , 2001)
Tulare	Almond	California	AF073242	Partial ITS	(Hendson <i>et al.</i> , 2001)
Contra Costa	Almond	California	AF073250	Partial ITS	(Hendson <i>et al.</i> , 2001)
Dixon	Almond	California	AF073251	Partial ITS	(Hendson <i>et al.</i> , 2001)
Fresno	Almond	California	DQ011259	Partial ITS	(Hernandez-Martinez <i>et al.</i> , 2006)
AZ03	Chitalpa	Arizona	EU714189	Partial ITS	(Randall <i>et al.</i> , 2009)
CA01	Chitalpa	California	EU714190	Partial ITS	(Randall <i>et al.</i> , 2009)
NM02	Chitalpa	New Mexico	EU714192	Partial ITS	(Randall <i>et al.</i> , 2009)
9a5c	Citrus	Brazil	AE003849	Complete genome	(Simpson <i>et al.</i> , 2000)
CI.52	Citrus	Brazil	AF203393	Partial ITS	(Mehta and Rosato, 2001)
CI.11067	Citrus	Brazil	AF237650	Partial ITS	(Mehta and Rosato, 2001)
CI.X0	Citrus	Brazil	AF237651	Partial ITS	(Mehta and Rosato, 2001)
CO.01	Coffee	Brazil	AF203394	Partial ITS	(Mehta and Rosato, 2001)
P3	Coffee	Brazil	AY388464	Partial ITS	(Martinati <i>et al.</i> , 2005)
ELM-1	Elm	Washington	AY388468	Partial ITS	(Martinati <i>et al.</i> , 2005)
Temecula 1	Grapevine	California	AE009442	Complete genome	(Van Sluys <i>et al.</i> , 2003)
XF GB514	Grapevine	Texas	CP002165	Complete genome	(Schreiber IV <i>et al.</i> , 2010)

(APPENDIX B continued)

Strain designation	Plant host	Geographical origin	GenBank accession no	Accession no description	Reference
<i>Xylella fastidiosa</i>					
PD 95-2	Grapevine	Florida	AF073220	Partial ITS	(Hendson <i>et al.</i> , 2001)
PD 95-4	Grapevine	Florida	AF073221	Partial ITS	(Hendson <i>et al.</i> , 2001)
P 95-9	Grapevine	Florida	AF073222	Partial ITS	(Hendson <i>et al.</i> , 2001)
R116V3	Grapevine	Florida	AF073223	Partial ITS	(Hendson <i>et al.</i> , 2001)
R116V3-4	Grapevine	Florida	AF073224	Partial ITS	(Hendson <i>et al.</i> , 2001)
Conn Creek	Grapevine	California	AF073225	Partial ITS	(Hendson <i>et al.</i> , 2001)
Santa Cruz	Grapevine	California	AF073229	Partial ITS	(Hendson <i>et al.</i> , 2001)
Preston Ranch	Grapevine	California	AF073232	Partial ITS	(Hendson <i>et al.</i> , 2001)
Moore Park	Grapevine	California	AF073236	Partial ITS	(Hendson <i>et al.</i> , 2001)
XF A-08	Grapevine	Louisiana	JN092384	Partial ITS	This study
			JN092393	<i>pglA</i> ^c	This study
Acer macrophylla	Maple	California	AF073219	Partial ITS	(Hendson <i>et al.</i> , 2001)
MUL-1	Mulberry	Massachusetts	AY388467	Partial ITS	(Martinati <i>et al.</i> , 2005)
88-9	Oak	Florida	AF073210	Partial ITS	(Hendson <i>et al.</i> , 2001)
92-3	Oak	Florida	AF073211	Partial ITS	(Hendson <i>et al.</i> , 2001)
92-10	Oak	Florida	AF073212	Partial ITS	(Hendson <i>et al.</i> , 2001)
OLS#2	Oak	Georgia	AF073213	Partial ITS	(Hendson <i>et al.</i> , 2001)
Stucky	Oak	Georgia	AF073214	Partial ITS	(Hendson <i>et al.</i> , 2001)
Ann1	Oleander	California	AF073215	Partial ITS	(Hendson <i>et al.</i> , 2001)
PF1	Oleander	California	AF073216	Partial ITS	(Hendson <i>et al.</i> , 2001)
H44	Oleander	California	AY603088	Partial ITS	(Costa <i>et al.</i> , 2004)
Riverside	Oleander	California	DQ011263	Partial ITS	(Hernandez-Martinez <i>et al.</i> , 2006)

(APPENDIX B continued)

Strain designation	Plant host	Geographical origin	GenBank accession no	Accession no description	Reference
<u>Xylella fastidiosa</u>					
Texas	Oleander	Texas	DQ011264	Partial ITS	(Hernandez-Martinez <i>et al.</i> , 2006)
XF Oleander	Oleander	Louisiana	JN092385	Partial ITS	This study
			JN092394	<i>pglA</i>	This study
5S2	Peach	Georgia	AF073206	Partial ITS	(Hendson <i>et al.</i> , 2001)
5R1	Peach	Georgia	AF073207	Partial ITS	(Hendson <i>et al.</i> , 2001)
4S3	Peach	Georgia	AF073208	Partial ITS	(Hendson <i>et al.</i> , 2001)
PE.PLS	Pear	Taiwan	AF203396	Partial ITS	(Mehta and Rosato, 2001)
XF A-05	Pecan	Louisiana	JN092378	Partial ITS	This study
			JN092387	<i>pglA</i>	This study
XF B-05	Pecan	Louisiana	JN092379	Partial ITS	This study
			JN092388	<i>pglA</i>	This study
XF C-05	Pecan	Louisiana	JN092380	Partial ITS	This study
			JN092389	<i>pglA</i>	This study
XF A-06	Pecan	Louisiana	JN092381	Partial ITS	This study
			JN092390	<i>pglA</i>	This study
XF D-07	Pecan	Louisiana	JN092383	Partial ITS	This study
			JN092392	<i>pglA</i>	This study
XF B-10	Pecan	Louisiana	JN092386	Partial ITS	This study
PWT-22	Periwinkle	Florida	AY388470	Partial ITS	(Martinati <i>et al.</i> , 2005)
2#4	Plum	Georgia	AF073209	Partial ITS	(Hendson <i>et al.</i> , 2001)
PL.788	Plum	Georgia	AF203395	Partial ITS	(Mehta and Rosato, 2001)
RGW-R	Ragweed	Florida	AY388469	Partial	(Martinati <i>et al.</i> , 2005)
XF A-07	Sycamore	Louisiana	JN092382	Partial ITS	This study
			JN092391	<i>pglA</i>	This study
<u>Xanthomonas campestris pv. campestris</u>					
LMG 568	--	--	AF209755	Complete ITS	(Gonçalves and Rosato, 2002)

(APPENDIX B continued)

^a Accession numbers for the complete genome of strains is listed. M12, an Almond Leaf Scorch (ALS) strain, is a *X. fastidiosa* subsp. *multiplex* strain; M23, an ALS strain, and Temecula1 and XF GB514, Pierce's Disease strains, are *X. fastidiosa* subsp. *fastidiosa* strains; and 9a5c, a citrus variegated chlorosis strain, is a *X. fastidiosa* subsp. *pauca* strain. Only a small portion of these genomes was extracted from each genome for phylogenetic analysis.

^b ITS = intergenic transcribed spacer region between the 16S and 23S ribosomal subunits described in NCBI's GenBank as the 16S-23S ribosomal RNA intergenic spacer.

^c *pglA* was designated as the sequence description for the strains used in this study based on the homology with the polygalacturonase gene in the complete genome sequences of *X. fastidiosa* strains 9a5c, Temecula1, M12, M23, and XF GB514 available in NCBI's GenBank.

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**APPENDIX C: RAXML PROGRAMS FOR MAXIMUM LIKELIHOOD SEARCHES OF
16S-23S ITS AND DATASETS**

RAxML program to run ITS sequence analysis

```
raxml -f a -x 12345 -p 12345 -# 1000 -m GTRMIX -s XF_ITS_curedml -n XFITS_cured_outfile
```

pause

RAxML program to run *pglA* sequence analysis

```
raxml -f a -x 12345 -p 12345 -# 1000 -m GTRMIX -s XF_PGLA -n XF_PGLA_outfile
```

pause

APPENDIX D: MRBAYES 3.1 PROGRAMS FOR MARKOV CHAIN MONTE CARLO (MCMC) SEARCHES OF 16S-23S ITS, *PGLA*, ERIC-PCR, REP-PCR, AND COMBINED DATASETS

*Note: Sequence data was omitted from this appendix for 16S-23S ITS, *pglA*, and 16S-23S, *pglA*, REP-PCR, and ERIC-PCR combined dataset programs, but was included in the actual MCMC searches.

MrBayes 3.1 program to run 16S-23S ITS MCMC Search*

```
BEGIN mrbayes;

set autoclose=yes nowarn=yes;
charset ITS = 1-503;

partition ITS = 1: ITS;
set partition = ITS;
lset applyto=(1) nst=6 rates=gamma;
lset coding = all;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
prset applyto=(all) ratepr=variable;

usertree =
(Pecan_XF_A05, (((Pecan_XF_B05, Pecan_XF_A06), (Sycamore_XF_A07, Pecan_XF_B10)), (
Pecan_XF_D07, (((AY388470_Periwinkle_PWT_22, AY388469_Ragweed_RGW_R), ((EU71418
9_Chitalpa_AZ03, EU714192_Chitalpa_NM02), EU714190_Chitalpa_CA01), (((DQ011263
_Oleander_Texas, DQ011264_Oleander_Riverside), (Oleander_XF_Oleander, AY603088_O
leander_H44)), (AF073216_Oleander_PF1, AF073215_Oleander_Ann1)), ((AF073223_Gra
pevine_R116V3, AF073232_Grapevine_Preston_Ranch), ((AF073220_Grapevine_PD_95_2,
(AF073221_Grapevine_PD_95_4, AF073219_Maple_Acer_macrophyta)), (AF073240_Almond
_ALS1, (((AF073236_Grapevine_Moore_Park, AF073229_Grapevine_Santa_Cruz), AF0732
25_Grapevine_Conn_Creek), AF073224_Grapevine_R118V3_4), AF073242_Almond_Tulare)
))), ((AY388467_Mulberry_MUL_1, (DQ011259_Almond_Fresno, Grapevine_XF_A08)), AY38
8468_Elm_ELM_1))), ((AF073251_Almond_Dixon, ((AF073250_Almond_Contra_Costa, AF0
73206_Peach_5S2), AF073207_Peach_5R1), AF073208_Peach_4S3)), ((AF073212_Oak_92
_10, AF073213_Oak_OLS2), AF073214_Oak_Stucky), (AF073210_Oak_88_9, AF073211_Oak_92
_3))))), ((AF203395_Plum_PL_788, ((AF203393_Citrus_CI_52, AF203393_Coffee_CO_01
), (AF237651_Citrus_CI_X0, AF237650_Citrus_CI_11067))), (AF209755_Xanthomonas_ca
mpestris_LMG568, AF203396_Pear_PE_PLS))))), Pecan_XF_C05);

mcmc startingtree=user ngen=100000000 temp=0.25 nruns=4 samplefreq=10
printfreq=500 nchains=4 savebrlens=yes
filename=XF_ITS_cured.nex stoprule=yes stopval=0.02;

[sump filename = XF_ITS_cured.nex;
sumt filename = XF_ITS_cured.nex;]

END;
```

MrBayes 3.1 program to run *pglA* MCMC Search*

```
BEGIN mrbayes;

set autoclose=yes nowarn=yes;
charset PGLA = 1-1636;
```

(APPENDIX D continued)

```
partition PGLA = 1: PGLA;
set partition = PGLA;
lset applyto=(1) nst=6 rates=gamma;

lset coding = all;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
prset applyto=(all) ratepr=variable;

mcmcp ngen=100000000 temp=0.25 nruns=4 samplefreq=100 printfreq=5000
nchains=4 savebrlens=yes
filename=XF_PGLA.nex stoprule=yes stopval=0.02;

[sump filename = XF_PGLA.nex;
sumt filename = XF_PGLA.nex;]

END;
```

MrBayes 3.1 program to run ERIC-PCR MCMC Search

```
BEGIN DATA;
    DIMENSIONS NTAX=10 NCHAR=10;
    FORMAT DATATYPE=standard MISSING=? GAP=- interleaved=yes;
MATRIX

Pecan_XF_A05          0111011010
Pecan_XF_B05          0111011010
Pecan_XF_C05          0111011010
Pecan_XF_A06          0111011010
Sycamore_XF_A07        0111011010
Pecan_XF_D07          0111011010
Grapevine_XF_A08      1011111100
Oleander_XF_Oleander  1000111101
Pecan_XF_A10          0111011010
Pecan_XF_B10          0111011010
;
END;

BEGIN mrbayes;

set autoclose=yes nowarn=yes;
charset REP = 1-10;

partition REP = 1: REP;
set partition = REP;
lset coding = noabsencesites;
lset coding = all;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
prset applyto=(all) ratepr=variable;

mcmcp ngen=100000000 temp=0.25 nruns=4 samplefreq=10 printfreq=500 nchains=4
savebrlens=yes
filename=XF_ERIC.nex stoprule=yes stopval=0.01;

[sump filename = XF_ERIC.nex;
```

(APPENDIX D continued)

```
sumt filename = XF_ERIC.nex;]
```

```
END;
```

MrBayes 3.1 program to run REP-PCR MCMC Search

```
BEGIN DATA;  
    DIMENSIONS NTAX=10 NCHAR=9;  
    FORMAT DATATYPE=standard MISSING=? GAP=- interleaved=yes;  
MATRIX
```

```
Pecan_XF_A05          110001010  
Pecan_XF_B05          110001010  
Pecan_XF_C05          110001010  
Pecan_XF_A06          100011010  
Sycamore_XF_A07        100011010  
Pecan_XF_D07          110001010  
Grapevine_XF_A08      001001000  
Oleander_XF_Oleander  100101100  
Pecan_XF_A10          110001001  
Pecan_XF_B10          110001010
```

```
;  
END;
```

```
BEGIN mrbayes;
```

```
set autoclose=yes nowarn=yes;  
charset REP = 1-9;
```

```
partition REP = 1: REP;  
set partition = REP;  
lset coding = noabsencesites;  
lset coding = all;  
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);  
prset applyto=(all) ratepr=variable;
```

```
mcmc ngen=100000000 temp=0.25 nruns=4 samplefreq=10 printfreq=500 nchains=4  
savebrlens=yes  
filename=XF_REP.nex stoprule=yes stopval=0.01;
```

```
[sump filename = XF_REP.nex;  
sumt filename = XF_REP.nex;]
```

```
END;
```

MrBayes 3.1 program to run REP-PCR and ERIC-PCR Combined Dataset MCMC Search

```
BEGIN DATA;  
    DIMENSIONS NTAX=10 NCHAR=19;  
    FORMAT DATATYPE=standard MISSING=? GAP=- interleaved=yes;  
MATRIX
```

```
Pecan_XF_A05          1100010100111011010  
Pecan_XF_B05          1100010100111011010
```


(APPENDIX D continued)

```
Pecan_XF_C05          1100010100111011010
Pecan_XF_A06          1000110100111011010
Sycamore_XF_A07        1000110100111011010
Pecan_XF_D07          1100010100111011010
Grapevine_XF_A08      0010010001011111100
Oleander_XF_Oleander  1001011001000111101
Pecan_XF_A10          1100010010111011010
Pecan_XF_B10          1100010100111011010
```

;

END;

BEGIN mrbayes;

```
set autoclose=yes nowarn=yes;
charset REP = 1-19;
partition REP = 1: REP;
set partition = REP;
lset coding = noabsencesites;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
prset applyto=(all) ratepr=variable;
```

```
mcmc ngen=100000000 temp=0.25 nruns=4 samplefreq=10 printfreq=500 nchains=4
savebrlens=yes
filename=XF_REP-ERIC.nex stoprule=yes stopval=0.01;
```

```
[sump filename = XF_REP-ERIC.nex;
sumt filename = XF_REP-ERIC.nex;]
```

END;

MrBayes 3.1 program to run 16S-23S ITS, *pglA*, and REP-PCR and ERIC-PCR Combined

Dataset MCMC Search*

BEGIN mrbayes;

```
set autoclose=yes nowarn=yes;
charset ITS = 1-503;
charset PGLA = 504-2139;
charset REP-PCR = 2140-2148;
charset ERIC-PCR = 2149-2158;
```

```
partition IPRE = 4: ITS, PGLA, REP-PCR, ERIC-PCR;
set partition = IPRE;
lset applyto=(1,2) nst=6 rates=gamma;
lset coding = all;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
prset applyto=(all) ratepr=variable;
```

```
usertree =
(Pecan_XF_A05, (((Pecan_XF_B05, Pecan_XF_A06), (Sycamore_XF_A07, Pecan_XF_B10)), (
Pecan_XF_D07, ((AY388470_Periwinkle_PWT_22, AY388469_Ragweed_RGW_R), ((EU71418
9_Chitalpa_AZ03, EU714192_Chitalpa_NM02), EU714190_Chitalpa_CA01), (((((DQ011263
_Oleander_Texas, DQ011264_Oleander_Riverside), (Oleander_XF_Oleander, AY603088_O
leander_H44))), (AF073216_Oleander_PF1, AF073215_Oleander_Ann1))), ((AF073223_Gra
```

(APPENDIX D continued)

```
pevine_R116V3,AF073232_Grapevine_Preston_Ranch),((AF073220_Grapevine_PD_95_2,
(AF073221_Grapevine_PD_95_4,AF073219_Maple_Acer_macrophylla)),(AF073240_Almond
_ALS1,(((AF073236_Grapevine_Moore_Park,AF073229_Grapevine_Santa_Cruz),AF0732
25_Grapevine_Conn_Creek),AF073224_Grapevine_R118V3_4),AF073242_Almond_Tulare)
))),((AY388467_Mulberry_MUL_1,(DQ011259_Almond_Fresno,Grapevine_XF_A08)),AY38
8468_Elm_ELM_1))),((AF073251_Almond_Dixon,((AF073250_Almond_Contra_Costa,AF0
73206_Peach_5S2),AF073207_Peach_5R1),AF073208_Peach_4S3)),((AF073212_Oak_92
_10,AF073213_Oak_OLS2),AF073214_Oak_Stucky),(AF073210_Oak_88_9,AF073211_Oak_92
_3))))) ,((AF203395_Plum_PL_788,((AF203393_Citrus_CI_52,AF203393_Coffee_CO_01
), (AF237651_Citrus_CI_X0,AF237650_Citrus_CI_11067))), (AF209755_Xanthomonas_ca
mpestris_LMG568,AF203396_Pear_PE_PLS))))) ,Pecan_XF_C05);
```

```
mcmcp startingtree=user ngen=5000000 temp=0.15 nruns=4 samplefreq=100
printfreq=5000 nchains=4 savebrelens=yes
filename=XF_IPRE.nex stoprule=yes stopval=0.02;
```

```
[sump filename = XF_IPRE.nex;
sumt filename = XF_IPRE.nex;]
```

```
END;
```

APPENDIX E: 16S-23S ITS NUCLEOTIDE SEQUENCES OF STRAINS OF XYLELLA FASTIDIOSA ISOLATED FROM PLANT HOSTS IN LOUISIANA

>XF_A-05_ITS [organism=*Xylella fastidiosa*][strain=XF A-05][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGAATATAATTGTC
TTATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTAT
GTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGGG
GTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGGT
TAGAGCGCACCCCTGATAAGGGTGAGGTTCGGTGGTTCGAGTCCCTCCAGACCCACCAATGTTAT
ATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGAGCTGTGAAGCGT
TCTTTTATAATTTGATGATGTAGCAAGCGTTTGAACCTTTTTATTAATAATTTCTCATTGGAAGC
CTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTATATGGTCAA
GCGAATAAGCGCACACGG

>XF_B-05_ITS [organism=*Xylella fastidiosa*][strain=XF B-05][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

GAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGA
ATATAATTGTCTTATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGG
TTTGGGTTTATGTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTT
GCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGTCTGTA
GCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTTCGGTGGTTCGAGTCCCTCCAGACCC
ACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGAG
CTGTGAAGCGTTCTTTTATAATTTGATGATGTAGCAAGCGTTTGAACCTTTTTATTAATAATTTCT
TCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGT
TATATGGTCAAGCGAATAAGCGCACACGGTGA

>XF_C-05_ITS [organism=*Xylella fastidiosa*][strain=XF C-05][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

CAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGAATATAATTGT
CTTATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTA
TGTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGG
GGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGG
TTAGAGCGCACCCCTGATAAGGGTGAGGTTCGGTGGTTCGAGTCCCTCCAGACCCACCAATGTTA
TATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGAGCTGTGAAGCG
TTCTTTTATAATTTGATGATGTAGCAAGCGTTTGAACCTTTTTATTAATAATTTCTCATTGGAAG
CCTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTATATGGTCA
AGCGAATAAGCGCACACGG

>XF_A-06_ITS [organism=*Xylella fastidiosa*][strain=XF A-06][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

GAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGA
ATATAATTGTCTTATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGG
TTTGGGTTTATGTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTT

(APPENDIX E continued)

GCAAGCAGGGGGTCGTCGGTTTCGATCCCAGCAGGCTCCACCATGAAAGTATTTATGGGTCTGTA
GCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCTCCCAGACCC
ACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTTATGCTTATCAGCCTTGGAG
CTGTGAAGCGTTCTTTTTATAATTTGATGATGTAGCAAGCGTTTGAACTTTTTATTAATAATTTTC
TCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGT
TATATGGTCAAGCGAATAAGCGCACACG

>XF_A-07_ITS [organism=*Xylella fastidiosa*][strain=XF A-07][host=sycamore][country=USA:
Louisiana][note=16S-23S intergenic transcribed spacer]

AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTTGAGTATGGTGAATATAATTGTC
TTATCAGGCGTCTCACAAAGTTACTTGCATTTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTAT
GTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGGG
GTCGTCGGTTCGATCCCAGCAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGGT
TAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCTCCCAGACCCACCAATGTTAT
ATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGGAGCTGTGAAGCGT
TCTTTTATAATTTGATGATGTAGCAAGCGTTTGAACTTTTTATTAATAATTTCTCATTGGAAGC
CTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTATATGGTCAA
GCGAATAAGCGCACACGGTG

>XF_D-07_ITS [organism=*Xylella fastidiosa*][strain=XF D-07][host=*Carya illinoensis*
(pecan) cultivar Cape Fear][country=USA: Louisiana][note=16S-23S intergenic transcribed
spacer]

AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTTGAGTATGGTGAATATAATTGTC
TTATCAGGCGTCTCACAAAGTTACTTGCATTTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTAT
GTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGGG
GTCGTCGGTTCGATCCCAGCAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGGT
TAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCTCCCAGACCCACCAATGTTAT
ATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGGAGCTGTGAAGCGT
TCTTTTATAATTTGATGATGTAGCAAGCGTTTGAACTTTTTATTAATAATTTCTCATTGGAAGC
CTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTATATGGTCAA
GCGAATAAGCGCACACGGTGGAT

>XF_A-08_ITS [organism=*Xylella fastidiosa*][strain=XF A-08][host=grapevine][country=USA:
Louisiana][note=16S-23S intergenic transcribed spacer]

AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTTGAGTATGGTGAATATAATTGTC
TTACCAGGCGTCTCACAAAGTTACTTGCATTTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTAT
GTTGGCGATTTTTGTTCTGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGGG
GTCGTCGGTTCGATCCCAGCAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGGT
TAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCTCCCAGACCCACCAATGTTAT
ATCAATTATTCTGAATGTAGTTTGCGCATTTTTTATGCTTATCAGCCTTGGAGCTGTGAAGCGTT
CTTTTATAATTTGATGATGTAGCAAGCGTTTGAATTTTTTATTAATAATTTCTCATTGGAAGC
CTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTATATGGTCAAG
CGAATAAGCGCACAC

(APPENDIX E continued)

>XF_Oleander_ITS [organism=*Xylella fastidiosa*][strain=XF Oleander][host=oleander]
[country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

GAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGA
ATATAATTGTCTTATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGG
TTTGGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTT
GCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATCAAAGTATTTATGGGTCTGTA
GCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTTCGGTGGTTCGAGTCCTCCAGACCC
ACCAATGTTATATCAATTATTCTGAATGTATTTTGCGCATTTTTATGCTTATCAGCCTTGGAGC
TGTGAAGCGTTCTTTTATAATTTGATGATGTAGCAAGCGTTTCAAATTTTTATTAATAATTTCT
CATTTGAAGCCTTAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTT
ATATGGTCAAGCGAATAAGCGCACACGGT

>XF_B-10_ITS [organism=*Xylella fastidiosa*][strain=XF B-10][host=*Carya illinoensis* (pecan)
cultivar Desirable][country=USA: Louisiana][note=16S-23S intergenic transcribed spacer]

GGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGAGTATGGTGAATATAATTGTCTT
ATCAGGCGTCCTCACAAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTTGGGTTTATGT
TGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTTTGCAAGCAGGGGGT
CGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGTCTGTAGCTCAGGTGGTTA
GAGCGCACCCCTGATAAGGGTGAGGTTCGGTGGTTCGAGTCCTCCAGACCCACCAATGTTATAT
CAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTTATCAGCCTTGGAGCTGTGAAGCGTTC
TTTTATAATTTGATGATGTAGCAAGCGTTTGAACTTTTTATTAATAATTTCTCATTGGAAGCCT
TAAGTGACAATGTTTATCCATTGTCTTGTAGATTTTGAGGCGACTTTGGGTTATATGGTCAAGC
GAATAAGCGCACACG

**APPENDIX F: CLUSTALW2 ALIGNMENT AND SUMMARY OF THE 16S-23S ITS
NUCLEOTIDE SEQUENCES OF STRAINS OF XYLELLA FASTIDIOSA ISOLATED
FROM PLANT HOSTS IN LOUISIANA**

ClustalW2 Alignment

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XF_A-05      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_B-05      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_C-05      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_A-06      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_A-07      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_D-07      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_B-10      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_A-08      AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
XF_Oleander  AAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTTGGAGTATGGTGAATATAAT 60
*****

XF_A-05      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_B-05      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_C-05      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_A-06      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_A-07      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_D-07      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_B-10      TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_A-08      TGTCTTACCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
XF_Oleander  TGTCTTATCAGGCGTCTCACAAGTTACTTGCATTCAGGGTTTGATGTTGGCATAGGTTT 120
*****

XF_A-05      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_B-05      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_C-05      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_A-06      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_A-07      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_D-07      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_B-10      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_A-08      GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
XF_Oleander  GGGTTTATGTTGGCGATTTTTGTTCTGGGGGCCTTAGCTCAGCTGGTAGAGCACCTGCTT 180
*****

XF_A-05      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_B-05      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_C-05      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_A-06      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_A-07      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_D-07      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_B-10      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_A-08      TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATGAAAGTATTTATGGGT 240
XF_Oleander  TGCAAGCAGGGGGTCGTCGGTTCGATCCCGACAGGCTCCACCATCAAAGTATTTATGGGT 240
*****

XF_A-05      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_B-05      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_C-05      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_A-06      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_A-07      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_D-07      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_B-10      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_A-08      CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
XF_Oleander  CTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAGGTCGGTGGTTCGAGTCCCT 300
*****

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(APPENDIX F continued)

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XF_A-05      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_B-05      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_C-05      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_A-06      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_A-07      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_D-07      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_B-10      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTGGTTTGCGCATTTTTTATGCTT 360
XF_A-08      CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTAGTTTGCGCATTTTT-ATGCTT 359
XF_Oleander  CCCAGACCCACCAATGTTATATCAATTATTCTGAATGTATTTTGCGCATTTTT-ATGCTT 359
              *****

XF_A-05      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_B-05      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_C-05      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_A-06      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_A-07      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_D-07      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_B-10      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 420
XF_A-08      ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 419
XF_Oleander  ATCAGCCTTGGAGCTGTGAAGCGTTCCTTTTATAATTTGATGATGTAGCAAGCGTTTGAAC 419
              *****

XF_A-05      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_B-05      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_C-05      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_A-06      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_A-07      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_D-07      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_B-10      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 480
XF_A-08      TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 479
XF_Oleander  TTTTTATTAATAATTTCTCATTGGAAGCCTTAAGTGACAATGTTTATCCATTGCTTGTA 479
              *****

XF_A-05      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_B-05      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_C-05      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_A-06      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_A-07      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_D-07      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_B-10      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 528
XF_A-08      GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 527
XF_Oleander  GATTTTGAGGCGACTTTGGGTTATATGGTCAAGCGAATAAGCGCACAC 527
              *****

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ClustalW2 Summary

SeqA	Name	Length	SeqB	Name	Length	Score
1	XF_A-05	528	2	XF_B-05	528	100
1	XF_A-05	528	3	XF_C-05	528	100
1	XF_A-05	528	4	XF_A-06	528	100
1	XF_A-05	528	5	XF_A-07	528	100
1	XF_A-05	528	6	XF_D-07	528	100
1	XF_A-05	528	7	XF_A-08	527	98

(APPENDIX F continued)

SeqA	Name	Length	SeqB	Name	Length	Score
1	XF_A-05	528	8	XF_Oleander	527	98
1	XF_A-05	528	9	XF_B-10	528	100
2	XF_B-05	528	3	XF_C-05	528	100
2	XF_B-05	528	4	XF_A-06	528	100
2	XF_B-05	528	5	XF_A-07	528	100
2	XF_B-05	528	6	XF_D-07	528	100
2	XF_B-05	528	7	XF_A-08	527	98
2	XF_B-05	528	8	XF_Oleander	527	98
2	XF_B-05	528	9	XF_B-10	528	100
3	XF_C-05	528	4	XF_A-06	528	100
3	XF_C-05	528	5	XF_A-07	528	100
3	XF_C-05	528	6	XF_D-07	528	100
3	XF_C-05	528	7	XF_A-08	527	98
3	XF_C-05	528	8	XF_Oleander	527	98
3	XF_C-05	528	9	XF_B-10	528	100
4	XF_A-06	528	5	XF_A-07	528	100
4	XF_A-06	528	6	XF_D-07	528	100
4	XF_A-06	528	7	XF_A-08	527	98
4	XF_A-06	528	8	XF_Oleander	527	98
4	XF_A-06	528	9	XF_B-10	528	100
5	XF_A-07	528	6	XF_D-07	528	100
5	XF_A-07	528	7	XF_A-08	527	98
5	XF_A-07	528	8	XF_Oleander	527	98
5	XF_A-07	528	9	XF_B-10	528	100
6	XF_D-07	528	7	XF_A-08	527	98
6	XF_D-07	528	8	XF_Oleander	527	98
6	XF_D-07	528	9	XF_B-10	528	100
7	XF_A-08	527	8	XF_Oleander	527	99
7	XF_A-08	527	9	XF_B-10	528	98
8	XF_Oleander	527	9	XF_B-10	528	98

APPENDIX G: BLAST SEARCH OF 16S-23S ITS NUCLEOTIDE SEQUENCES OF STRAINS OF *XYLELLA FASTIDIOSA* ISOLATED FROM PLANT HOSTS IN LOUISIANA

BLAST Query Results: XF A-05 (Identical to all LA pecan and sycamore ITS sequences)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP000941.1	Xylella fastidiosa M12, complete genome	974	1948	99%	0.0	100%
AF003849.1	Xylella fastidiosa 9a5c, complete genome	952	1904	99%	0.0	99%
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	933	1867	99%	0.0	98%
CP001011.1	Xylella fastidiosa M23, complete genome	933	1867	99%	0.0	98%
AF009442.1	Xylella fastidiosa Temecula1, complete genome	933	1867	99%	0.0	98%
AF073215.1	Xylella fastidiosa strain Ann1 16S-23S ribosomal RNA intergenic spacer, partial sequence	883	883	96%	0.0	98%

BLAST Query Results: XF A-08 (LA grapevine strain)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	972	1944	99%	0.0	100%
CP001011.1	Xylella fastidiosa M23, complete genome	972	1944	99%	0.0	100%
AF009442.1	Xylella fastidiosa Temecula1, complete genome	972	1944	99%	0.0	100%
CP000941.1	Xylella fastidiosa M12, complete genome	933	1867	99%	0.0	98%
AF003849.1	Xylella fastidiosa 9a5c, complete genome	911	1823	99%	0.0	97%
AF073215.1	Xylella fastidiosa strain Ann1 16S-23S ribosomal RNA intergenic spacer, partial sequence	898	898	96%	0.0	98%

BLAST Query Results: XF Oleander (LA oleander strain)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	950	1900	99%	0.0	99%
CP001011.1	Xylella fastidiosa M23, complete genome	950	1900	99%	0.0	99%
AF009442.1	Xylella fastidiosa Temecula1, complete genome	950	1900	99%	0.0	99%
CP000941.1	Xylella fastidiosa M12, complete genome	933	1867	99%	0.0	98%
AF073215.1	Xylella fastidiosa strain Ann1 16S-23S ribosomal RNA intergenic spacer, partial sequence	920	920	96%	0.0	99%
AF003849.1	Xylella fastidiosa 9a5c, complete genome	911	1823	99%	0.0	97%

APPENDIX H: PGLA NUCLEOTIDE SEQUENCES OF STRAINS OF XYLELLA FASTIDIOSA ISOLATED FROM PLANT HOSTS IN LOUISIANA

>XF_A-05_PGLA [organism=*Xylella fastidiosa*][strain=XF A-05][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=pglA]

ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCATTGTTTTGCCGCAATGGGCGGCA
CTGCTGATGTCTTTCGAGTGTACAGCTGTCTCATCCGATCTTCCGAGCCGGTATCGGTGAA
AACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACGGTATTGCCTGCG
CGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAAC TAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTGAGCGGGCCGTTGCACTTGAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTA CTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGGTGTGATTGATGGGCGTGGCGGTAGCATTTTGACT
GGCGGTAAGCATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATAACCACGCCGGGTACCACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCAGCATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCAGTGCTGCTAGCGTACTCCTACATCAGCACCGGGGATGAC
CACGTTGCCATCAAAGCGCGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TtGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTTCGACCATGTCACCTACTCCAAAATATGCATGCGTCTGAAAC
GTCCGCTGGCGTTTACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTGAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGTTGAGTCTGGATAACGTCGTATTCG
ACGGTTTTTTGCCAACATTGATAGCGCCTCCCAGCAGTGTCTGATTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAAGTGTGGGCAACCATAACGATTGTTTCAGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTTCGCCTATCTAA

>XF_B-05_PGLA [organism=*Xylella fastidiosa*][strain=XF B-05][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=pglA]

ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCATTGTTTTGCCGCAATGGGCGGCA
CTGCTGATGTCTTTCGAGTGTACAGCTGTCTCATCCGATCTTCCGAGCCGGTATCGGTGAA
AACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACGGTATTGCCTGCG
CGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAAC TAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTGAGCGGGCCGTTGCACTTGAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACgACAAAGGCAATG
GTACGTGCGGTA CTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGGTGTGATTGATGGGCGTGGCGGTAGCATTTTGACT
GGCGGTAAGCATGCTCGGCAGCGTACCTGgtGGGACcTGGCCTATCAGaACAAGCGCCAtgCac
tGCATCAaCAGGTACCcCGGTTGATCCAAATCAGGGGCGGTAAcGacTTCACGTTGTaCCGTGT
tGCCATCGAaAATGCACcTAAcTTCCATGTGGTTGcTGATACGGTCAGCGGTGTCACCGTATGG

(APPENDIX H continued)

GGCATCCGCATCCTGACCCCAAGCTTGGTCTATAACCACGCCGGGTACCACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACCGGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTTCGACCATGTCACCTACTCCAAAATATGCATGCGTTCGTCTGAAAC
GTCCGCTGGCGTTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTCAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGTTGAGTCTGGATAACGTCGTATTTCG
ACGGTTTTTTTGCCAACATTTGATAGCGCCTCCCAGCAGTGTTCGTATTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTTCGCCTATCTAA

>XF_C-05_PGLA [organism=*Xylella fastidiosa*][strain=XF C-05][host=*Carya illinoensis*
(pecan) cultivar Cape Fear][country=USA: Louisiana][note=p gla]

ATGAACCTTGACCGTTTTCTCCCTAGTGTGGACTGCATTGTTTTGCCGCAATGGGCGGCA
CTGCTGATGTCTTTCGAGTGTACAGCTGTCTCATCCGATCTTTCGAGCCGGTATCGGTGAA
AACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACGGTATTGCCTGCG
CGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAACCTAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTTGAGCGGGCCGTTGCACTTCAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACgACAAAgGCAATG
GTACGTGCGGTACTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCaA
CACCACCGGTAGCGGTATCGTgGGTGGGGGTGTGAtTGATGGGCGTGGCgGtAGCATTTTGACT
GGCGGTAAGCATGCTCGGCAGCGTAcctGGTGGGACcTGgCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATAACCACGCCGGGTACCACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACCGGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACaCGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTTCGACCATGTCACCTACTCCAAAATATGCATGCGTTCGTCTGAAAC
GTCCGCTGGCGTTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTCAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGTTGAGTCTGGATAACGTCGTATTTCG
ACGGTTTTTTTGCCAACATTTGATAGCGCCTCCCAGCAGTGTTCGTATTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTTCGCCTATCTAA

(APPENDIX H continued)

>XF_A-06_PGLA [organism=*Xylella fastidiosa*][strain=XF A-06][host=*Carya illinoensis* (pecan) cultivar Cape Fear][country=USA: Louisiana][note=p gla]

ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCATTGTTTTGCCGCAATGGGCGGCA
CTGCTGATGTCTTTCGAGTGTCCACAGCTGTCTCATCCGATCTTTCGAGCCGGTATCGGTGAA
AACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACGGTATTGCCTGCG
CGCCTGACTCCTAAACATGGTTCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAAC TAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTTGAGCGGGCCGTTGCACTTGAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTACTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGGTGTGATTGATGGGCGTGGCGGTAGCATTTTGACT
GGCGGTAAGCATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACC ACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCAGTGTCTGCTAGCGTACTCCTACATCAGCACC GGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTTCGACCATGTCACCTACTCCAAAATATGCATGCGTCTGAAAC
GTCCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTGAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
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ACGGTTTTTTGCCAACATTGATAGCGCCTCCCAGCAGTGTCTGATTTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGAAGTCCAAGTGTGGGCAACCCATACGATTGTTT CAGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTTCGCTATCTAA

>XF_A-07_PGLA [organism=*Xylella fastidiosa*][strain=XF A-07][host=sycamore][country= USA: Louisiana][note=p gla]

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AACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACGGTATTGCCTGCG
CGCCTGACTCCTAAACATGGTTCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAAC TAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTTGAGCGGGCCGTTGCACTTGAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTACTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGGTGTGATGATGGGCGTGGCGGTAGCATTTTGACT
GGCGGTAAGCATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACC ACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG

(APPENDIX H continued)

CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACCCGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTCGACCATGTCACCTACTCCAAAATATGCATGCGTTCGTCTGAAAC
GTCCGCTGGCGTTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTGAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGTTGAGTCTGGATAACGTTCGTATTTCG
ACGTTTTTTTTGCCAACATTGATAGCGCCTCCCAGCAGTGTTCGTATTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTTCGCCTATCTAA

>XF_D-07_PGLA [organism=*Xylella fastidiosa*][strain=XF D-07][host=*Carya illinoensis*
(pecan) cultivar Cape Fear][country=USA: Louisiana][note=p gla]

ATGAACCTTGACCGTTTTCTCCCCCTAGTGTTTGGACTGCATTGTTTTGCCGCAATGGGCGGCA
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CGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCACAGGCTTCCAAGCCTG
ATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGTAGCGCGGTCAAAC TAGTGAT
CGACAGTCATCGCAAATCCGGCTTTTTGAGCGGGCCGTTGCACTTGAAATCTAGGGTGACGTTG
TGGATTGACGATGGCGTCACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTACTGCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGTGTGATTGATGGGCGTGGCGGTAGCATTTTACT
GGCGGTAAGCATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGG
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CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACCCGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGTTTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTCGACCATGTCACCTACTCCAAAATATGCATGCGTTCGTCTGAAAC
GTCCGCTGGCGTTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATCGTGCTGCAAGATATTCATGTGCTTGAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGTTGAGTCTGGATAACGTTCGTATTTCG
ACGTTTTTTTTGCCAACATTGATAGCGCCTCCCAGCAGTGTTCGTATTTGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCA
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>XF_A-08_PGLA [organism=*Xylella fastidiosa*][strain=XF A-08][host=grapevine][country=
USA: Louisiana][note=p gla]

ATGAACCTTGACCGTTTTCTCCCCCTAGTGTTTGGACTGCACTGTTTTGCCGCAATGGGCGGCA

(APPENDIX H continued)

