

US011788052B2

(12) **United States Patent**
Gonzalez et al.

(10) **Patent No.:** **US 11,788,052 B2**
(45) **Date of Patent:** ***Oct. 17, 2023**

(54) **METHOD FOR TREATMENT AND CONTROL OF PLANT DISEASE**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 771 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **16/702,154**

(22) Filed: **Dec. 3, 2019**

(65) **Prior Publication Data**

US 2020/0178539 A1 Jun. 11, 2020

Related U.S. Application Data

(63) Continuation of application No. 15/174,589, filed on Jun. 6, 2016, now Pat. No. 10,499,651, which is a
(Continued)

(51) **Int. Cl.**
C12N 1/00 (2006.01)
C12N 15/82 (2006.01)
(Continued)

(52) **U.S. Cl.**
CPC **C12N 1/00** (2013.01); **A01N 63/40** (2020.01); **C12N 7/00** (2013.01); **C12N 15/8281** (2013.01);
(Continued)

(58) **Field of Classification Search**

CPC C12N 1/00; C12N 7/00; C12N 15/8281;
C12N 2795/10121; C12N 2795/10131;
(Continued)

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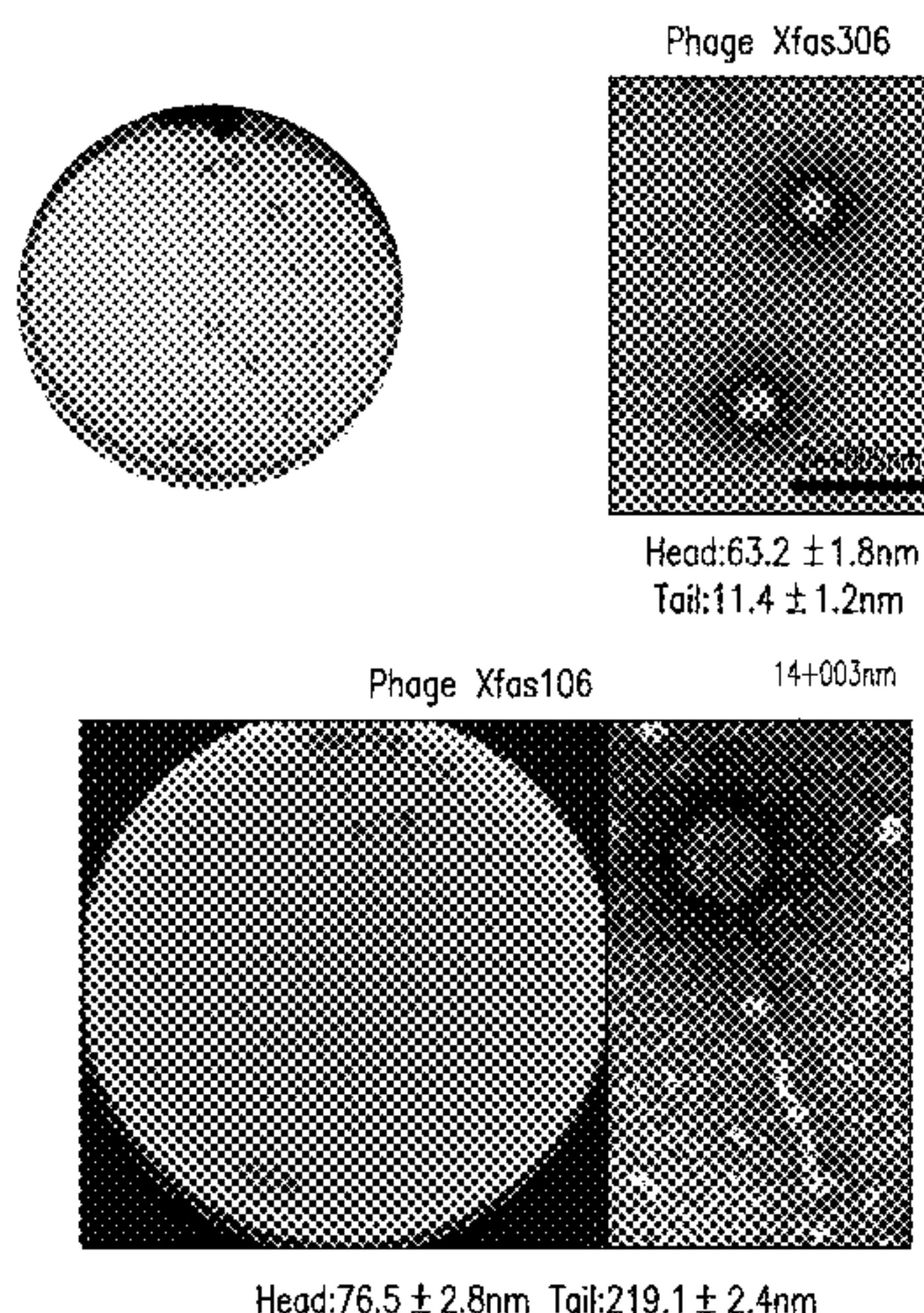
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(57) **ABSTRACT**

Methods and compositions are provided for preventing or reducing symptoms or disease associated with *Xylella fastidiosa* or *Xanthomonas axonopodis* in a plant. The invention provides novel bacteriophages virulent to *Xylella fastidiosa* or *Xanthomonas axonopodis*, including XfaMija and XfaMijo, and further provides methods for treating or preventing Pierce's Disease or Citrus Canker in plants.

13 Claims, 15 Drawing Sheets

Specification includes a Sequence Listing.



Related U.S. Application Data

continuation-in-part of application No. 14/057,851, filed on Oct. 18, 2013, now Pat. No. 9,357,785.