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CGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCAAAGGTTTCCAAGCCTG
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CGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTGCACTTGAAATCTGGGGTGACGTTG
TGGATTGACGAGGGTGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTAAGTGTCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
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GGCGGTAAGTATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTTAGCGGTGTCACCGCATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGATATGGAAGT
CAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGCAGATGAAATCTGAT
GCCGATCATGGCGGAGTGGTTCGACCATGTCACCTACTCCAAAATATGCATGCGTTCGTCTGAAAC
GTCCGCTGGCGTTTTCGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
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ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGCTGAGCATGGATAACGTCGTATTCG
ACGGTTTTTTTGGCAACATTTGATAGCGCCTCCCAGCAGTGTTCGTATTCGCCAATCCGCAGGCAGT
GCATTTTCACTTCGGTCCCGGTCCGGTTCAGTTTCGCTCCTTTGATTACCCCTCGGTTGCTTAC
GATGTGACTGTGAGTGGAAAGTCCAGGTGTGGGCAACCATAACGATTGTTTCGGCGGCATTTATCA
ATTTTTCCAGCGTATTTCTGATTCGCCTATCTAA

>XF_Oleander_PGLA [organism=*Xylella fastidiosa*][strain=XF Oleander][host=oleander]
[country=USA: Louisiana][note=pgla]

ATGAACCTTGACCGTTTCTTCCCCCTAGTGTGGACTGCATTGTTTTGCCGCAATGGGGCGGCA
CTGCTGATGTCTTTTCGAGTGTACAGCTGTCCCTCATCCGATCTTTCCGAGCCGGTATCTGTGAA
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CGCCTGACTCCTAAACATGGCTCCATTGACGCACTTGATGCCAATCCAAAGGTTTCCAAGCCTG
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CGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTGCACTTGAAATCTGGGGTGACGTTG
TGGATTGACGATGGTGTACGCTGTTTGCATCGCGCAACCCCAAGGATTACGACAAAGGCAATG
GTACGTGCGGTAAGTGTCAACGTCAACTCATGAGTTCAGTTGTATGCCTTTGATCTCCGCGATCAA
CACCACCGGTAGCGGTATCGTGGGTGGGGGTGTGATTGATGGGCGTGGCGGTAGCATTTTGACT
GGCGGTAAGTATGCTCGGCAGCGTACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCAC
TGCATCAACAGGTACCACGGTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGT
TGCCATCGAAAATGCACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGCATGG
GGCATCCGCATCCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTA
CCACGCCGGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGG
CTTTGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGAC
CACGTTGCCATCAAAGCGCGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAACCACT
TTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGATATGGAAGT

(APPENDIX H continued)

CAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGCTTGCATATGAAATCTGAT
GCCGATCATGGCGGAGTGGTCGACCATGTCACCTACTCCAAAATATGCATGCGTCGTCTGAAAC
GTCCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAATTCTTATCCACTCTTCAAAAA
TATTGTGTTGCAAGATATTCATGTGCTTGAAAGCCCTGTCTTTGGTGCTGGTCAGCTGCTTTTC
ATGGGGATCCTGGGCAGTGGGAATAATCTGCCAATGACGCTGAGCATGGATAACGTCGTATTTCG
ACGGTTTTTTGCCAACATTGATAGCGCCTCCCAGCAGTATCGTATTTCGCCAATCCGCAGGCAGC
GCATTTTCACTTCGGTCCCGGTCCGGTCAGTTTCGCTCCTTTGATTACCCCTCTGTTGCTTAC
GATGTGACTGTGAGTGGAAGTCCAGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCA
ATTTTTCCAGCATATTTCTGATTCGCCTATCTAA

**APPENDIX I: CLUSTALW2 ALIGNMENT AND SUMMARY OF THE PGLA
NUCLEOTIDE SEQUENCES OF STRAINS OF XYLELLA FASTIDIOSA ISOLATED
FROM PLANT HOSTS IN LOUISIANA AND USED IN THIS STUDY**

ClustalW2 Alignment

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XF_A-08          ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
M23_ALSD        ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
Temecula1_PD    ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_GB514        ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_Oleander     ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_A-05         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_B-05         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_C-05         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_A-06         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_A-07         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
XF_D-07         ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
M12_ALSD        ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
9a5c_CVC        ATGAACCTTGACCGTTTCCTCCCCCTAGTGTTGGACTGCACTGTTTTGCCGCAATGGGC 60
*****

XF_A-08          GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
M23_ALSD        GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
Temecula1_PD    GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_GB514        GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_Oleander     GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_A-05         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_B-05         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_C-05         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_A-06         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_A-07         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
XF_D-07         GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
M12_ALSD        GGCACCTGCTGATGTCTTTCGAGTGTACAGCTGTCCCTCATCAGATCTTTCGAGCCGGTA 120
9a5c_CVC        GGCACCTGCTGATGTCTTTCGAGGATACAGCCTTCCCTATCCGATCTTTCGAGCCGGTA 120
*****

XF_A-08          TCGGTGAAAACGCTATGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
M23_ALSD        TCGGTGAAAACGCTATGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
Temecula1_PD    TCGGTGAAAACGCTATGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_GB514        TCGGTGAAAACGCTATGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_Oleander     TCTGTGAAAACGCTATGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_A-05         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_B-05         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_C-05         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_A-06         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_A-07         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
XF_D-07         TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
M12_ALSD        TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
9a5c_CVC        TCGGTGAAAACGCTCTGGGGCGAGGTGCAACGTCCCAGCCTACCTACCCACGTGTGTACG 180
** *****

XF_A-08          GTATTGCCTGCGCGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCA 240
M23_ALSD        GTATTGCCTGCGCGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCA 240
Temecula1_PD    GTATTGCCTGCGCGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCA 240
XF_GB514        GTATTGCCTGCGCGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCA 240
XF_Oleander     GTATTGCCTGCGCGCCTGACTCCTAAACATGGCTCCATTGACGCACTCGATGCCAATCCA 240
XF_A-05         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
XF_B-05         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
XF_C-05         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
XF_A-06         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
XF_A-07         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
XF_D-07         GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
M12_ALSD        GTATTGCCTGCGCGCCTGACTCCTAAACATGGTTCCATTGACGCACTCGATGCCAATCCA 240
9a5c_CVC        GTATTGCCTGCGCGCCTGACTCCTGAACATGGCTCCCTTGACGCACTCGATGCCAATCCA 240
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(APPENDIX I continued)

XF_A-08 AAGGTTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
M23_ALSD AAGGTTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
Temecula1_PD AAGGTTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_GB514 AAGGTTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_Oleander AAGGTTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_A-05 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_B-05 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_C-05 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_A-06 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_A-07 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
XF_D-07 CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
M12_ALSD CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
9a5c_CVC CAGGCTTCCAAGCCTGATACCAAGCGTTTACAGGATGCCATTGATGATTGTCCCGCCGGT 300
** *****

XF_A-08 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
M23_ALSD AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
Temecula1_PD AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_GB514 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_Oleander AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_A-05 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_B-05 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_C-05 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_A-06 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_A-07 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
XF_D-07 AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
M12_ALSD AGCGCGGTCAAACCTAGTGATCGACAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
9a5c_CVC AGCGCGGTCAAACCTAGTGATGGATAGTCATCGCAAATCCGGCTTTTTGAGTGGGCCGTTG 360
***** ** *****

XF_A-08 CACTTGAAATCTGGGGTGACGTTGTGGATTGACGAGGGTGTACGCTGTTTGCATCGCGC 420
M23_ALSD CACTTGAAATCTGGGGTGACGTTGTGGATTGACGAGGGTGTACGCTGTTTGCATCGCGC 420
Temecula1_PD CACTTGAAATCTGGGGTGACGTTGTGGATTGACGAGGGTGTACGCTGTTTGCATCGCGC 420
XF_GB514 CACTTGAAATCTGGGGTGACGTTGTGGATTGACGAGGGTGTACGCTGTTTGCATCGCGC 420
XF_Oleander CACTTGAAATCTGGGGTGACGTTGTGGATTGACGATGGTGTACGCTGTTTGCATCGCGC 420
XF_A-05 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
XF_B-05 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
XF_C-05 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
XF_A-06 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
XF_A-07 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
XF_D-07 CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
M12_ALSD CACTTGAAATCTAGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGC 420
9a5c_CVC CACTTGAAATCTGGGGTGACGTTGTGGATTGACGATGGCGTCACGCTGTTTGCATCGCGT 420
***** ** *****

XF_A-08 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
M23_ALSD AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
Temecula1_PD AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_GB514 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_Oleander AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_A-05 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_B-05 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_C-05 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_A-06 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_A-07 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
XF_D-07 AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
M12_ALSD AACCCCAAGGATTACGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
9a5c_CVC AACCCCAAGGACTATGACAAAGGCAATGGTACGTGCGGTACTGCAACGTCAACTCATGAG 480
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(APPENDIX I continued)

XF_A-08 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
M23_ALSD TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
Temecula1_PD TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_GB514 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_Oleander TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_A-05 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_B-05 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_C-05 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_A-06 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_A-07 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
XF_D-07 TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
M12_ALSD TTCAGTTGTATGCCTTT-GATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 539
9a5c_CVC TTCAGTTGTATGCCATTAGATCTCCGCGATCAACACCACCGGTAGCGGTATCGTGGGTGG 540
***** * * *****

XF_A-08 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
M23_ALSD GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
Temecula1_PD GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_GB514 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_Oleander GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_A-05 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_B-05 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_C-05 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_A-06 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_A-07 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
XF_D-07 GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
M12_ALSD GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGCGGTAAGTATGCTCGGCAGCG 599
9a5c_CVC GGGTGTCAATTGATGGGCGTGGCGGTAGCATTTTACTGGTGGTAAGCATGCTCGGCAGCG 600
***** *****

XF_A-08 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
M23_ALSD TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
Temecula1_PD TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_GB514 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_Oleander TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_A-05 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_B-05 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_C-05 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_A-06 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_A-07 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
XF_D-07 TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
M12_ALSD TACCTGGTGGGACCTGGCCTATCAGAACAAGCGCCATGCACTGCATCAACAGGTACCACG 659
9a5c_CVC TACCTGGTGGGATCTGGCCTATCAGAACAAGCACCATGCACTGCATCAACAGGTACCACG 660
***** *****

XF_A-08 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
M23_ALSD GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
Temecula1_PD GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_GB514 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_Oleander GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_A-05 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_B-05 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_C-05 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_A-06 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_A-07 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
XF_D-07 GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
M12_ALSD GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 719
9a5c_CVC GTTGATCCAAATCAGGGGCGGTAACGACTTCACGTTGTACCGTGTGGCCATCGAAAATGC 720
***** *****

(APPENDIX I continued)

XF_A-08 ACCTAACTTCCATGTGGTTGCTGATACGGTTAGCGGTGTCACCGCATGGGGCATCCGCAT 779
M23_ALSD ACCTAACTTCCATGTGGTTGCTGATACGGTTAGCGGTGTCACCGCATGGGGCATCCGCAT 779
Temecula1_PD ACCTAACTTCCATGTGGTTGCTGATACGGTTAGCGGTGTCACCGCATGGGGCATCCGCAT 779
XF_GB514 ACCTAACTTCCATGTGGTTGCTGATACGGTTAGCGGTGTCACCGCATGGGGCATCCGCAT 779
XF_Oleander ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGCATGGGGCATCCGCAT 779
XF_A-05 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
XF_B-05 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
XF_C-05 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
XF_A-06 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
XF_A-07 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
XF_D-07 ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
M12_ALSD ACCTAACTTCCATGTGGTTGCTGATACGGTCAGCGGTGTCACCGTATGGGGCATCCGCAT 779
9a5c_CVC ACCTAACTTCCATGTGGTTGCTGATACGGTCAGTGGTGTACCGCATGGGGCATCCGCAT 780
***** ** ***** **

XF_A-08 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
M23_ALSD CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
Temecula1_PD CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_GB514 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_Oleander CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_A-05 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_B-05 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_C-05 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_A-06 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_A-07 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
XF_D-07 CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
M12_ALSD CCTGACCCCAAGCTTGGTCTATACCACGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 839
9a5c_CVC CCTGACCCCAAGCTTGGTCTATACCATGCCGGGGTACCACTGTCCGCCCGGTACCACGCC 840
***** *****

XF_A-08 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
M23_ALSD GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
Temecula1_PD GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_GB514 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_Oleander GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_A-05 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_B-05 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_C-05 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_A-06 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_A-07 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
XF_D-07 GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
M12_ALSD GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 899
9a5c_CVC GGATGTTGTGACGCCGGCGACATGCTTTACCCCGGACACGGTCAAGAACACCGATGGCTT 900
***** *****

XF_A-08 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
M23_ALSD TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
Temecula1_PD TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_GB514 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_Oleander TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_A-05 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_B-05 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_C-05 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_A-06 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_A-07 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
XF_D-07 TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
M12_ALSD TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 959
9a5c_CVC TGATCCTGGGCAATCAAACCACGTGCTGCTAGCGTACTCCTACATCAGCACTGGGGATGA 960
***** *****

(APPENDIX I continued)

XF_A-08 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
M23_ALSD CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
Temecula1_PD CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_GB514 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_Oleander CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_A-05 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_B-05 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_C-05 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_A-06 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_A-07 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
XF_D-07 CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
M12_ALSD CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1019
9a5c_CVC CCACGTTGCCATCAAAGCGGGGGCAAGATGCCAAGCTACGCTCTGAGCTTCTTACACAA 1020

XF_A-08 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1079
M23_ALSD CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1079
Temecula1_PD CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1079
XF_GB514 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1079
XF_Oleander CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1079
XF_A-05 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
XF_B-05 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
XF_C-05 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
XF_A-06 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
XF_A-07 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
XF_D-07 CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
M12_ALSD CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACATCGAGTCAGGTGTACACGA 1079
9a5c_CVC CCACTTTGGCTATGGACATGGCATGTCCATCGGTAGCGACACCGAGTCAGGTGTACACGA 1080

XF_A-08 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
M23_ALSD TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
Temecula1_PD TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_GB514 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_Oleander TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_A-05 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_B-05 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_C-05 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_A-06 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_A-07 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
XF_D-07 TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
M12_ALSD TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1139
9a5c_CVC TATGGAAGTCAGTGATTTGAGTATCGACGGCTTTGACAGCCCTAACAGCAATGGTTTGA 1140

XF_A-08 GATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
M23_ALSD GATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
Temecula1_PD GATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_GB514 GATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_Oleander TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_A-05 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_B-05 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_C-05 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_A-06 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_A-07 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
XF_D-07 TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
M12_ALSD TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1199
9a5c_CVC TATGAAATCTGATGCCGATCATGGCGGAGTGGTCGACCATGTACCTACTCCAAAATATG 1200

(APPENDIX I continued)

XF_A-08 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
M23_ALSD CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
Temecula1_PD CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_GB514 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_Oleander CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_A-05 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_B-05 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_C-05 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_A-06 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_A-07 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
XF_D-07 CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
M12_ALSD CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1259
9a5c_CVC CATGCGTCGTCTGAAACGTCGCTGGCGTTTGACACCTTCTACAAACCTTCCAACGGGAA 1260

XF_A-08 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
M23_ALSD TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
Temecula1_PD TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_GB514 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_Oleander TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_A-05 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_B-05 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_C-05 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_A-06 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_A-07 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
XF_D-07 TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
M12_ALSD TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1319
9a5c_CVC TTCTTATCCACTCTTCAAAAATATCGTGCTGCAAGATATTCATGTGCTTGAAAGTCTGT 1320

XF_A-08 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
M23_ALSD CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
Temecula1_PD CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_GB514 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_Oleander CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_A-05 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_B-05 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_C-05 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_A-06 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_A-07 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
XF_D-07 CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
M12_ALSD CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1379
9a5c_CVC CTTTGGTGCTGGTCAGCTGCTTTTTTCATGGGGATCCTGGGCAGTGGGAATAATCTGCCAAT 1380

XF_A-08 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
M23_ALSD GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
Temecula1_PD GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_GB514 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_Oleander GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_A-05 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_B-05 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_C-05 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_A-06 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_A-07 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
XF_D-07 GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
M12_ALSD GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1439
9a5c_CVC GACGCTGAGCATGGATAACGTCGTATTCGACGGTTTTTTTGCCAACATTGATAGCGCTCC 1440

(APPENDIX I continued)

XF_A-08 CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
M23_ALSD CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
Temecula1_PD CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_GB514 CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_Oleander CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_A-05 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_B-05 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_C-05 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_A-06 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_A-07 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
XF_D-07 CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
M12_ALSD CAGCAGTGTGCGTATTTGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1499
9a5c_CVC CAGCAGTGTGCGTATTCGCCAATCCGCAGGCAGTGCATTTTCACTTCGGTCCCGGTCCGGT 1500

XF_A-08 CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
M23_ALSD CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
Temecula1_PD CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_GB514 CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_Oleander CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_A-05 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_B-05 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_C-05 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_A-06 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_A-07 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
XF_D-07 CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
M12_ALSD CAGTTTCGCTCCTTTGATTACCTCCTCTGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1559
9a5c_CVC CAGTTTCGCTCCTTTGATTACCCCCCTCGGTTGCTTACGATGTGACTGTGAGTGGAAGTCC 1560

XF_A-08 AGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
M23_ALSD AGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
Temecula1_PD AGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_GB514 AGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_Oleander AGGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCATATTTC 1619
XF_A-05 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_B-05 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_C-05 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_A-06 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_A-07 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
XF_D-07 AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
M12_ALSD AAGTGTGGGCAACCCATACGATTGTTTCAGCGGCATTTATCAATTTTTCCAGCGTATTTC 1619
9a5c_CVC AAGTGTGGGCAACCCATACGATTGTTTCGGCGGCATTTATCAATTTTTCCAGCGTATTTC 1620

XF_A-08 TGATTTCGCCTATCTAA 1635
M23_ALSD TGATTTCGCCTATCTAA 1635
Temecula1_PD TGATTTCGCCTATCTAA 1635
XF_GB514 TGATTTCGCCTATCTAA 1635
XF_Oleander TGATTTCGCCTATCTAA 1635
XF_A-05 TGATTTCGCCTATCTAA 1635
XF_B-05 TGATTTCGCCTATCTAA 1635
XF_C-05 TGATTTCGCCTATCTAA 1635
XF_A-06 TGATTTCGCCTATCTAA 1635
XF_A-07 TGATTTCGCCTATCTAA 1635
XF_D-07 TGATTTCGCCTATCTAA 1635
M12_ALSD TGATTTCGCCTATCTAA 1635
9a5c_CVC TGATTTCGCCTATCTAA 1636

(APPENDIX I continued)

ClustalW2 Summary

SeqA	Name	Length	SeqB	Name	Length	Score
1	XF_A-05	1635	2	XF_B-05	1635	100
1	XF_A-05	1635	3	XF_C-05	1635	100
1	XF_A-05	1635	4	XF_A-06	1635	100
1	XF_A-05	1635	5	XF_A-07	1635	100
1	XF_A-05	1635	6	XF_D-07	1635	100
1	XF_A-05	1635	7	XF_A-08	1635	98
1	XF_A-05	1635	8	XF_Oleander	1635	98
1	XF_A-05	1635	9	M23_ALSD	1635	98
1	XF_A-05	1635	10	Temecula1_PD	1635	98
1	XF_A-05	1635	11	M12_ALSD	1635	99
1	XF_A-05	1635	12	9a5c_CVC	1636	97
1	XF_A-05	1635	13	XF_GB514	1635	98
2	XF_B-05	1635	3	XF_C-05	1635	100
2	XF_B-05	1635	4	XF_A-06	1635	100
2	XF_B-05	1635	5	XF_A-07	1635	100
2	XF_B-05	1635	6	XF_D-07	1635	100
2	XF_B-05	1635	7	XF_A-08	1635	98
2	XF_B-05	1635	8	XF_Oleander	1635	98
2	XF_B-05	1635	9	M23_ALSD	1635	98
2	XF_B-05	1635	10	Temecula1_PD	1635	98
2	XF_B-05	1635	11	M12_ALSD	1635	99
2	XF_B-05	1635	12	9a5c_CVC	1636	97
2	XF_B-05	1635	13	XF_GB514	1635	98
3	XF_C-05	1635	4	XF_A-06	1635	100
3	XF_C-05	1635	5	XF_A-07	1635	100
3	XF_C-05	1635	6	XF_D-07	1635	100
3	XF_C-05	1635	7	XF_A-08	1635	98
3	XF_C-05	1635	8	XF_Oleander	1635	98
3	XF_C-05	1635	9	M23_ALSD	1635	98
3	XF_C-05	1635	10	Temecula1_PD	1635	98
3	XF_C-05	1635	11	M12_ALSD	1635	99
3	XF_C-05	1635	12	9a5c_CVC	1636	97
3	XF_C-05	1635	13	XF_GB514	1635	98
4	XF_A-06	1635	5	XF_A-07	1635	100
4	XF_A-06	1635	6	XF_D-07	1635	100
4	XF_A-06	1635	7	XF_A-08	1635	98
4	XF_A-06	1635	8	XF_Oleander	1635	98
4	XF_A-06	1635	9	M23_ALSD	1635	98
4	XF_A-06	1635	10	Temecula1_PD	1635	98

(APPENDIX I continued)

SeqA	Name	Length	SeqB	Name	Length	Score
4	XF_A-06	1635	11	M12_ALSD	1635	99
4	XF_A-06	1635	12	9a5c_CVC	1636	97
4	XF_A-06	1635	13	XF_GB514	1635	98
5	XF_A-07	1635	6	XF_D-07	1635	100
5	XF_A-07	1635	7	XF_A-08	1635	98
5	XF_A-07	1635	8	XF_Oleander	1635	98
5	XF_A-07	1635	9	M23_ALSD	1635	98
5	XF_A-07	1635	10	Temecula1_PD	1635	98
5	XF_A-07	1635	11	M12_ALSD	1635	99
5	XF_A-07	1635	12	9a5c_CVC	1636	97
5	XF_A-07	1635	13	XF_GB514	1635	98
6	XF_D-07	1635	7	XF_A-08	1635	98
6	XF_D-07	1635	8	XF_Oleander	1635	98
6	XF_D-07	1635	9	M23_ALSD	1635	98
6	XF_D-07	1635	10	Temecula1_PD	1635	98
6	XF_D-07	1635	11	M12_ALSD	1635	99
6	XF_D-07	1635	12	9a5c_CVC	1636	97
6	XF_D-07	1635	13	XF_GB514	1635	98
7	XF_A-08	1635	8	XF_Oleander	1635	98
7	XF_A-08	1635	9	M23_ALSD	1635	100
7	XF_A-08	1635	10	Temecula1_PD	1635	100
7	XF_A-08	1635	11	M12_ALSD	1635	98
7	XF_A-08	1635	12	9a5c_CVC	1636	97
7	XF_A-08	1635	13	XF_GB514	1635	100
8	XF_Oleander	1635	9	M23_ALSD	1635	98
8	XF_Oleander	1635	10	Temecula1_PD	1635	98
8	XF_Oleander	1635	11	M12_ALSD	1635	98
8	XF_Oleander	1635	12	9a5c_CVC	1636	97
8	XF_Oleander	1635	13	XF_GB514	1635	98
9	M23_ALSD	1635	10	Temecula1_PD	1635	100
9	M23_ALSD	1635	11	M12_ALSD	1635	98
9	M23_ALSD	1635	12	9a5c_CVC	1636	97
9	M23_ALSD	1635	13	XF_GB514	1635	100
10	Temecula1_PD	1635	11	M12_ALSD	1635	98
10	Temecula1_PD	1635	12	9a5c_CVC	1636	97
10	Temecula1_PD	1635	13	XF_GB514	1635	100
11	M12_ALSD	1635	12	9a5c_CVC	1636	97
11	M12_ALSD	1635	13	XF_GB514	1635	98
12	9a5c_CVC	1636	13	XF_GB514	1635	97

APPENDIX J: BLAST SEARCH OF *PGLA* NUCLEOTIDE SEQUENCES OF STRAINS OF *XYLELLA FASTIDIOSA* ISOLATED FROM PLANT HOSTS IN LOUISIANA

BLAST Query Results: XF A-05 (Identical to all LA pecan and sycamore ITS sequences)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP000941.1	Xylella fastidiosa M12, complete genome	3014	3014	100%	0.0	99%
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	2859	2859	100%	0.0	98%
CP001011.1	Xylella fastidiosa M23, complete genome	2859	2859	100%	0.0	98%
AE009442.1	Xylella fastidiosa Temecula1, complete genome	2859	2859	100%	0.0	98%
AE003849.1	Xylella fastidiosa 9a5c, complete genome	2765	2765	100%	0.0	97%

BLAST Query Results: XF A-08 (LA grapevine strain)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	3020	3020	100%	0.0	100%
CP001011.1	Xylella fastidiosa M23, complete genome	3020	3020	100%	0.0	100%
AE009442.1	Xylella fastidiosa Temecula1, complete genome	3020	3020	100%	0.0	100%
CP000941.1	Xylella fastidiosa M12, complete genome	2854	2854	100%	0.0	98%
AE003849.1	Xylella fastidiosa 9a5c, complete genome	2771	2771	100%	0.0	97%

BLAST Query Results: XF Oleander (LA oleander strain)

<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>
CP002165.1	Xylella fastidiosa subsp. fastidiosa GB514, complete genome	2915	2915	100%	0.0	98%
CP001011.1	Xylella fastidiosa M23, complete genome	2915	2915	100%	0.0	98%
AE009442.1	Xylella fastidiosa Temecula1, complete genome	2915	2915	100%	0.0	98%
CP000941.1	Xylella fastidiosa M12, complete genome	2859	2859	100%	0.0	98%
AE003849.1	Xylella fastidiosa 9a5c, complete genome	2743	2743	100%	0.0	96%

**APPENDIX K: PGLA AMINO ACID SEQUENCES OF STRAINS OF XYLELLA
FASTIDIOSA ISOLATED FROM PLANT HOSTS IN LOUISIANA (TRANSLATED
FROM THE PGLA NUCLEOTIDE SEQUENCES)**

>XF_A-05_PGLA

Met N L D R F L P L V F G L H C F A A **Met** G G T A D V F R V S Q L S S S D L S
 E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
 D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
 L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
 A T S T H E F S C **Met** P L I S A I N T T G S G I V G G G V I D G R G G S I L T
 G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
 L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
 G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
 L A Y S Y I S T G D D H V A I K A R G K **Met** P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D **Met** E V S D L S I D G F D S P N S N G L H **Met** K
 S D A D H G G V V D H V T Y S K I C **Met** R R L K R P L A F D T F Y K P S N G N
 S Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F **Met** G I L G S G N N L
P Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G
 P G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F
 S S V F P D S P I **Stop**

>XF_B-05_PGLA

Met N L D R F L P L V F G L H C F A A **Met** G G T A D V F R V S Q L S S S D L S
 E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
 D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
 L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
 A T S T H E F S C **Met** P L I S A I N T T G S G I V G G G V I D G R G G S I L T
 G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
 L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
 G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
 L A Y S Y I S T G D D H V A I K A R G K **Met** P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D **Met** E V S D L S I D G F D S P N S N G L H **Met** K S
 D A D H G G V V D H V T Y S K I C **Met** R R L K R P L A F D T F Y K P S N G N S
 Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F **Met** G I L G S G N N L P
Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G P
 G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F S
 S V F P D S P I **Stop**

>XF_C-05_PGLA

Met N L D R F L P L V F G L H C F A A **Met** G G T A D V F R V S Q L S S S D L S
 E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
 D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
 L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
 A T S T H E F S C **Met** P L I S A I N T T G S G I V G G G V I D G R G G S I L T
 G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
 L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
 G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
 L A Y S Y I S T G D D H V A I K A R G K **Met** P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D **Met** E V S D L S I D G F D S P N S N G L H **Met** K S
 D A D H G G V V D H V T Y S K I C **Met** R R L K R P L A F D T F Y K P S N G N S
 Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F **Met** G I L G S G N N L P
Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G P
 G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F S
 S V F P D S P I **Stop**

(APPENDIX K continued)

>XF_A-06_PGLA

Met N L D R F L P L V F G L H C F A A Met G G T A D V F R V S Q L S S S D L S
E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
A T S T H E F S C Met P L I S A I N T T G S G I V G G G V I D G R G G S I L T
G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
L A Y S Y I S T G D D H V A I K A R G K Met P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D Met E V S D L S I D G F D S P N S N G L H Met K S
D A D H G G V V D H V T Y S K I C Met R R L K R P L A F D T F Y K P S N G N S
Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F Met G I L G S G N N L P
Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G P
G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F S
S V F P D S P I Stop

>XF_A-07_PGLA

Met N L D R F L P L V F G L H C F A A Met G G T A D V F R V S Q L S S S D L S
E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
A T S T H E F S C Met P L I S A I N T T G S G I V G G G V I D G R G G S I L T
G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
L A Y S Y I S T G D D H V A I K A R G K Met P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D Met E V S D L S I D G F D S P N S N G L H Met K S
D A D H G G V V D H V T Y S K I C Met R R L K R P L A F D T F Y K P S N G N S
Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F Met G I L G S G N N L P
Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G P
G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F S
S V F P D S P I Stop

>XF_D-07_PGLA

Met N L D R F L P L V F G L H C F A A Met G G T A D V F R V S Q L S S S D L S
E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
D A N P Q A S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
L S G P L H L K S R V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
A T S T H E F S C Met P L I S A I N T T G S G I V G G G V I D G R G G S I L T
G G K H A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
L Y R V A I E N A P N F H V V A D T V S G V T V W G I R I L T P S L V Y T T P
G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
L A Y S Y I S T G D D H V A I K A R G K Met P S Y A L S F L H N H F G Y G H G
Met S I G S D I E S G V H D Met E V S D L S I D G F D S P N S N G L H Met K S
D A D H G G V V D H V T Y S K I C Met R R L K R P L A F D T F Y K P S N G N S
Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F Met G I L G S G N N L P
Met T L S L D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G P
G P V S F A P L I T S S V A Y D V T V S G S P S V G N P Y D C S A A F I N F S
S V F P D S P I Stop

(APPENDIX K continued)

>XF_A-08_PGLA

Met N L D R F L P L V F G L H C F A A **Met** G G T A D V F R V S Q L S S S D L S
E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
D A N P K V S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
L S G P L H L K S G V T L W I D E G V T L F A S R N P K D Y D K G N G T C G T
A T S T H E F S C **Met** P L I S A I N T T G S G I V G G G V I D G R G G S I L T
G G K Y A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
L Y R V A I E N A P N F H V V A D T V S G V T A W G I R I L T P S L V Y T T P
G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
L A Y S Y I S T G D D H V A I K A R G K **Met** P S Y A L S F L H N H F G Y G H G
Met S I G S D T E S G V H D **Met** E V S D L S I D G F D S P N S N G L Q **Met** K S
D A D H G G V V D H V T Y S K I C **Met** R R L K R P L A F D T F Y K P S N G N S
Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F **Met** G I L G S G N N L P
Met T L S **Met** D N V V F D G F L P T L I A P P S S V V F A N P Q A V H F H F G
P G P V S F A P L I T P S V A Y D V T V S G S P G V G N P Y D C S A A F I N F
S S V F P D S P I **Stop**

>XF_Oleander_PGLA

Met N L D R F F P L V F G L H C F A A **Met** G G T A D V F R V S Q L S S S D L S
E P V S V K T L W G E V Q R P S L P T H V C T V L P A R L T P K H G S I D A L
D A N P K V S K P D T K R L Q D A I D D C P A G S A V K L V I D S H R K S G F
L S G P L H L K S G V T L W I D D G V T L F A S R N P K D Y D K G N G T C G T
A T S T H E F S C **Met** P L I S A I N T T G S G I V G G G V I D G R G G S I L T
G G K Y A R Q R T W W D L A Y Q N K R H A L H Q Q V P R L I Q I R G G N D F T
L Y R V A I E N A P N F H V V A D T V S G V T A W G I R I L T P S L V Y T T P
G Y H C P P G T T P D V V T P A T C F T P D T V K N T D G F D P G Q S N H V L
L A Y S Y I S T G D D H V A I K A R G K **Met** P S Y A L S F L H N H F G Y G H G
Met S I G S D T E S G V H D **Met** E V S D L S I D G F D S P N S N G L H **Met** K S
D A D H G G V V D H V T Y S K I C **Met** R R L K R P L A F D T F Y K P S N G N S
Y P L F K N I V L Q D I H V L E S P V F G A G Q L L F **Met** G I L G S G N N L P
Met T L S **Met** D N V V F D G F L P T L I A P P S S I V F A N P Q A A H F H F G
P G P V S F A P L I T P S V A Y D V T V S G S P G V G N P Y D C S A A F I N F
S S I F P D S P I **Stop**

**APPENDIX L: CONSENSUS DATASET OF BANDS PRESENT IN ERIC-PCR AND
REP-PCR**

Table L1. Consensus Dataset^a of ERIC-PCR Data Used in Phylogenetic Analyses

Band size ^b (bp)	Strain of <i>Xylella fastidiosa</i>									
	XF A-05	XF B-05	XF C-05	XF A-06	XF D-07	XF A-10	XF B-10	XF A-08	XF Oleander	XF A-07
1,275	0	0	0	0	0	0	0	0	1	0
950	1	1	1	1	1	1	1	0	0	1
880	0	0	0	0	0	0	0	1	1	0
800	1	1	1	1	1	1	1	1	1	1
575	1	1	1	1	1	1	1	1	1	1
550	0	0	0	0	0	0	0	1	1	0
420	1	1	1	1	1	1	1	1	0	1
300	1	1	1	1	1	1	1	1	0	1
160	1	1	1	1	1	1	1	0	0	1
155	0	0	0	0	0	0	0	1	1	0

^a A ‘0’ indicates the absence of a band in a particular band class, while a ‘1’ indicates the presence of a band in a particular band class. The dataset was created using distinguishable bands that regularly appeared between 100 bp and 1,650 bp in ERIC-PCR fingerprints.

^b Band sizes are approximate sizes based on the location of a band in comparison to the bands of known size present in the DNA marker. Bands present at a particular size make up a ‘class’.

Table L2. Consensus Dataset^a of REP-PCR Data Used in Phylogenetic Analyses

Band size ^b (bp)	Strain of <i>Xylella fastidiosa</i>									
	XF A-05	XF B-05	XF C-05	XF A-06	XF D-07	XF A-10	XF B-10	XF A-08	XF Oleander	XF A-07
1,950	0	0	0	0	0	1	0	0	0	0
1,900	1	1	1	1	1	0	1	0	0	1
1,600	0	0	0	0	0	0	0	0	1	0
950	1	1	1	1	1	1	1	1	1	1
900	0	0	0	1	0	0	0	0	0	1
750	0	0	0	0	0	0	0	0	1	0
600	0	0	0	0	0	0	0	1	0	0
520	1	1	1	0	1	1	1	0	0	0
460	1	1	1	1	1	1	1	0	1	1

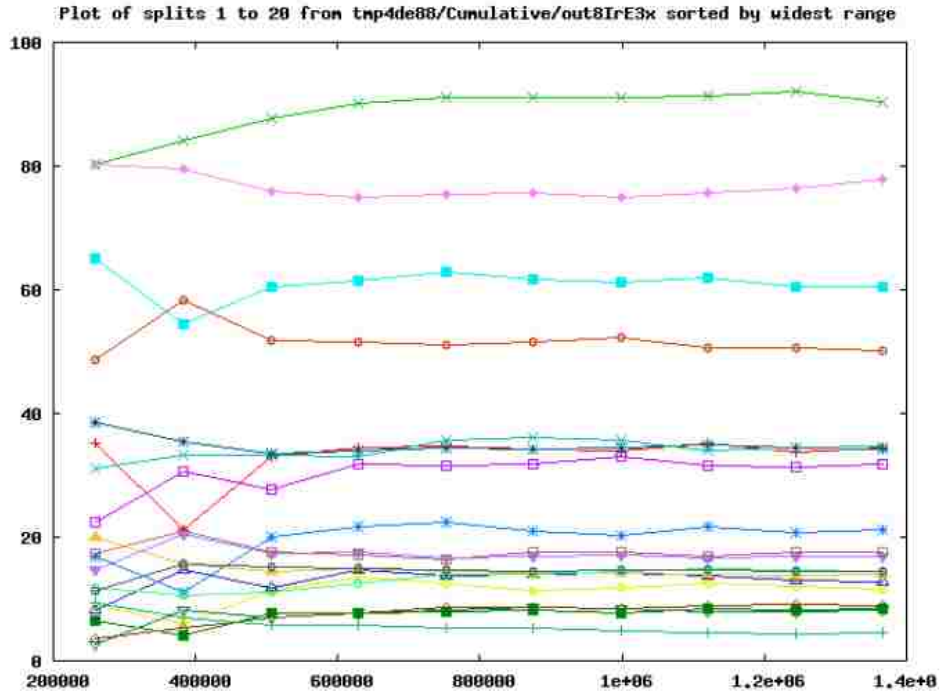
^a A ‘0’ indicates the absence of a band in a particular band class, while a ‘1’ indicates the presence of a band in a particular band class. The dataset was created using distinguishable bands that regularly appeared between 400 bp and 2,000 bp in REP-PCR fingerprints.

^b Band sizes are approximate sizes based on the location of a band in comparison to bands of known size present in the DNA marker. Bands present at a particular size make up a ‘class’.

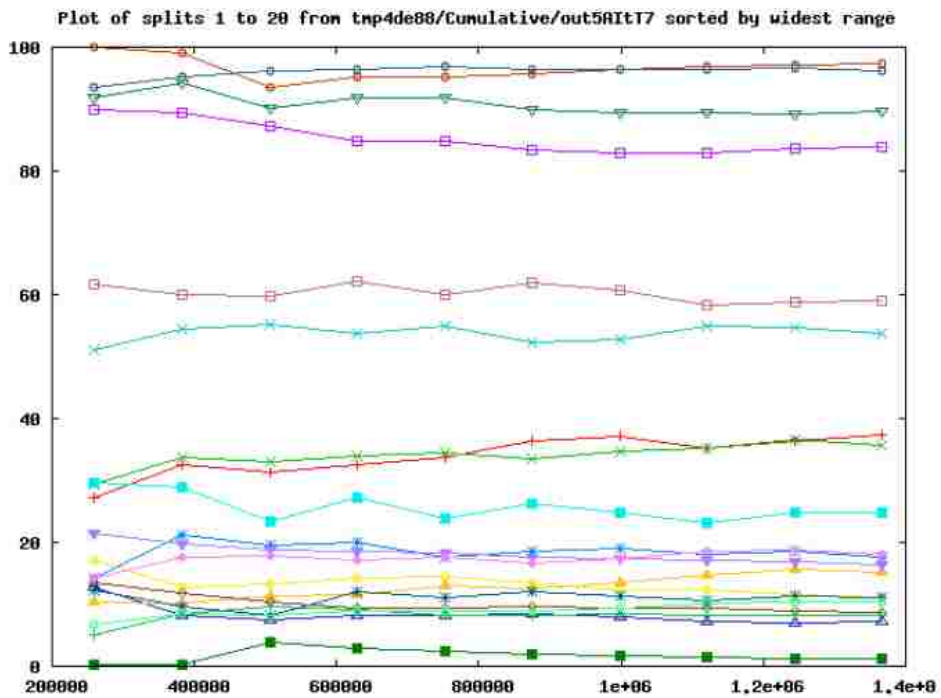
APPENDIX M: AWTY CUMULATIVE AND COMPARE TEST PLOTS FOR CONVERGENCE OF BAYESIAN ANALYSES

AWTY Cumulative Plots XF-ITS cured (stopval=0.01)