- (60) Provisional application No. 61/785,535, filed on Mar. 14, 2013, provisional application No. 61/716,245, filed on Oct. 19, 2012.

(51) **Int. Cl.**

C12N 7/00 (2006.01)

A01N 63/40 (2020.01)

C12R 1/91 (2006.01)

(52) **U.S. Cl.**

CPC *C12N 2795/10121* (2013.01); *C12N 2795/10131* (2013.01); *C12N 2795/10221* (2013.01); *C12N 2795/10231* (2013.01); *C12N 2795/10321* (2013.01); *C12N 2795/10331* (2013.01); *C12R 2001/91* (2021.05)

(58) **Field of Classification Search**

CPC *C12N 2795/10221*; *C12N 2795/10231*; *C12N 2795/10321*; *C12N 2795/10331*; *A01N 63/40*; *C12R 2001/91*

See application file for complete search history.

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Fig. 1

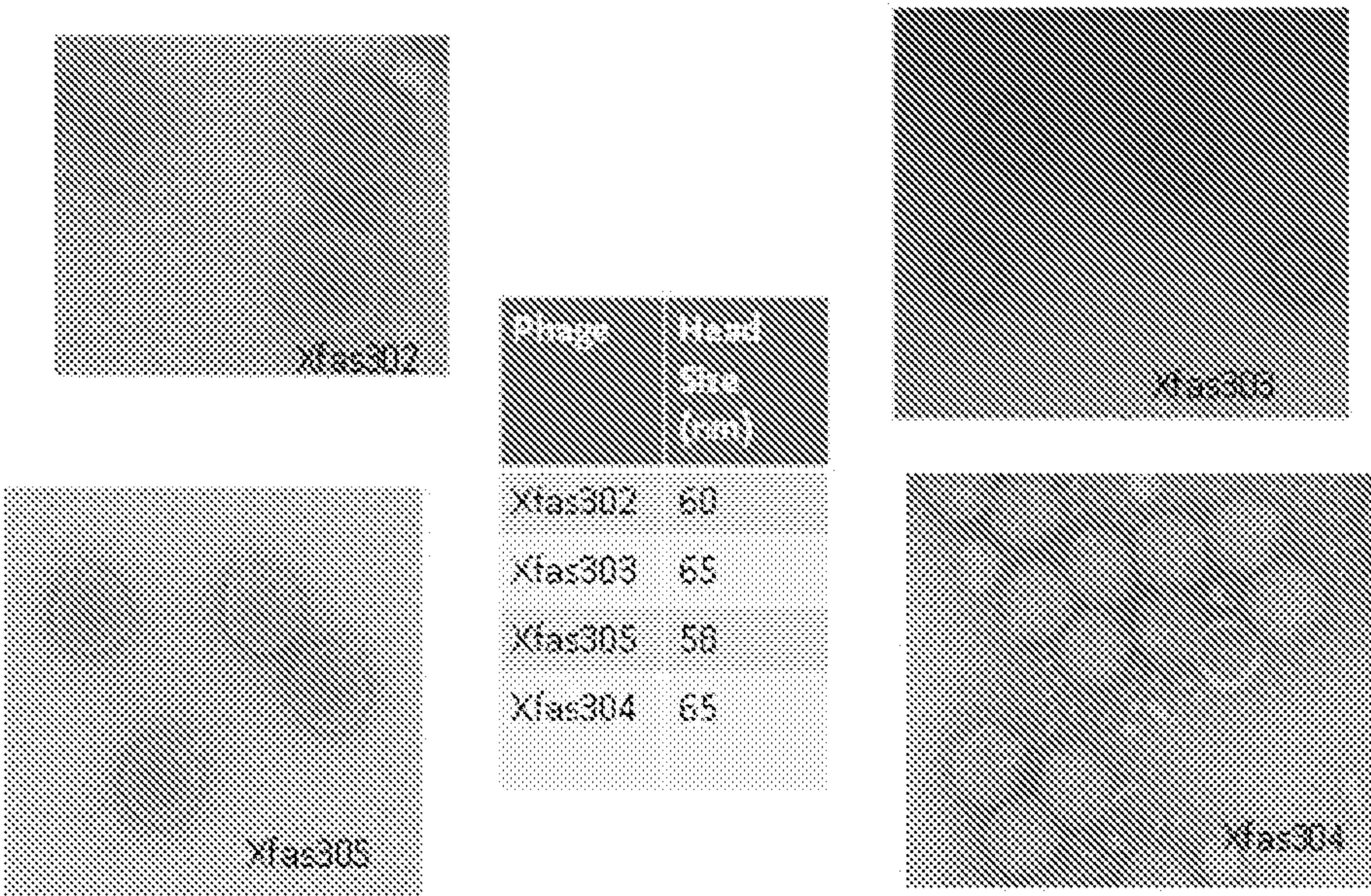
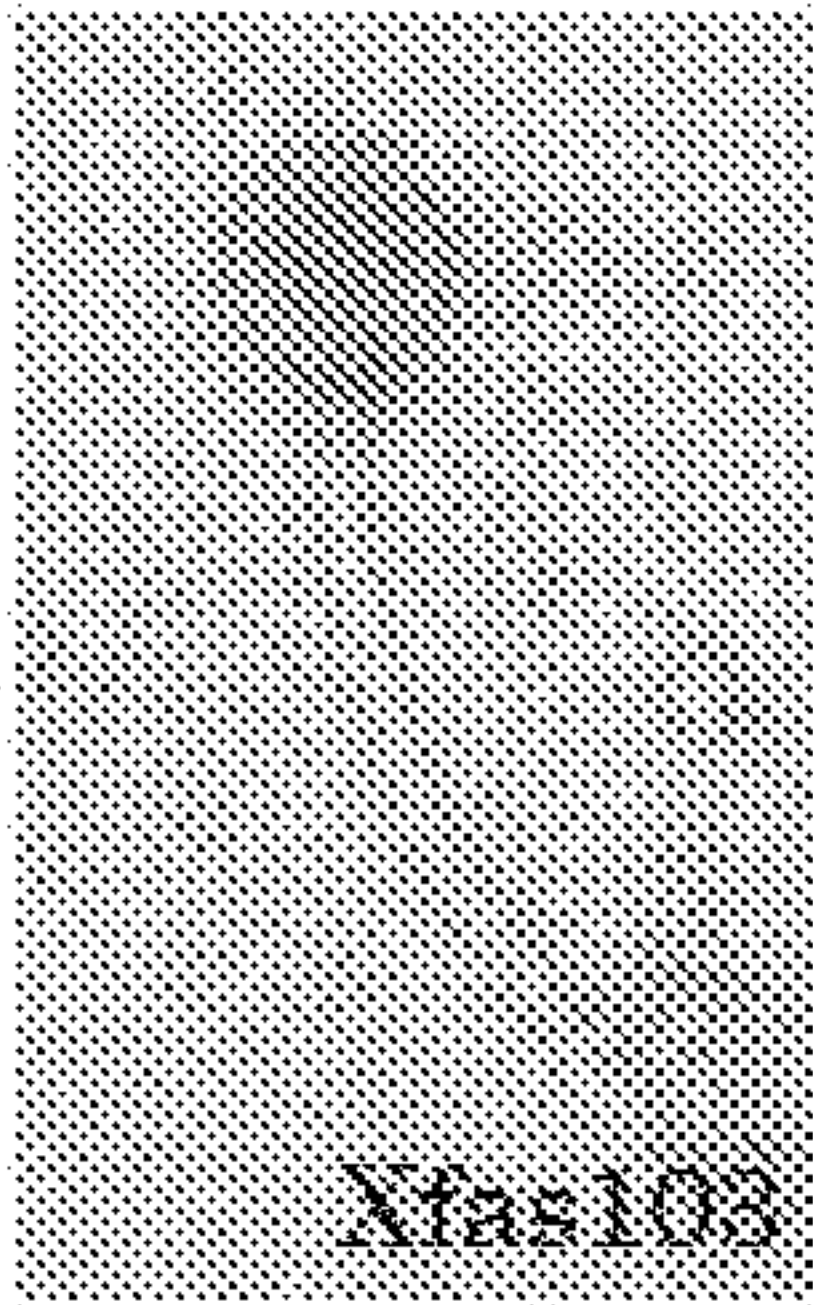
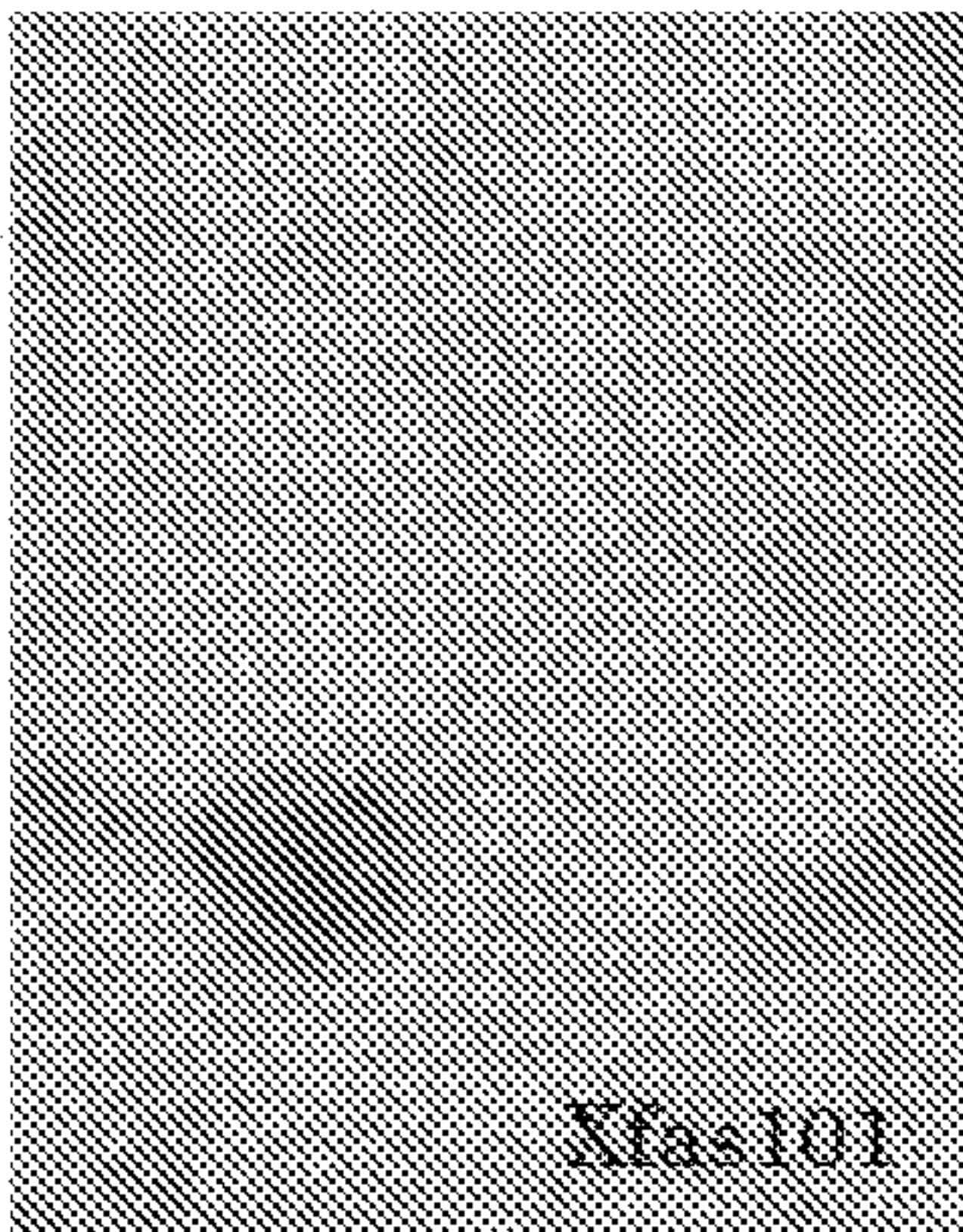
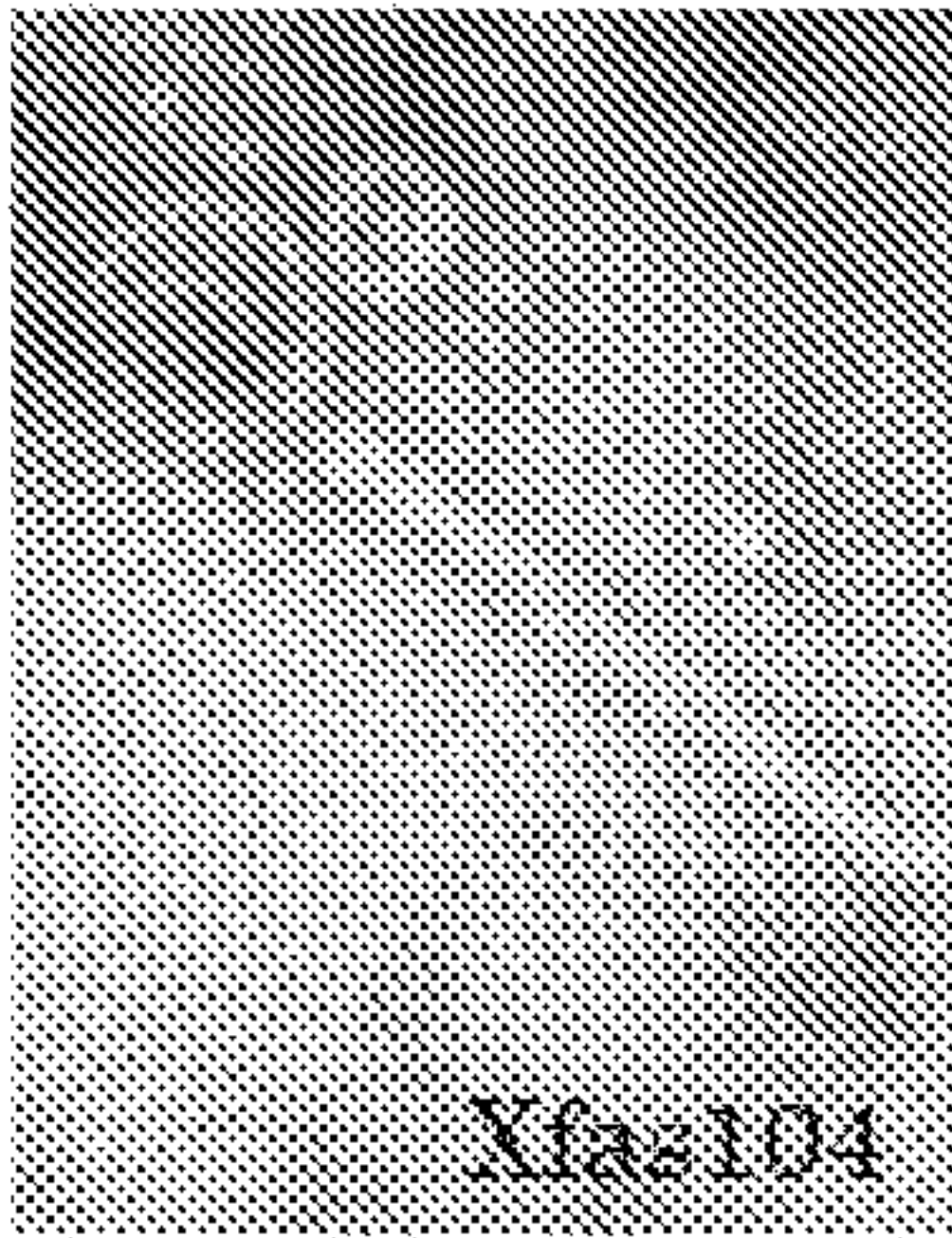
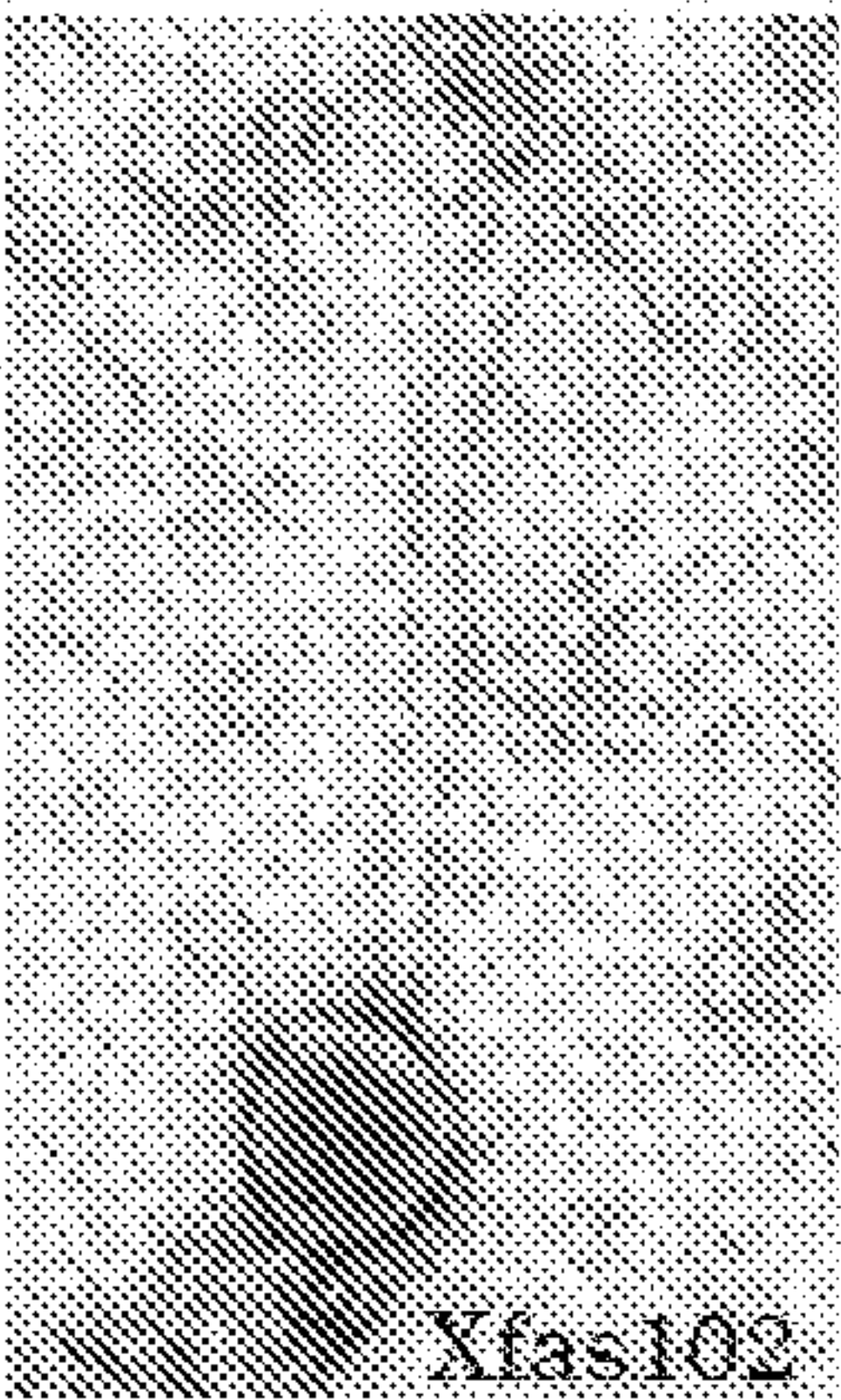