XF- ITS_cured (stopval=0.01) Cumulative Plot 1

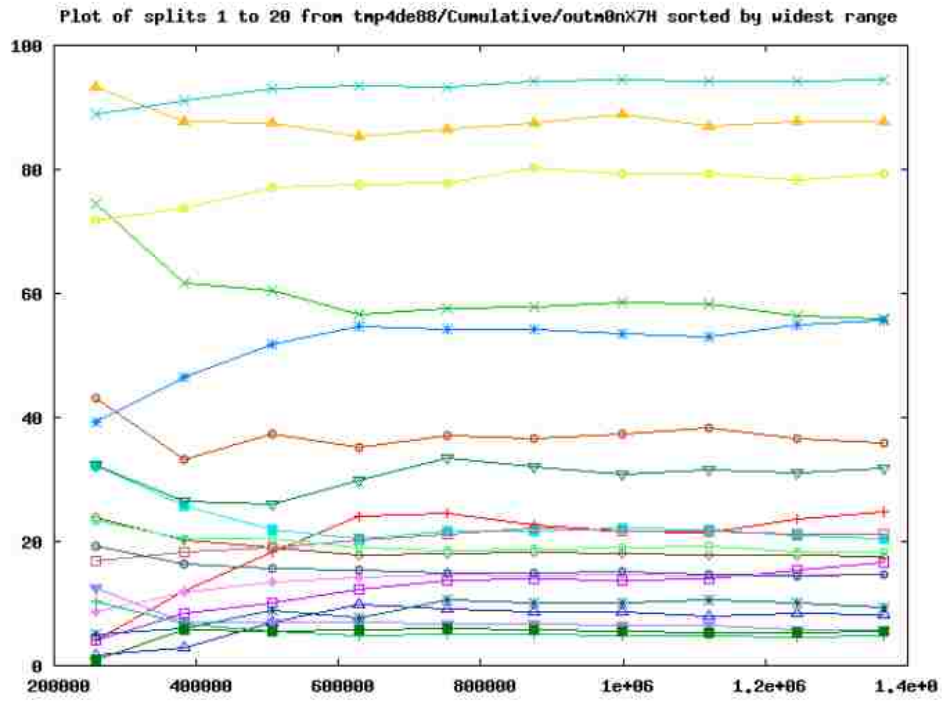


XF- ITS_cured (stopval=0.01) Cumulative Plot 2

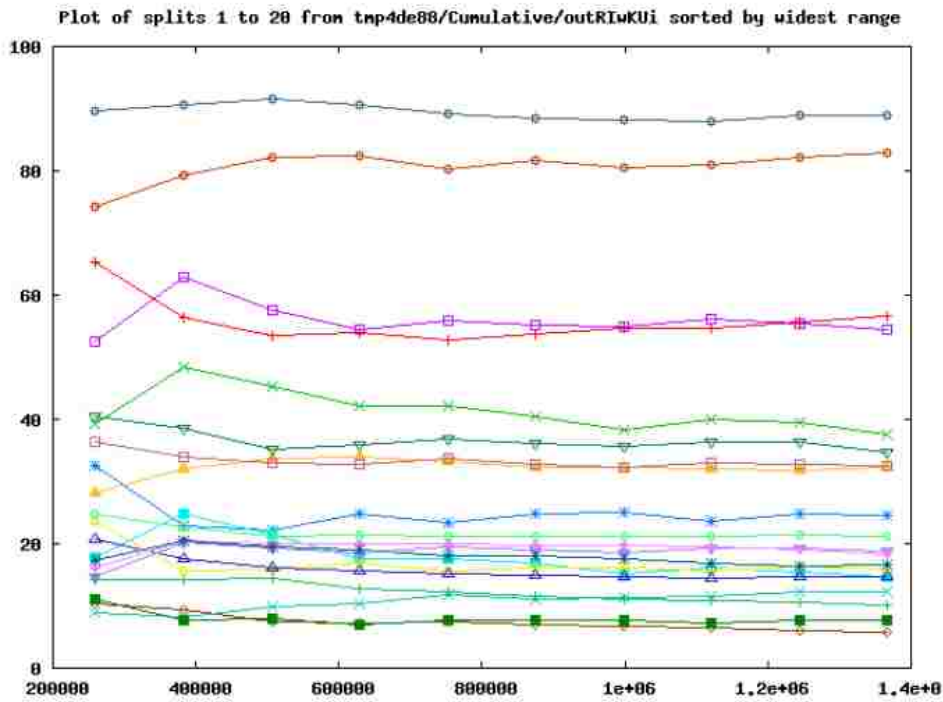


(APPENDIX M continued)

XF- ITS_cured (stopval=0.01) Cumulative Plot 3



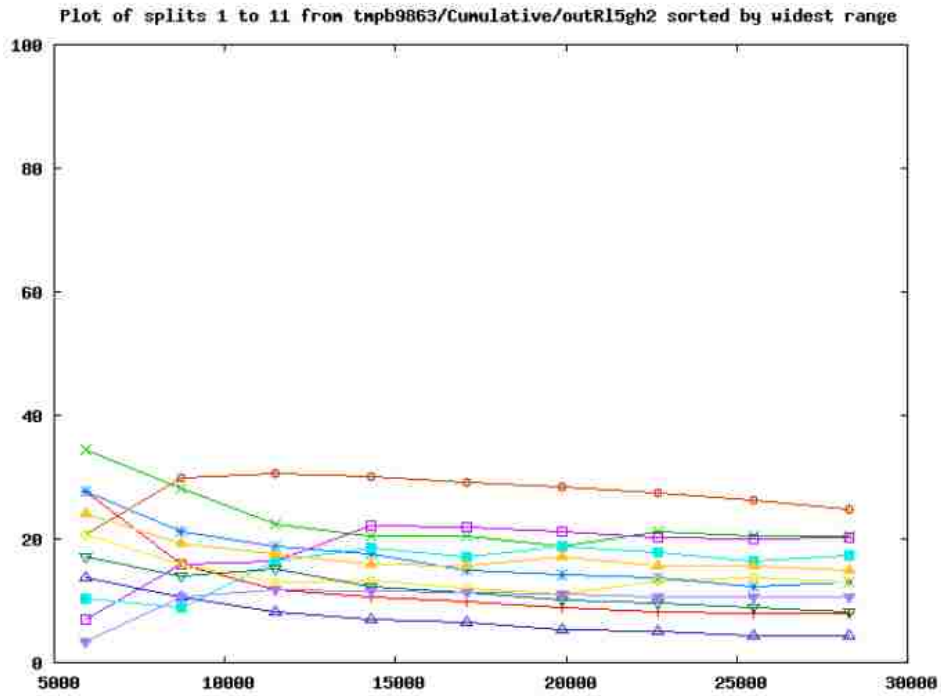
XF- ITS_cured (stopval=0.01) Cumulative Plot 4



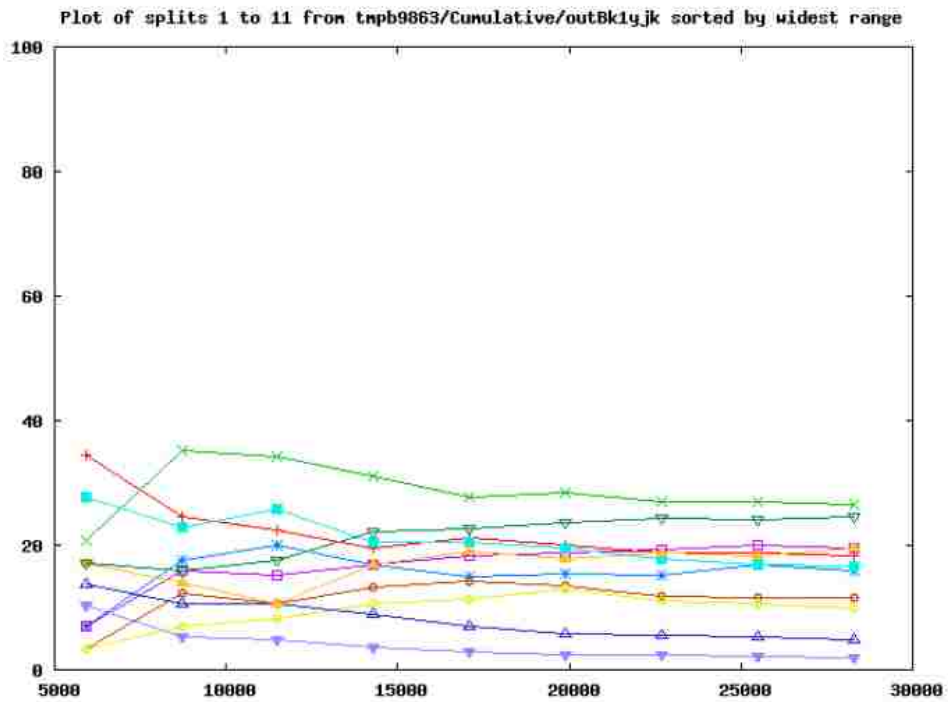
(APPENDIX M continued)

AWTY Cumulative Plots XF-PGLA

XF-PGLA Cumulative Plot 1

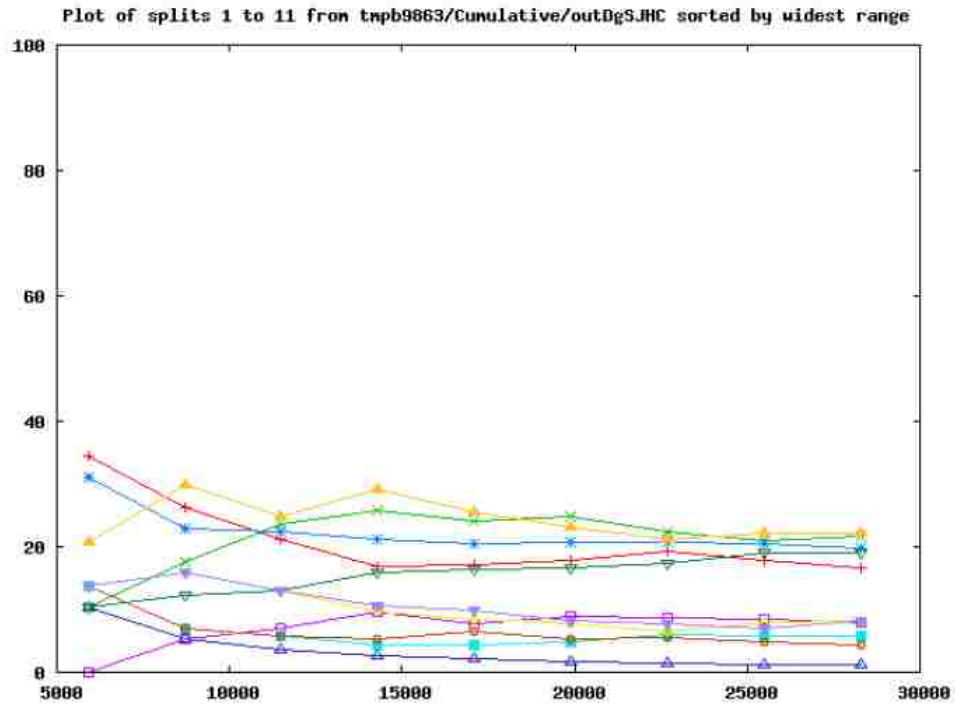


XF-PGLA Cumulative Plot 2

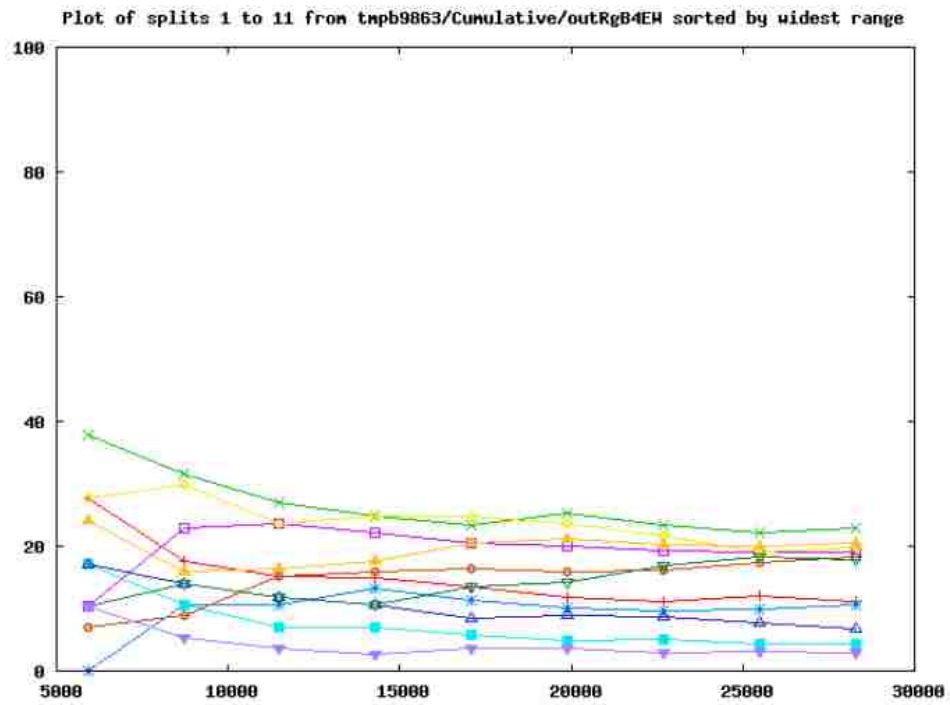


(APPENDIX M continued)

XF-PGLA Cumulative Plot 3



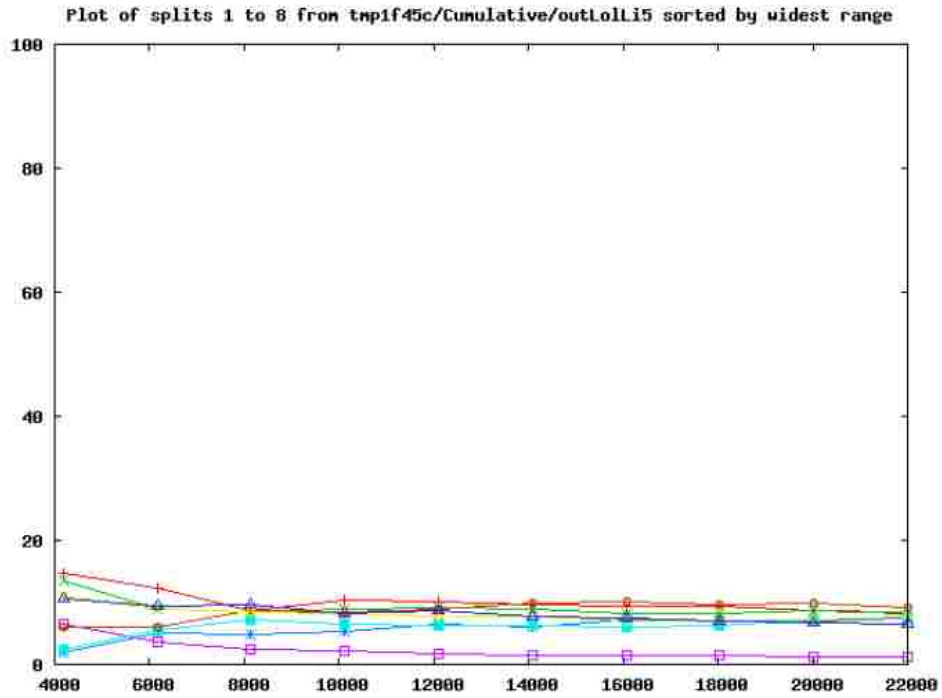
XF-PGLA Cumulative Plot 4



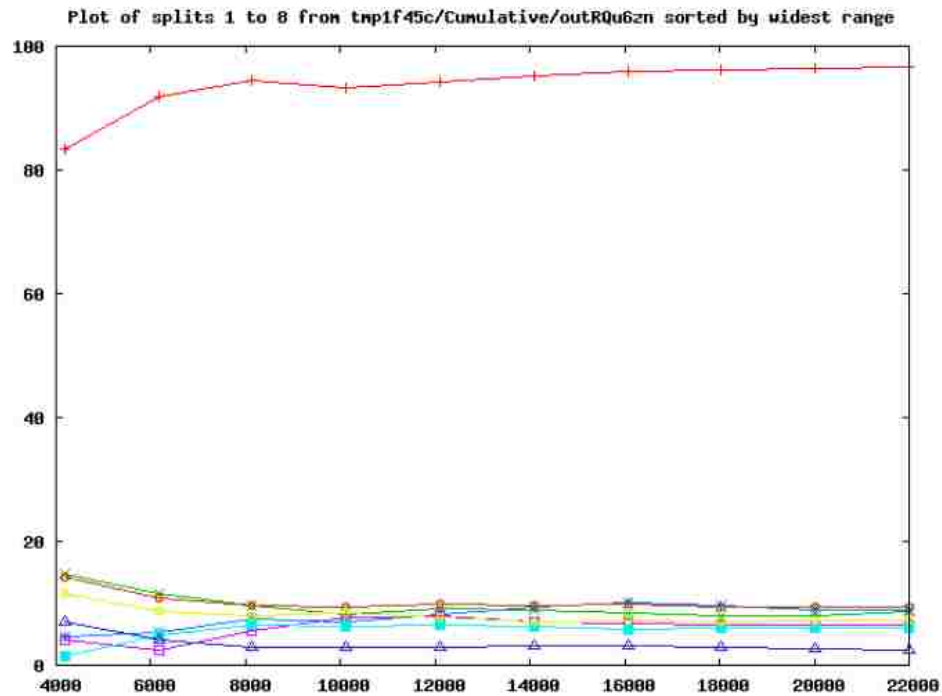
(APPENDIX M continued)

AWTY Cumulative Plots XF-ERIC

XF-ERIC Cumulative Plot 1

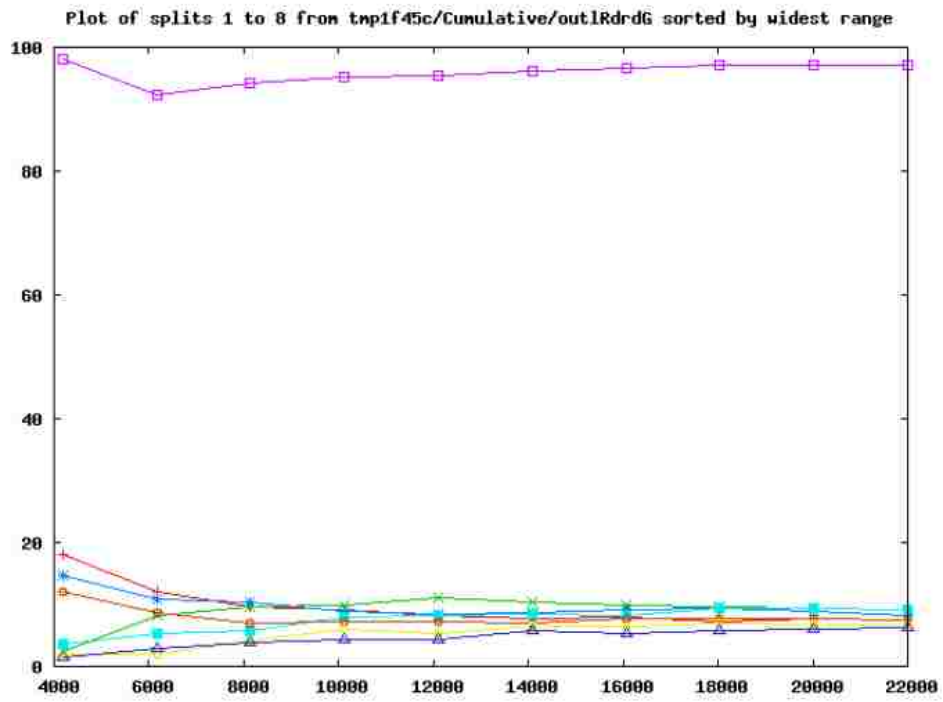


XF-ERIC Cumulative Plot 2

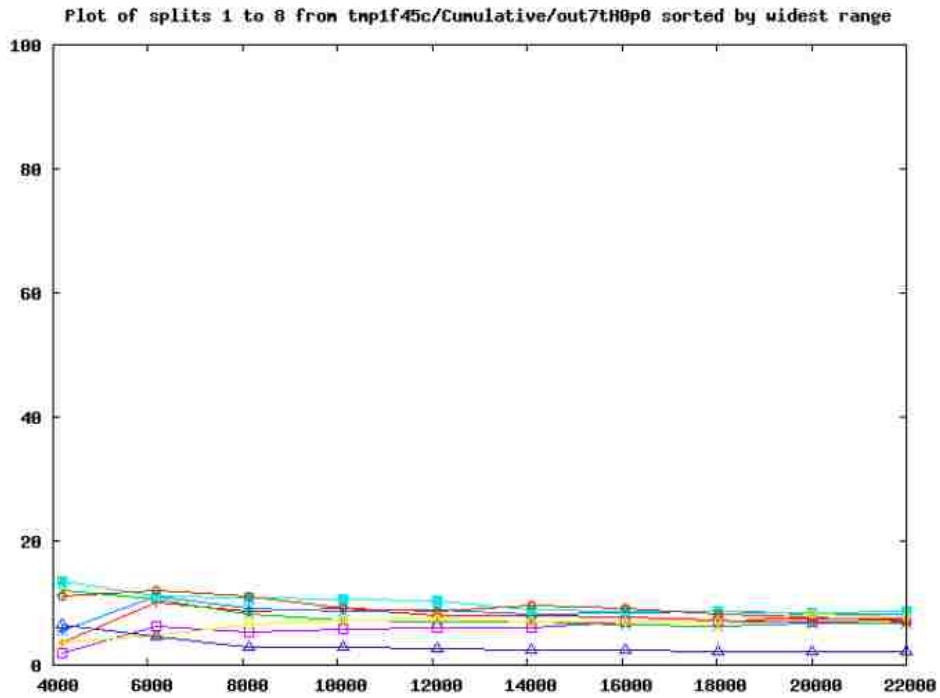


(APPENDIX M continued)

XF-ERIC Cumulative Plot 3



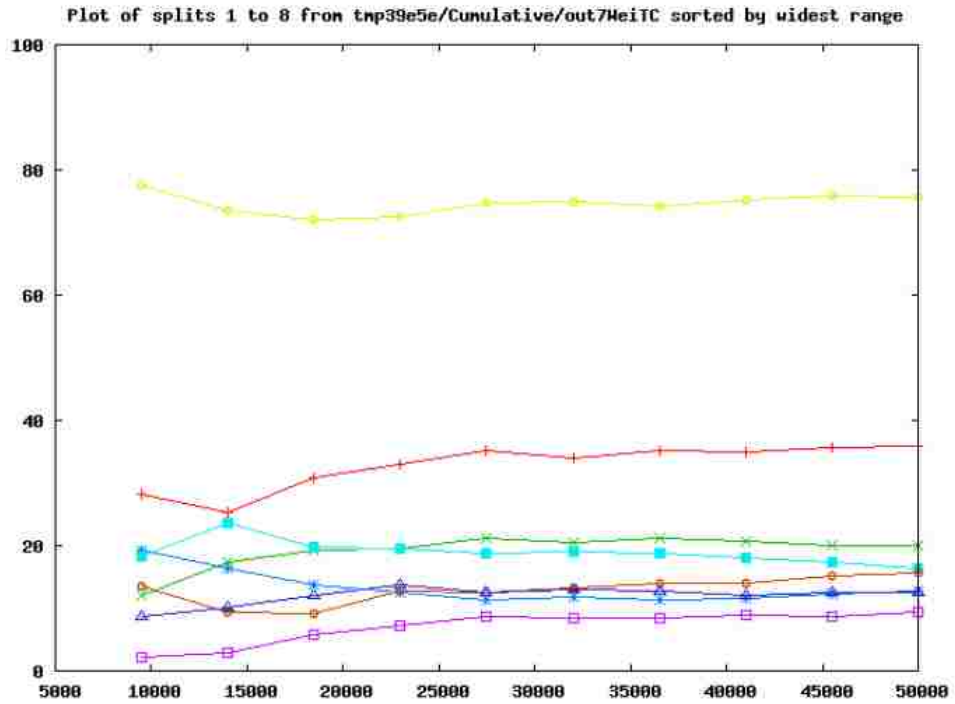
XF-ERIC Cumulative Plot 4



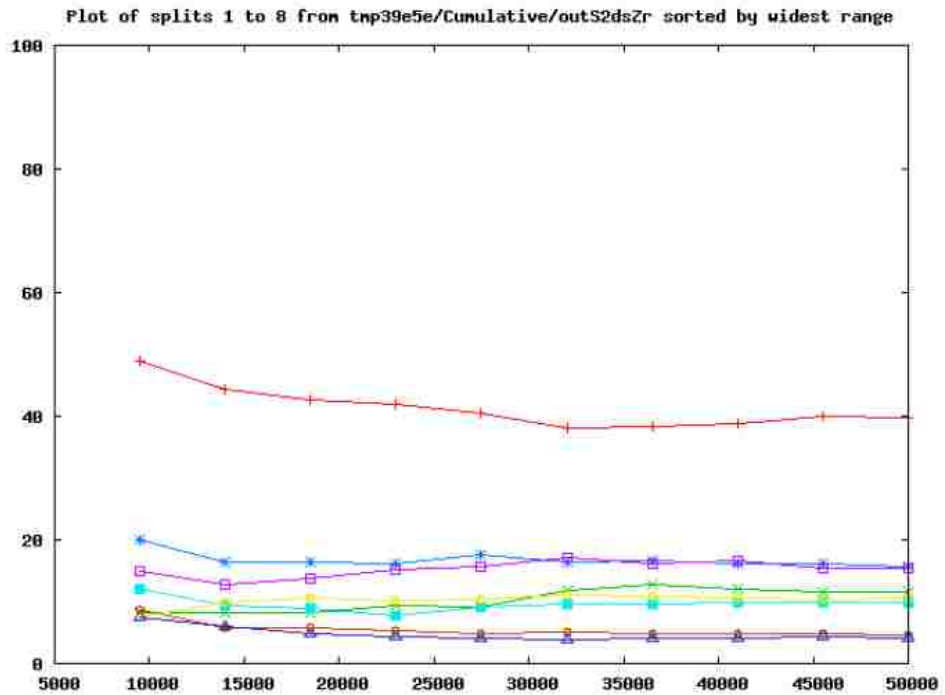
(APPENDIX M continued)

AWTY Cumulative Plots XF-REP

XF-REP Cumulative Plot 1

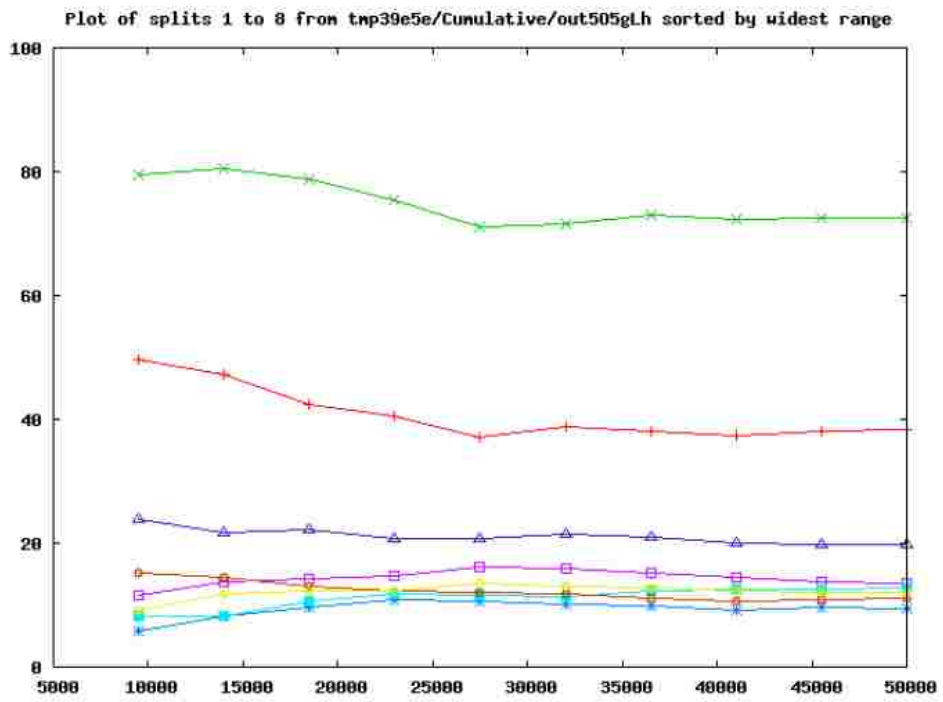


XF-REP Cumulative Plot 2

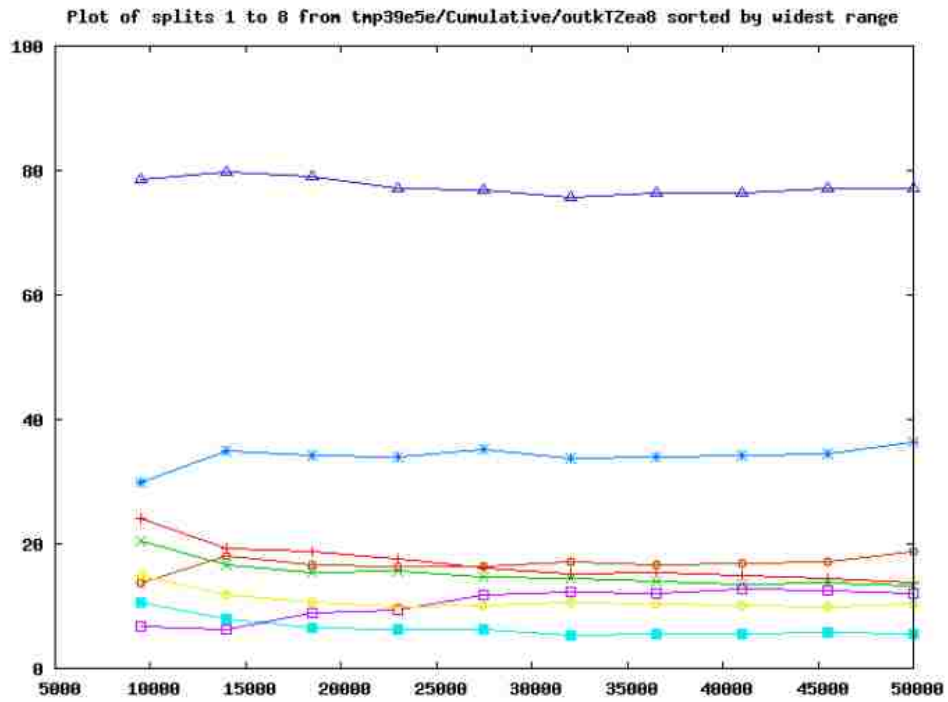


(APPENDIX M continued)

XF-REP Cumulative Plot 3



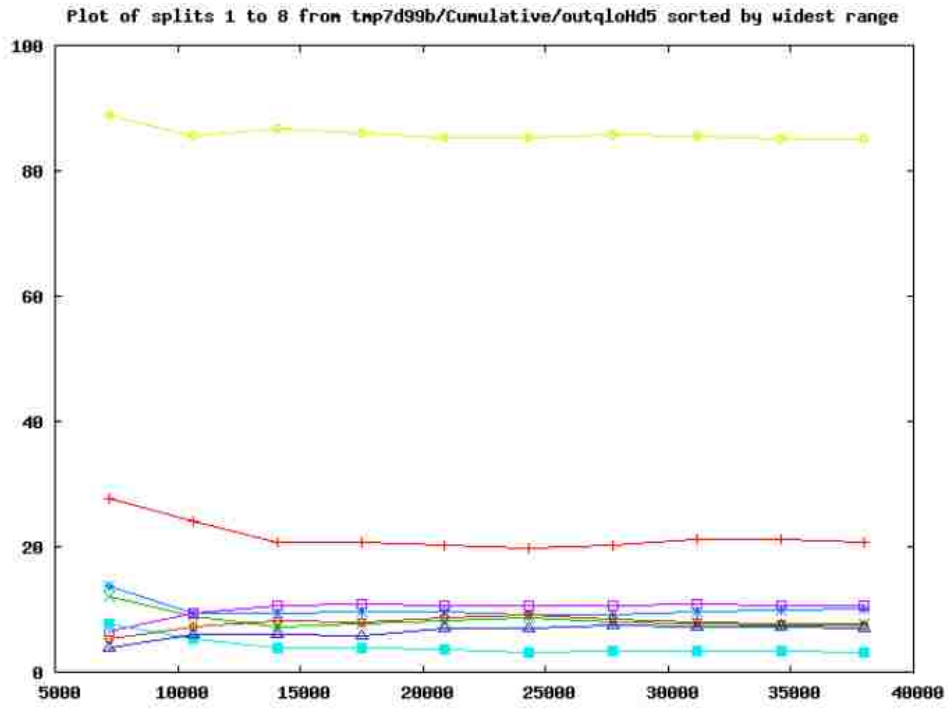
XF-REP Cumulative Plot 4



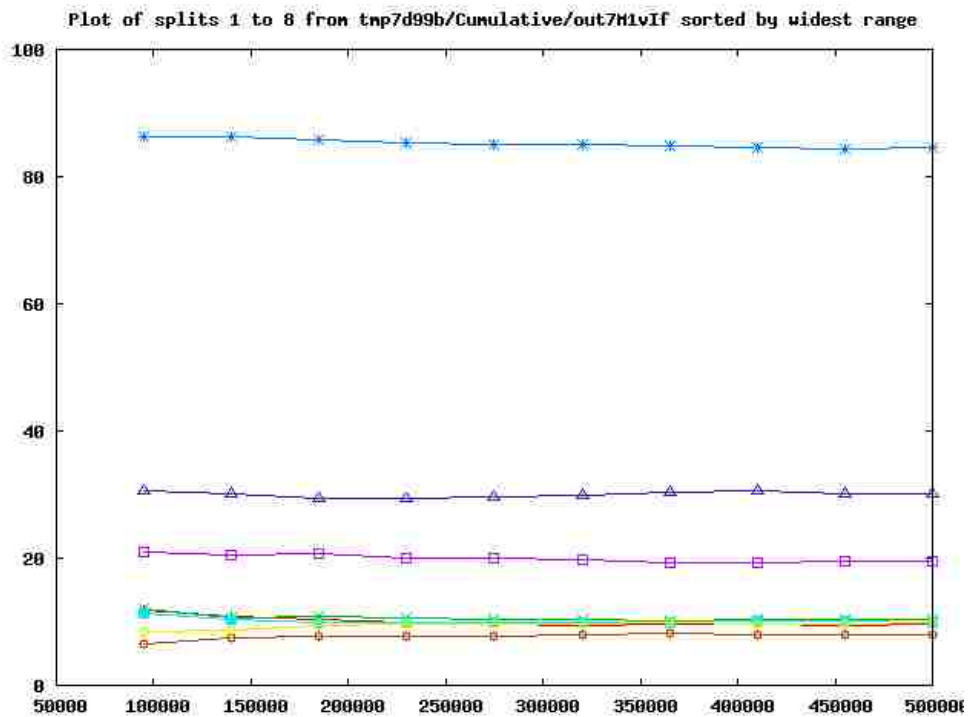
(APPENDIX M continued)

AWTY Cumulative Plots XF-REP-ERIC

XF-REP-ERIC Cumulative Plot 1

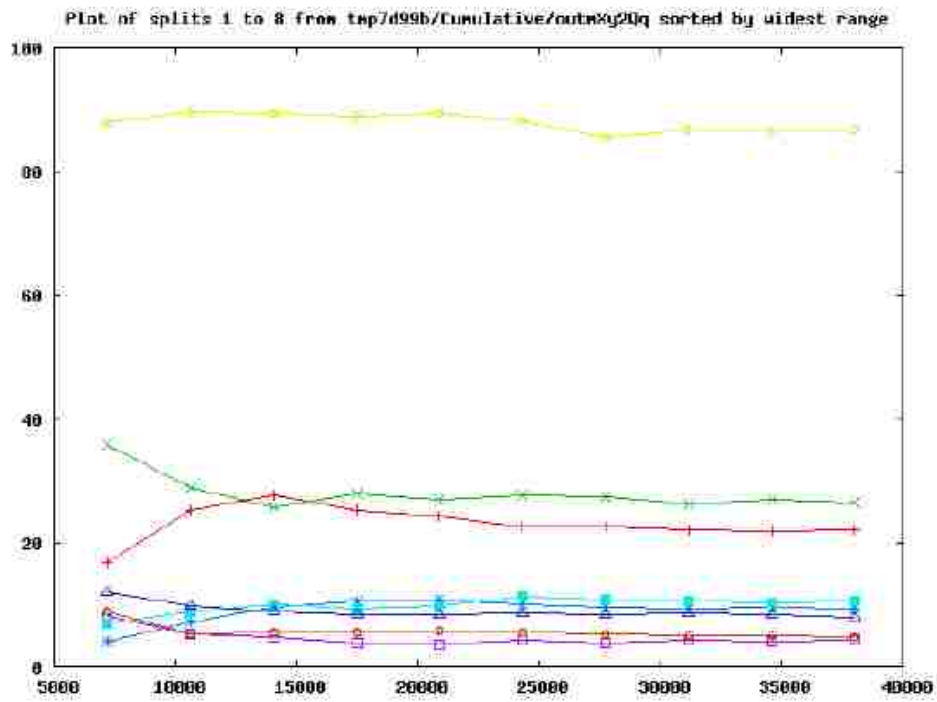


XF-REP-ERIC Cumulative Plot 2

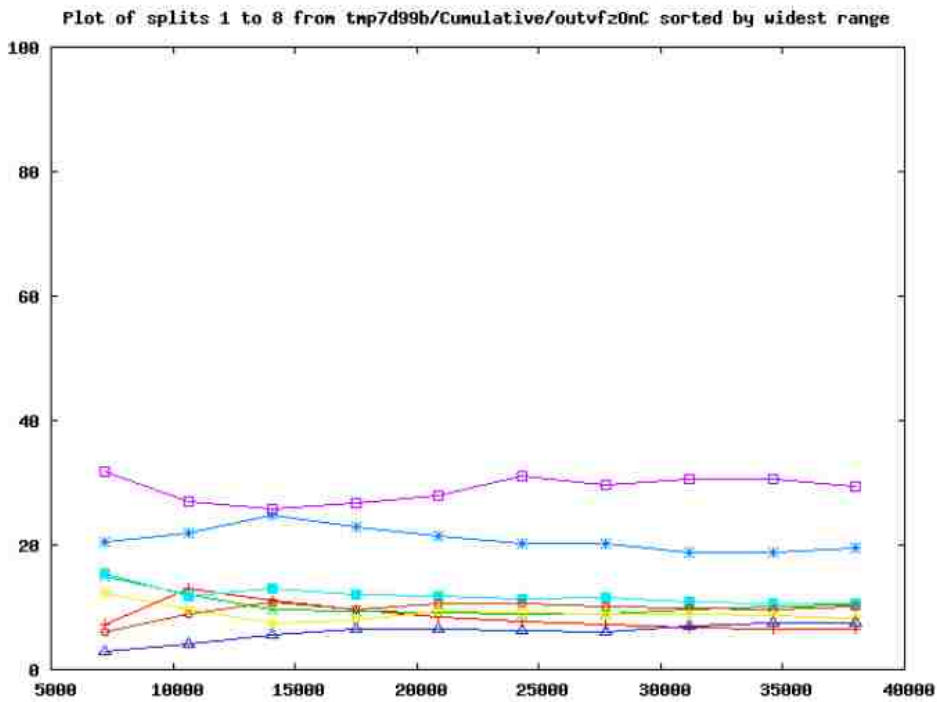


(APPENDIX M continued)