Fig. 2



Phage	Head Size (nm)	Tail Size (nm)
Xfas101	63.4	262
Xfas102	55	200
Xfas103	64	210
Xfas104	64	230



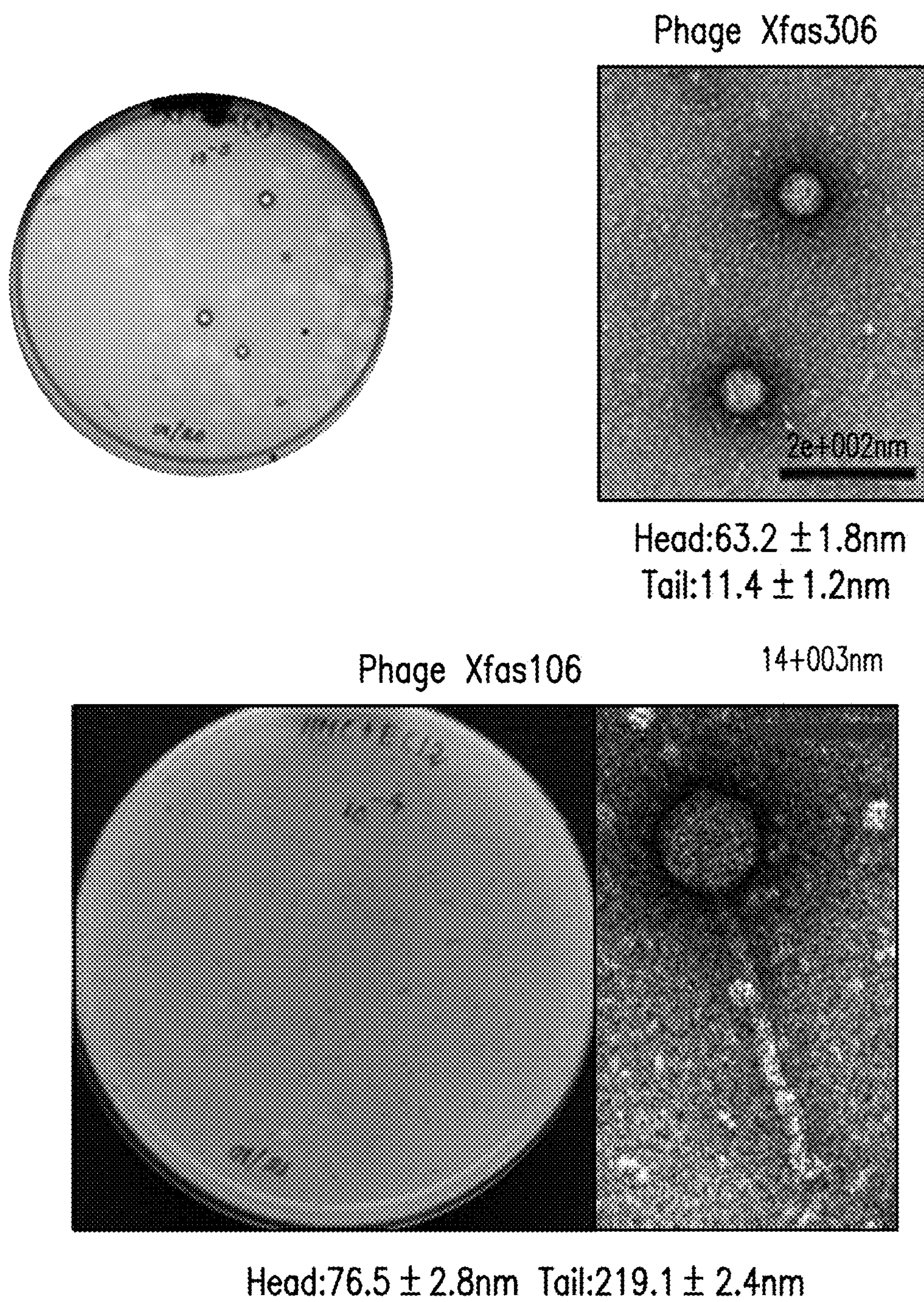


FIG. 3

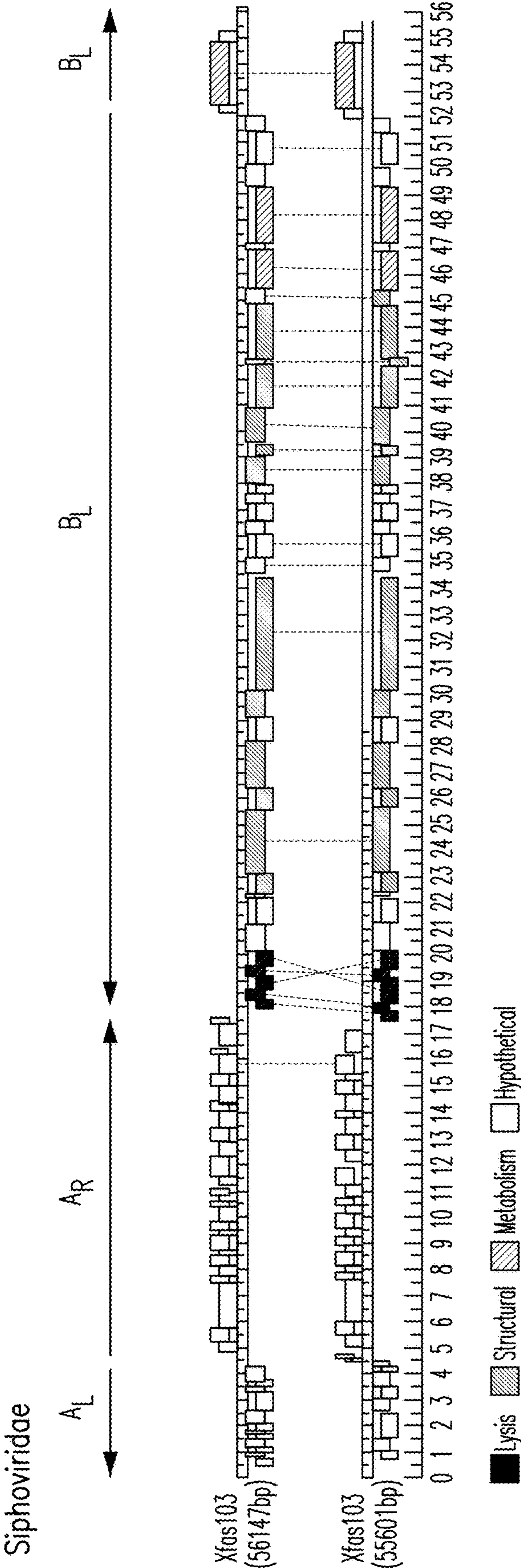


FIG. 4

Podoviridae

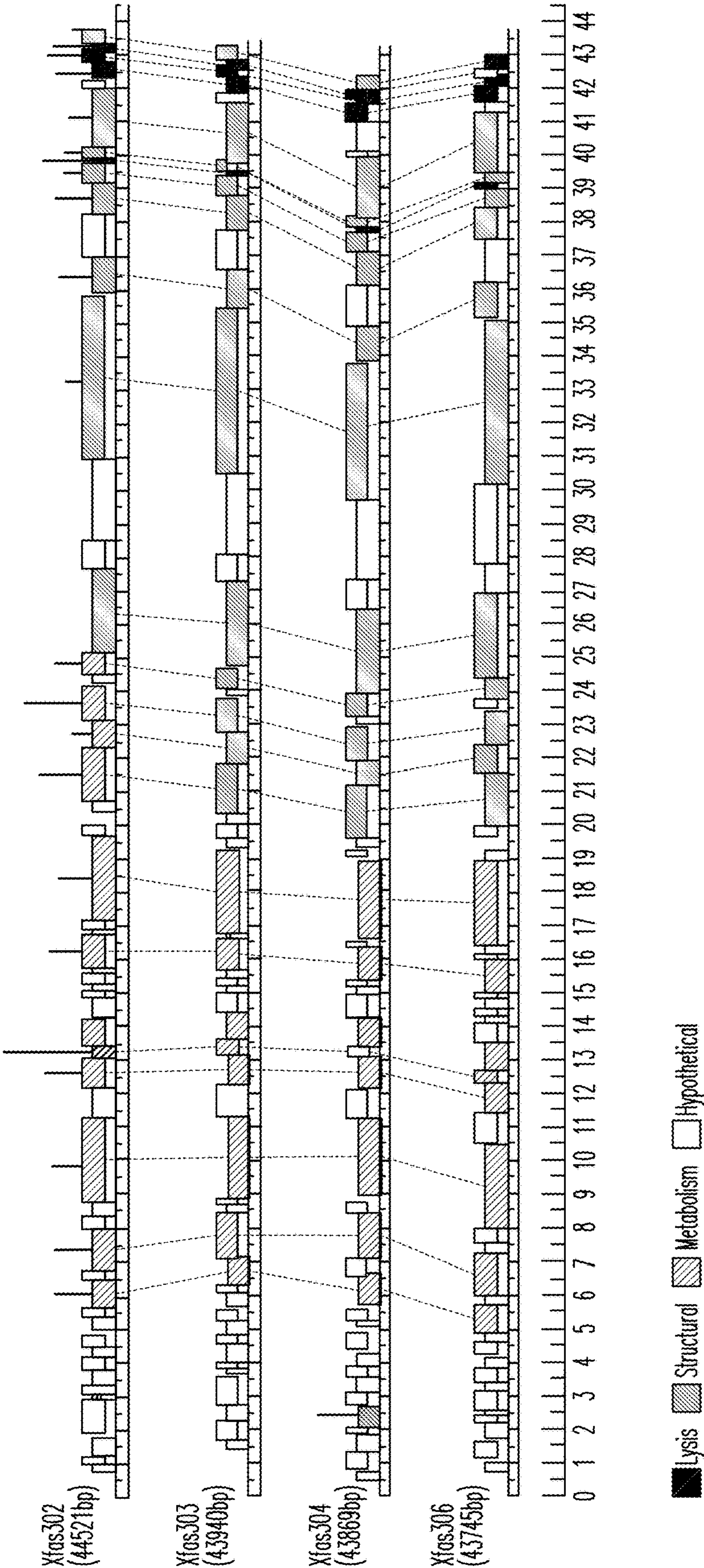


FIG. 5

Fig. 6



Observation for PD symptoms*	Vines Inoculated with XF, Phage or Buffer				Inoculated with XF & Challenged with Phage		Inoculated with Phage & Challenged with XF-15 (6)*
	XF-15 XF-54 Phage Xfas304 ** Buffer			XF-15(15)*	XF-54(15)*		
	(15)*	(15)*	(24)*			(6)*	
Wk. 0 (10/05/11)	0***	0	0	0	0	0	0
Wk. 1 (10/12/11)	0	0	0	0	0	0	0
Wk. 2 (10/19/11)	0	0	0	0	0	0	0
Wk. 3 (10/26/11)	1	1	0	0	1	1	0
Wk. 4 (10/31/11)	2	2	0	0	2	2	0
Wk. 4 (11/04/11)	3	3	0	0	3	2	0
Wk. 5 (11/07/11)	5	4	0	0	5	4	0
Wk. 5 (11/11/11)	7	6	0	0	5	4	0
Wk. 6 (11/14/11)	9	6	0	0	5	4	0