XF-REP-ERIC Cumulative Plot 3



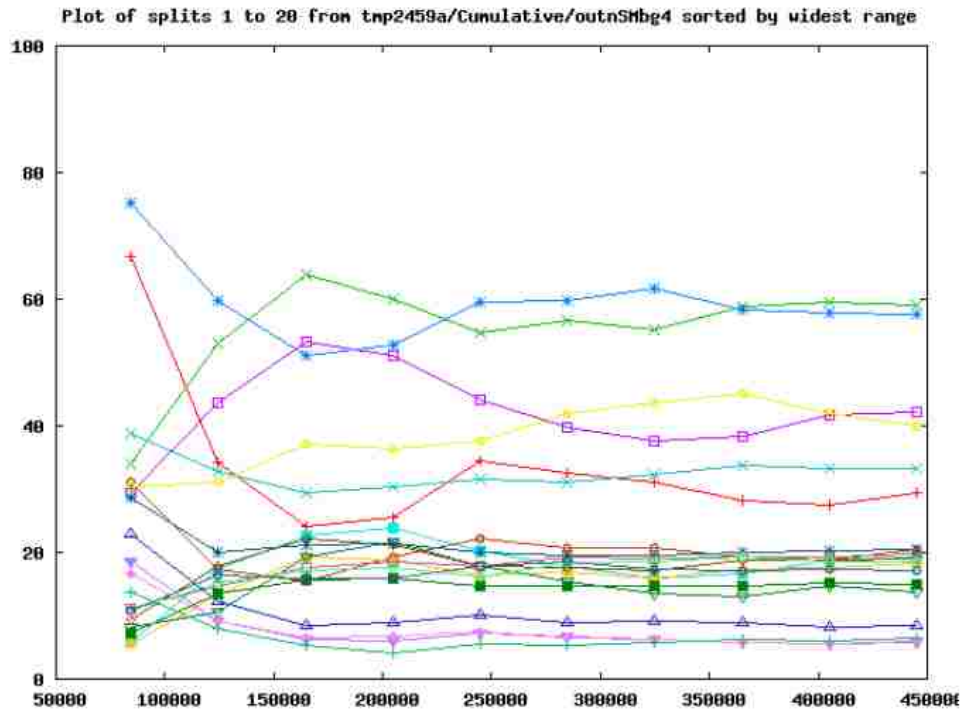
XF-REP-ERIC Cumulative Plot 4



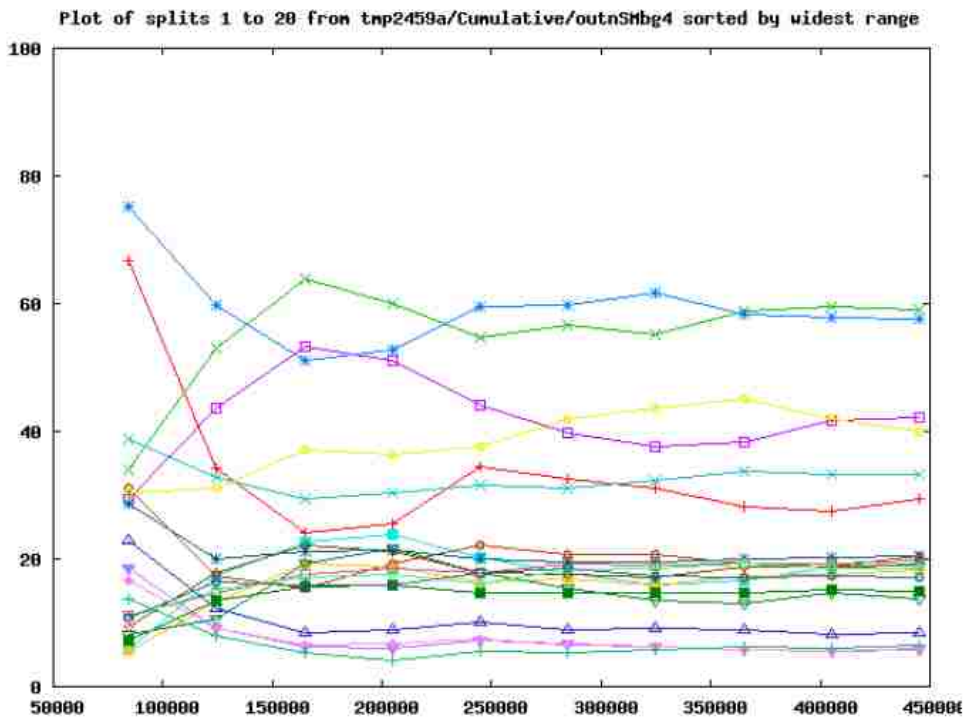
(APPENDIX M continued)

AWTY Cumulative Plots XF-IPRE (Total combined dataset)

XF-IPRE Cumulative Plot 1

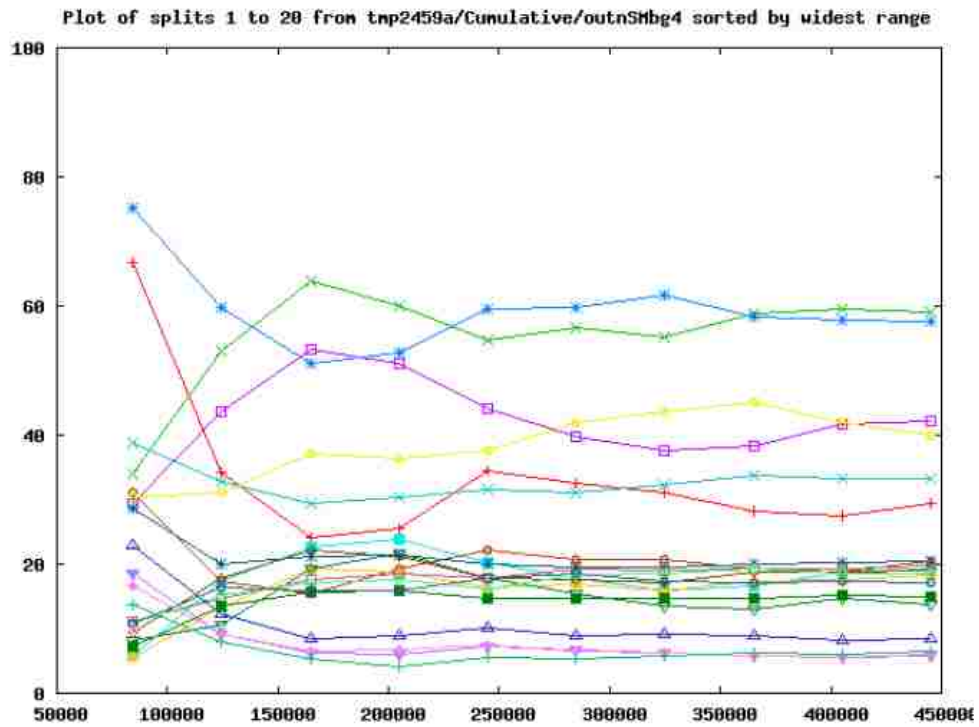


XF-IPRE Cumulative Plot 2

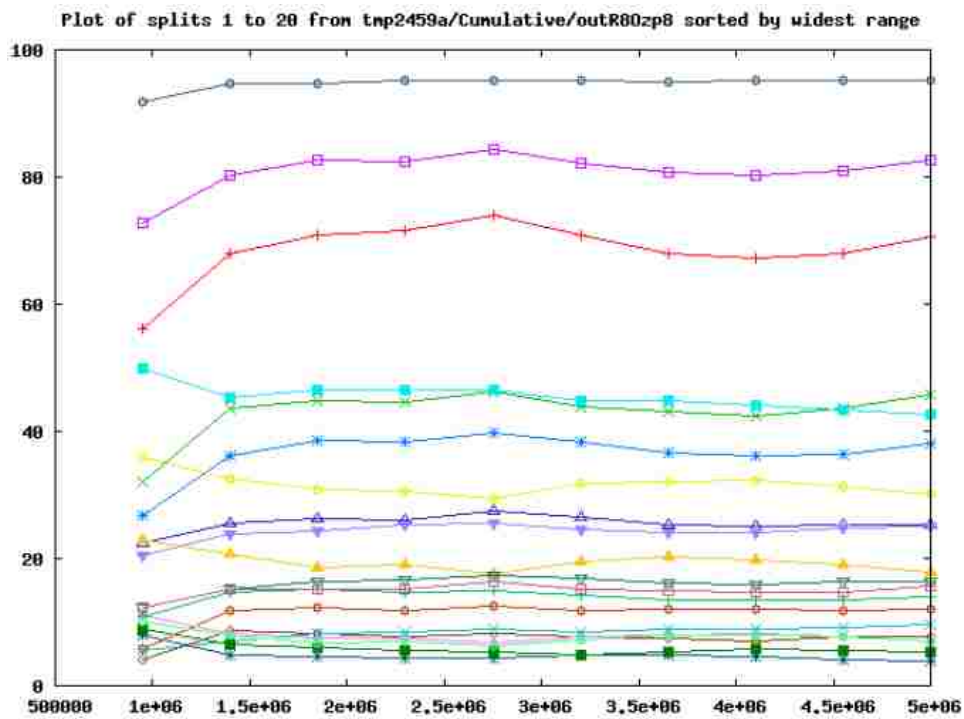


(APPENDIX M continued)

XF-IPRE Cumulative Plot 3

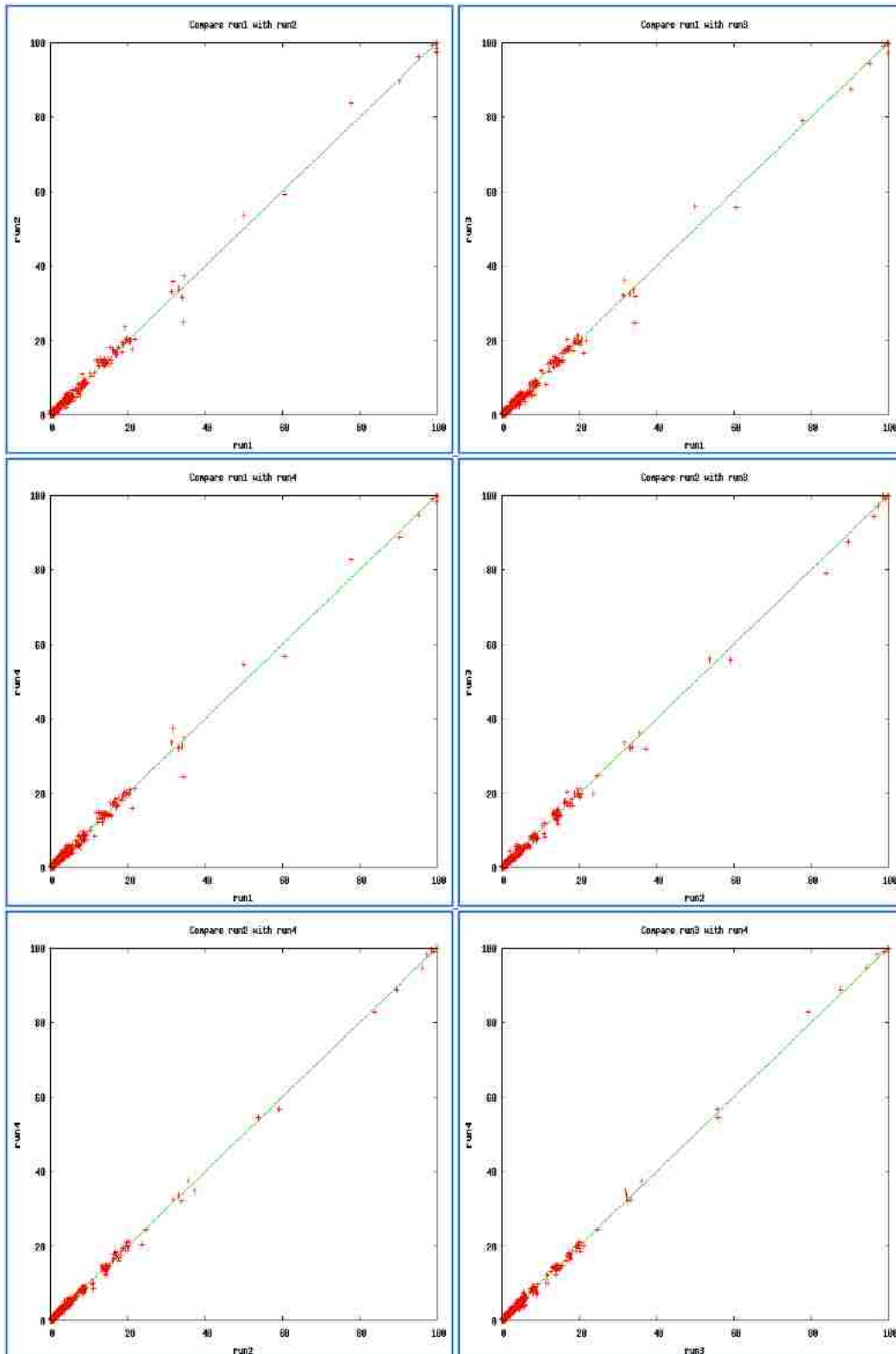


XF-IPRE Cumulative Plot 4



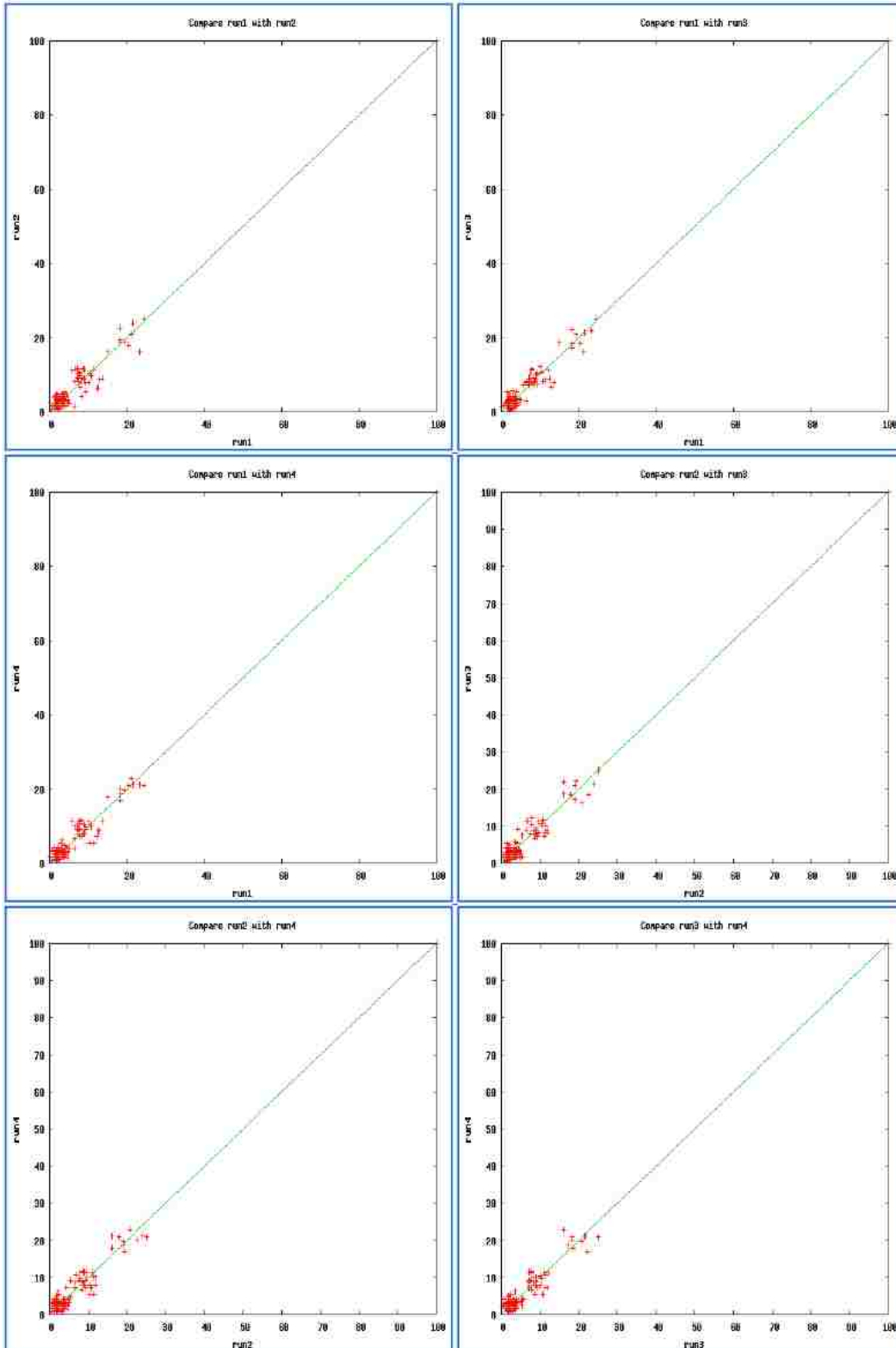
(APPENDIX M continued)

AWTY Compare Plots XF-ITS cured (stopval=0.01)



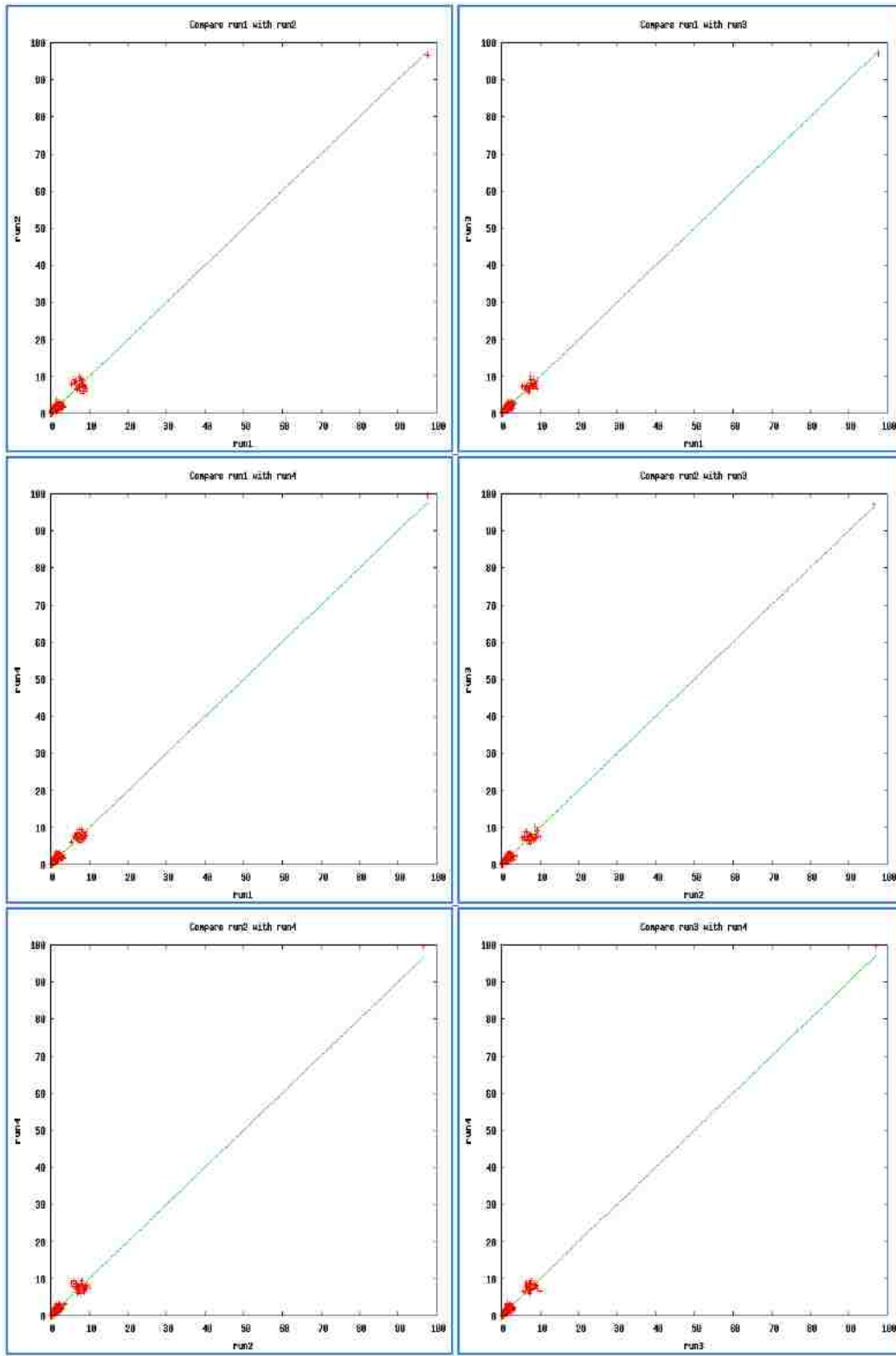
(APPENDIX M continued)

AWTY Compare Plots PGLA



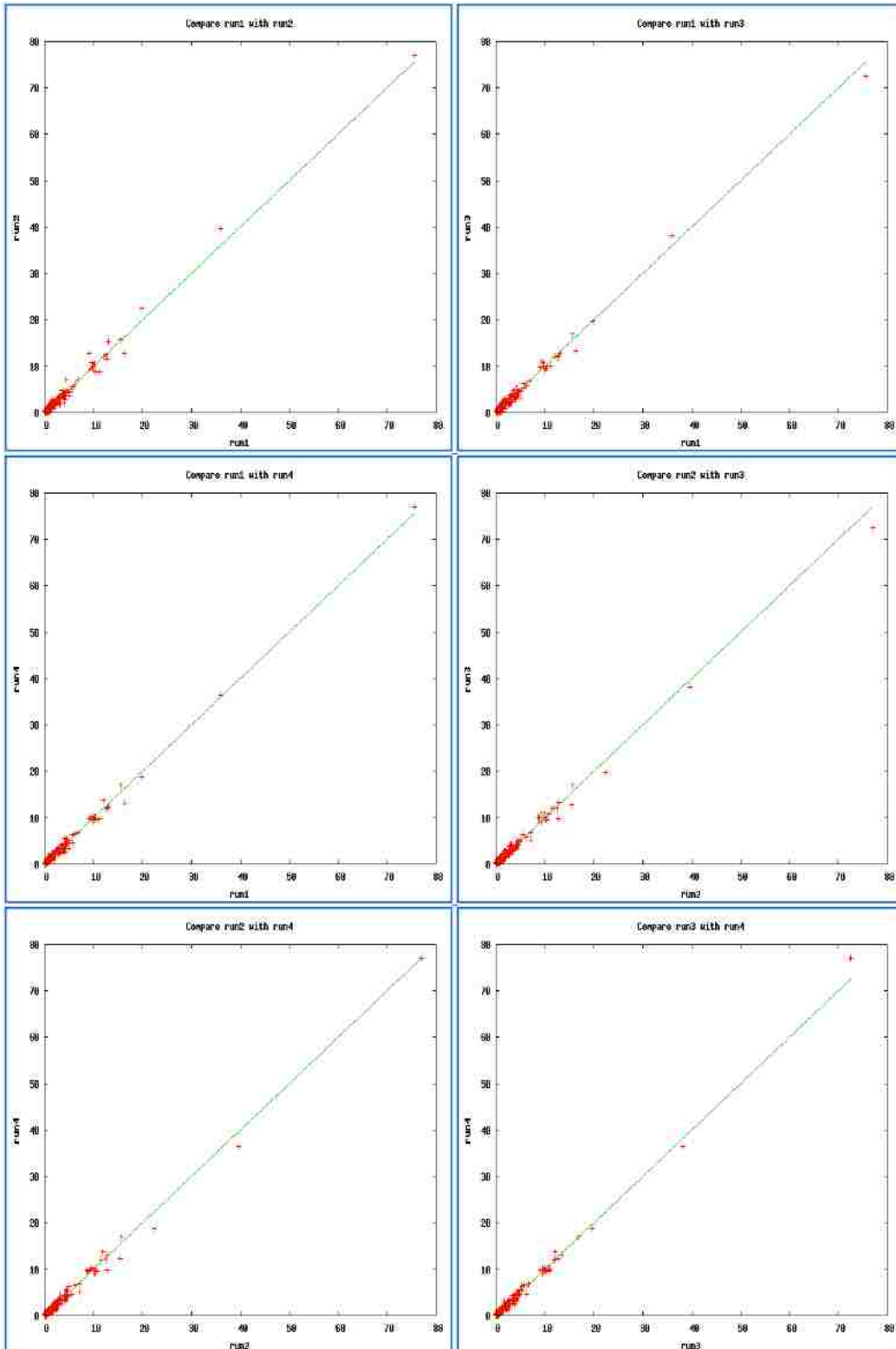
(APPENDIX M continued)

AWTY Compare Plots ERIC-PCR



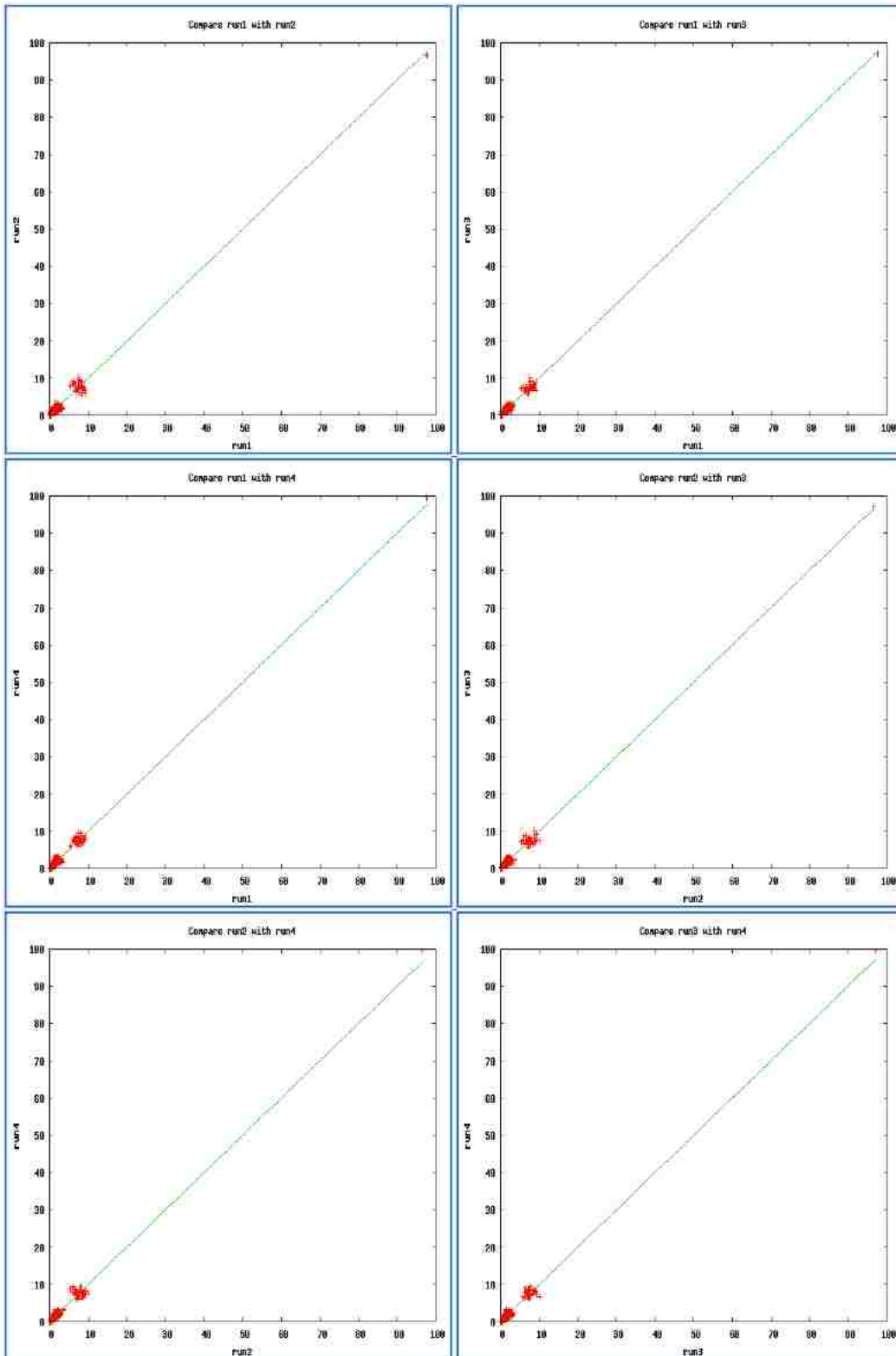
(APPENDIX M continued)

AWTY Compare Plots REP-PCR



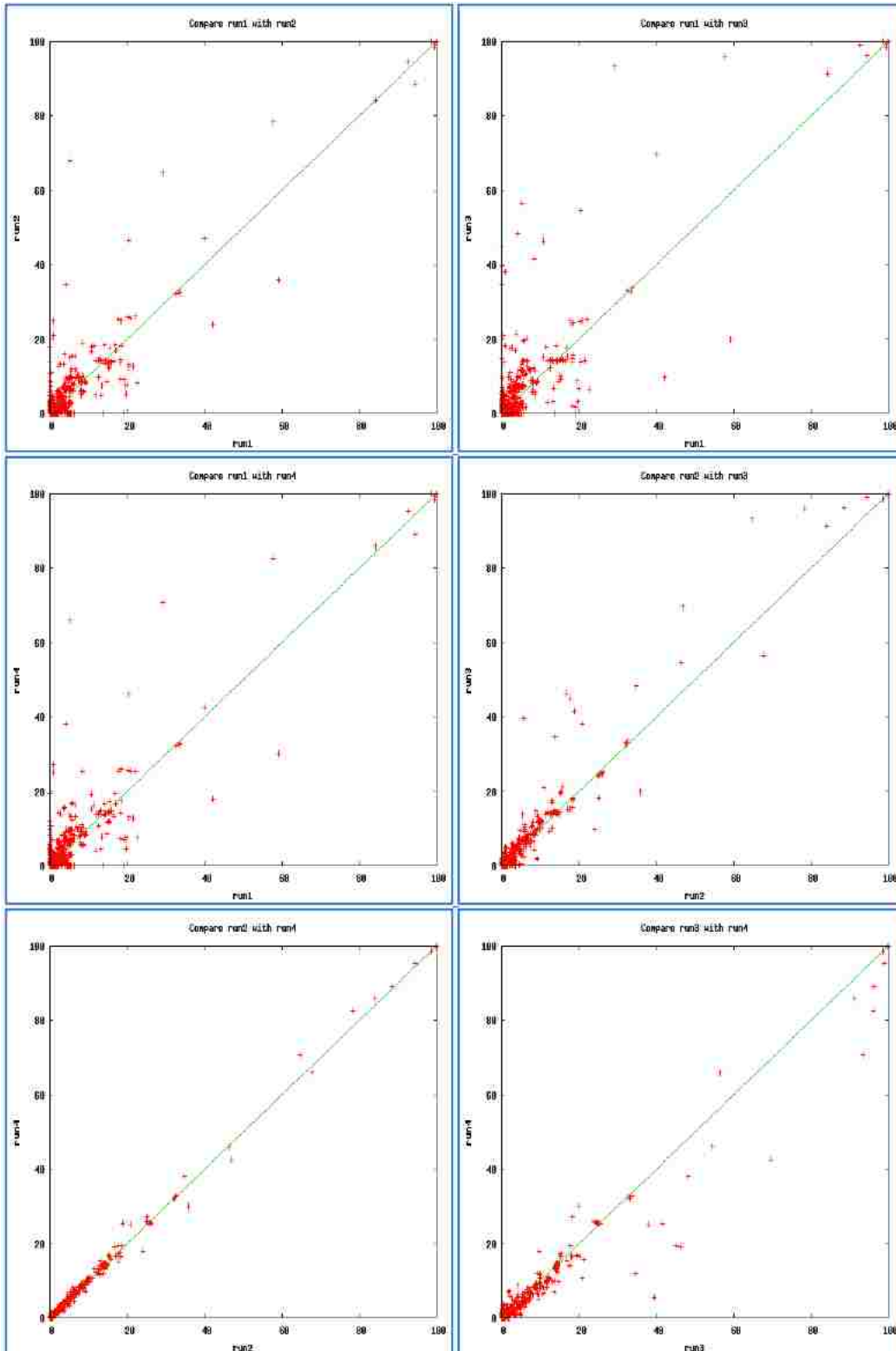
(APPENDIX M continued)

AWTY Compare Plots ERIC-PCR and REP-PCR Combined Dataset



(APPENDIX M continued)

AWTY Compare Plots Total Combined Dataset



APPENDIX N: PROCEDURE FOR SEQUENCING GENES USED IN A MULTILOCUS SEQUENCE TYPING SYSTEM FOR *XYLELLA FASTIDIOSA*

Primers for six different housekeeping genes (Table N1) used in a multilocus sequence typing (MLST) system (Schuenzel *et al.*, 2005) were used to amplify the partial sequences of these genes from five strains of *X. fastidiosa*, XF A-05, XF B-05, XF C-05, XF A-07, and XF A-08 (Table 1). The PCR cycling parameters and procedure, modified from Schuenzel *et al.*, (2005), are described in Table N2.

Table N1. Multilocus Sequence Typing Genes and Primers Used for Gene Amplification

Gene ID	Gene length (bp)	Primer name ^a	Primer sequence (5' → 3') ^b
<i>cysG</i>	1,170	cysG_F	GGCGGCGGTAAGGTTG
		cysG_R	GCGTATGTCTGTGCGGTGTGC
<i>gltT</i>	951	gltT_F	TTGGGTGTGGGTACGTTGCTG
		gltT_R	CGCTGCCTCGTAAACCGTTGT
<i>holC</i>	342	holC_F	GATTTCCAAACCGCGCTTTC
		holC_R	TCATGTGCAGGCCGCGTCTCT
<i>petC</i>	531	petC_F	CTGCCATTCGTTGAAGTACCT
		petC_R	CGTCCTCCCAATAAGCCT
<i>pilU</i>	873	pilU_F	CAATGAAGATTCACGGCAATA
		pilU_R	ATAGTTAATGGCTCCGCTATG
<i>rfbD</i>	429	rfbD_F	TTTGGTGATTGAGCCGAGGGT
		rfbD_R	CCATAAACGGCCGCTTTC

^a Primer names were assigned for the purposes of ordering.

^b Primer sequences were obtained from Schuenzel *et al.*, (2005).

Aliquots of the PCR products were tested by gel electrophoresis as described in Table N2 to confirm PCR product. The remaining PCR products were purified using the QuickClean 5M PCR Purification Kit (GenScript, Piscataway, NJ). Purified PCR products were sequenced by Macrogen Inc., Seoul, Korea.

MLST gene sequences were analyzed with Geneious Pro 5.4 (Biomatters LTD, Auckland, New Zealand) (Drummond *et al.*, 2011). When possible, sequences from two independent PCRs for each gene for each strain were aligned to ensure correct base

(APPENDIX N continued)

identification. When only a single readable sequence was returned, the HQ% DNA for the edited sequence was recorded (Appendix O).

Table N2. PCR and Electrophoresis Conditions to Amplify and Visualize Multilocus Sequence Typing Gene Sequences and PCR Products

Genes amplified	PCR reaction components ^s	PCR program ^b	Gel electrophoresis ^c
<i>cysG</i> , <i>gltT</i> , <i>holC</i> , <i>petC</i> , <i>pilU</i> , <i>rfdD</i>	50 µL volume: 2 µl of template DNA, 5.0 µl of 10X PCR Buffer, 2.0 µl each of the appropriate primers, 1.5 µl of MgCl ₂ , 1.0 µl of dNTP mix, 1.5 µl of <i>Taq</i> polymerase	94°C for 3 min; 20 cycles: 94°C for 30 s, 60°C for 30 s, 72°C for 1 min for products <1000 bp or 90 s for >1000 bp; 72°C for 5 min	0.7 to 1.0% agarose gel

^a PCR reagents and DNA template solutions were used at the following concentrations: 10X PCR Buffer; homemade *Taq* polymerase, ~ 1.0 U/µl; primers, 10 µM; MgCl₂, 50mM; dNTP mix, 10 mM; DNA template, 1 ng/µl. Sterile ddH₂O was used to bring the volume up to the desired reaction volume.

^b PCR was performed in a DNA Engine Peltier Thermal Cycler (Bio-Rad, Hercules, CA). Program was modified from Schuenzel *et al.*, (2005).

^c Agarose gels contained ethidium bromide for visualization of PCR products under UV light. PCR products were visualized and photographed with a KODAK Gel Logic 1500 Imaging System (Eastman Kodak Company, Rochester, New York). Unless specified, gels were run under standard conditions in 1X Tris-borate EDTA (TBE) buffer (Sambrook and Russell, 2001).

References

Drummond, A. J., Ashton, B., Buxton, S., Cheung, M., Cooper, A., Duran, C., Field, M., Heled, J., Kearse, M., Markowitz, S., Moir, R., Stones-Havas, S., Sturrock, S., Thierer, T. and Wilson, A. 2011. Geneious v5.4, available from <http://www.geneious.com/>.

Sambrook, J. and Russell, D. W. *Molecular cloning: A laboratory manual*. 3rd edition. Cold Spring Harbor Laboratory Press. 2001. 2344 pages.

Schuenzel, E. L., Scally, M., Stouthamer, R. and Nunney, L. 2005. A multigene phylogenetic study of clonal diversity and divergence in North American strains of the plant pathogen *Xylella fastidiosa*. *Applied and Environmental Microbiology* 71:3832-3839.

APPENDIX O: NUCLEOTIDE SEQUENCES OF GENES USED IN THE MULTILOCUS SEQUENCE TYPING ANALYSIS FOR XYLELLA FASTIDIOSA FROM STRAINS OF XYLELLA FASTIDIOSA FROM LOUISIANA

Gene Nucleotide Sequence Summary

Strain designation	<i>cysG</i> ^a		<i>glfT</i> ^a		<i>holC</i> ^a		<i>petC</i> ^a		<i>pilU</i> ^b		<i>rfdD</i> ^a	
	HQ %	Size (bp)	HQ %	Size (bp)	HQ %	Size (bp)	HQ %	Size (bp)	HQ %	Size (bp)	HQ %	Size (bp)
XF A-05	92.0	697	59.7	698	98.4	313	84.8	492	--	839	69.9	412
XF B-05	68.5	588	88.6	623	98.1	311	74.8	480	--	752	34.3	426
XF C-05	52.7	412	53.3	499	92.5	306	--	--	--	532	40.1	419
XF A-07	84.5	503	63.6	503	67.1	286	49.0	480	--	546	--	--
XF A-08	97.5	674	82.9	702	96.4	308	96.1	490	--	753	46.9	397

^a Sequences obtained from a single independent PCR product.

^b Two independent PCR products were used to obtain sequences for *pilU*.

Nucleotide Sequences

cysG

>XF_A-05_ *cysG*

GATTATCGGCGCCCCCTCTCTGACCACATCGTTACAGCGCTGGGCCGAAACCGGCCGCATCACG
 TGCGGCAAGGGACGTTTGAAGACAGCTGGCTGCAAGAAGATATTTGGTTGGTCATCGCCGCCA
 CCGATCAACCCGAAGTGAACCACGCCGCGCGCTGCAGCACATGCGCAACGGTTATTCGTCAA
 CGTGGTTCGACGACATTGCACTCTCCAACGTGCAGGTCCCGGCCGTGGTTCGAACGCGGCCCGTTG
 CGGATCGCGATTTCTAGCGGCGGTGGCGCACCGATGGTGGCAGCTATCTGCGACAACAACACTGG
 AAAGCCTCATTGACGATAGTTGGGGACGACTGACCACACTGTTTCGCGCAACGCCGCGACACTAT
 CCGCGCCCGCTATCCAAACATAGAAGCACGCCGCCGCTTCTTTGAAACCCAACACTCGCCGGCCCA
 CTCCAACGACTGCTACGCAAGCAACGCCACGCAGAGGCCGAAGCAGTGCTGGAAGCAGCACTCG
 CCGAGACTCCCCCTCACGGAGTCCGGCAGCGTCACCCTAGTGGGCGCTGGCGCCGGCGACGCCGG
 GCTACTGACCTTAAATGCACTGCGCGCCTTGAATGAAGCCGACATCATCCTCTACGACCGCCTG
 GTCAGCGACACCGTGTTACAGATGGCACGGCGCGATGCGGAGCAGATCGAAGTAGGC

>XF_B-05_ *cysG*

GCCCCCTCTCTGACCACATCGTTACAGCGCTGGGCCGAAACCGGCCGCATCACGTGGCGGCAAG
 GGACGTTTGAAGACAGCTGGCTGCAAGAAGATATTTGGTTGGTCATCGCCGCCACCGATCAACC
 CGAAGTGAACCACGCCGCGCGCTGCAGCACATGCGCAACGGTTATTCGTCAACGTGGTTCGAC
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VITA

Rebecca A. Melanson grew up in Marrero, Louisiana, where she attended Concordia Lutheran School and Immaculata High School. She attended Centenary College of Louisiana in Shreveport, Louisiana, from 1999 to 2003 and earned a Bachelor of Science in biology with minors in chemistry and psychology in 2003. Following graduation, she worked as an entomology student worker at the Louisiana State University (LSU) Agricultural Center (LSU AgCenter) Red River Research Station in Bossier City, Louisiana. In January 2004, she became the research associate in plant pathology at the LSU AgCenter Pecan Research-Extension Station in Shreveport, Louisiana, where she worked until August 2008. During her time as a research associate, she conducted research with Dr. R. S. Sanderlin on the transmission of *Xylella fastidiosa*, the causal agent of pecan bacterial leaf scorch, in pecan, as well as on pecan scab disease. She was also the Content Management System's Content Reviewer for the LSU AgCenter's Pecan Research-Extension Station website and, eventually, for the LSU AgCenter's Northwest Region. In August 2008, she joined Louisiana State University's Department of Plant Pathology and Crop Physiology as a graduate student under Dr. Jong Hyun Ham where she continued working with *Xylella fastidiosa* and began characterizing the function of a negative regulator for toxoflavin production in *Burkholderia glumae*, the causal agent of bacterial panicle blight in rice. As a graduate student, she served as the editor of the Department of Plant Pathology and Crop Physiology newsletter and as the president of the Department of Plant Pathology and Crop Physiology Graduate Student Association. She received travel awards from the LSU Graduate School, the Department of Plant Pathology and Crop Physiology Graduate Student Association, and the American Phytopathological Society - Southern Division to attend American Phytopathological Society's national and regional meetings in 2009, 2010, and 2011.

She also received the 2010 Louisiana Agricultural Consultants Association Scholarship. Rebecca will continue her graduate studies in the Department of Plant Pathology and Crop Physiology at LSU under Dr. Jong Hyun Ham.