Wk. 6 (11/18/11)	9	7	0	0	5	4	0
Wk. 7 (11/21/11)	10	8	0	0	5	4	0
Wk. 7 (11/25/11)	10	9	0	0	5	4	0
Wk. 8 (11/28/11)	11	10	0	0	5	4	0
Wk. 8 (12/02/11)	11	10	0	0	5	4	0
Wk. 9 (12/05/11)	11	11	0	0	5	4	0
Wk. 9 (12/09/11)	12	11	0	0	5	4	0
Wk. 10 (12/12/11)	12	12	0	0	5	4	0
Wk. 10 (12/16/11)	12	12	0	0	5	4	0
Wk. 11 (12/19/11)	12	12	0	0	5	4	0
Wk. 11 (12/23/11)	12	12	0	0	5	4	0
Wk. 12 (12/26/11)	12	12	0	0	5	4	0
Wk. 12 (12/30/11)	12	12	0	0	5	4	0

Vines in column 2
and 3 challenged
with phage. vines in
column 8 challenged
wit XF15

* Total No. of vines in each category is within parentheses. Note: 3 vines we harvested at time zero to determine input.
** Phage movement data in vines will be presented separately.
*** Number indicated equals vines exhibiting Pierce's Disease symptoms
* Data collected on dates indicated in parentheses

FIG. 7

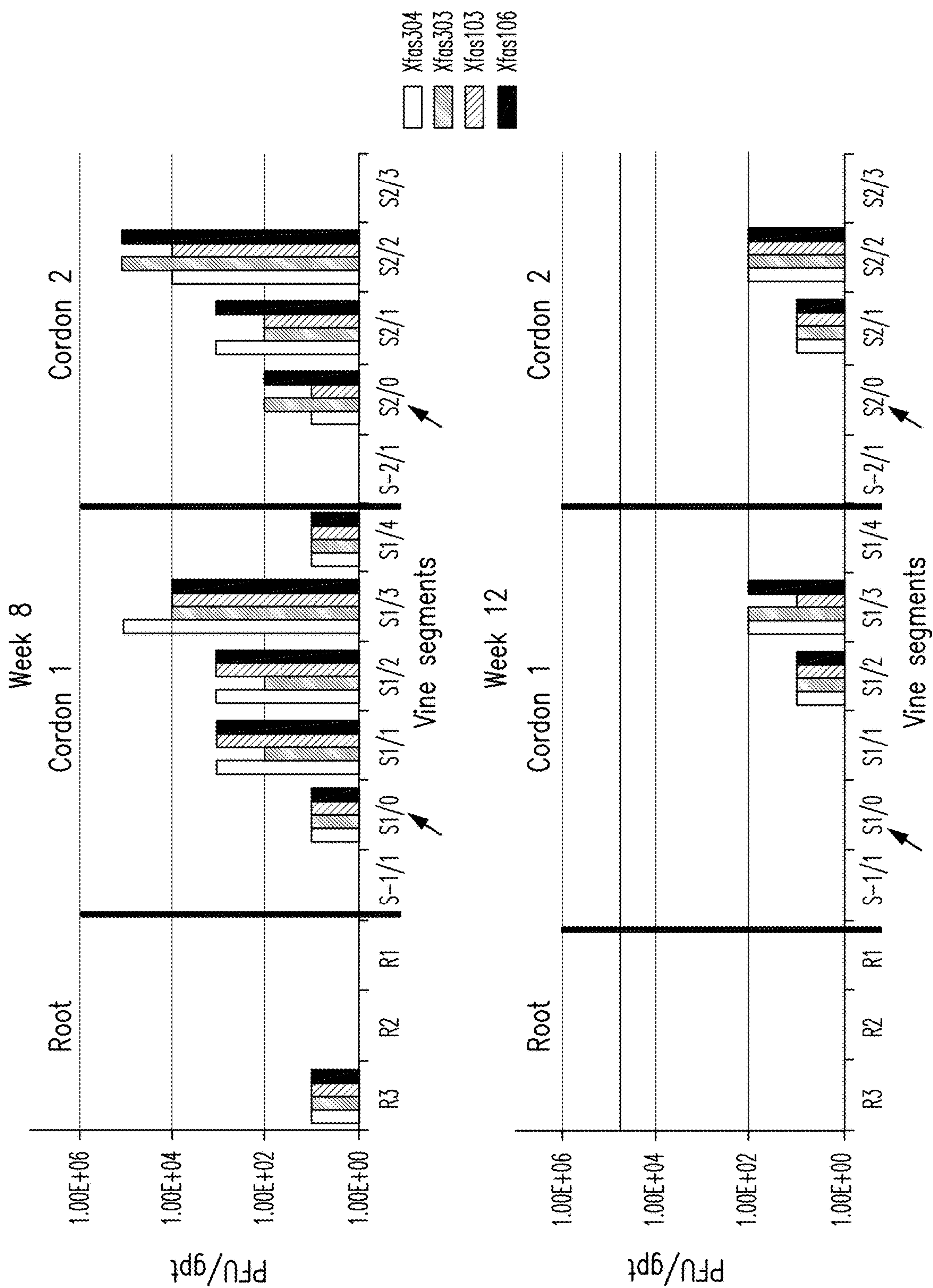


FIG. 8

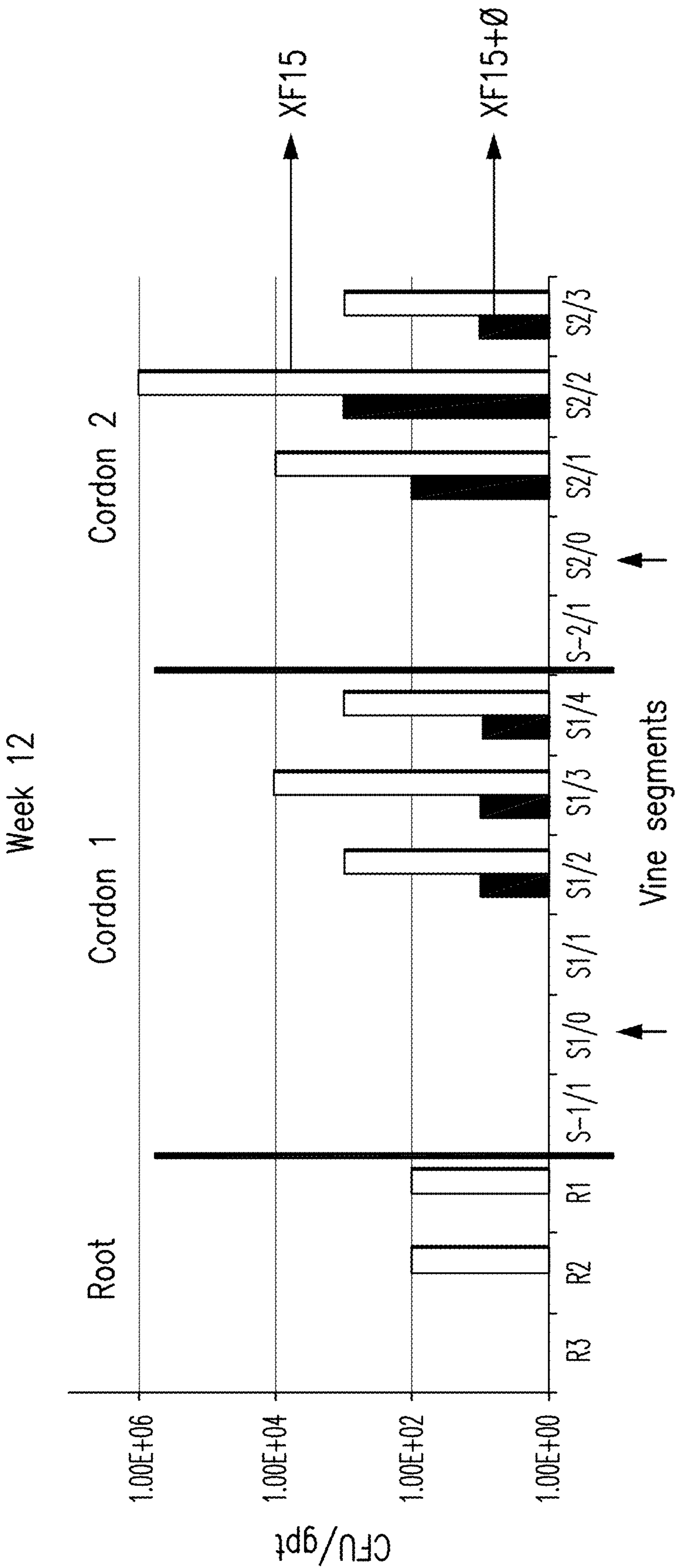


FIG. 9

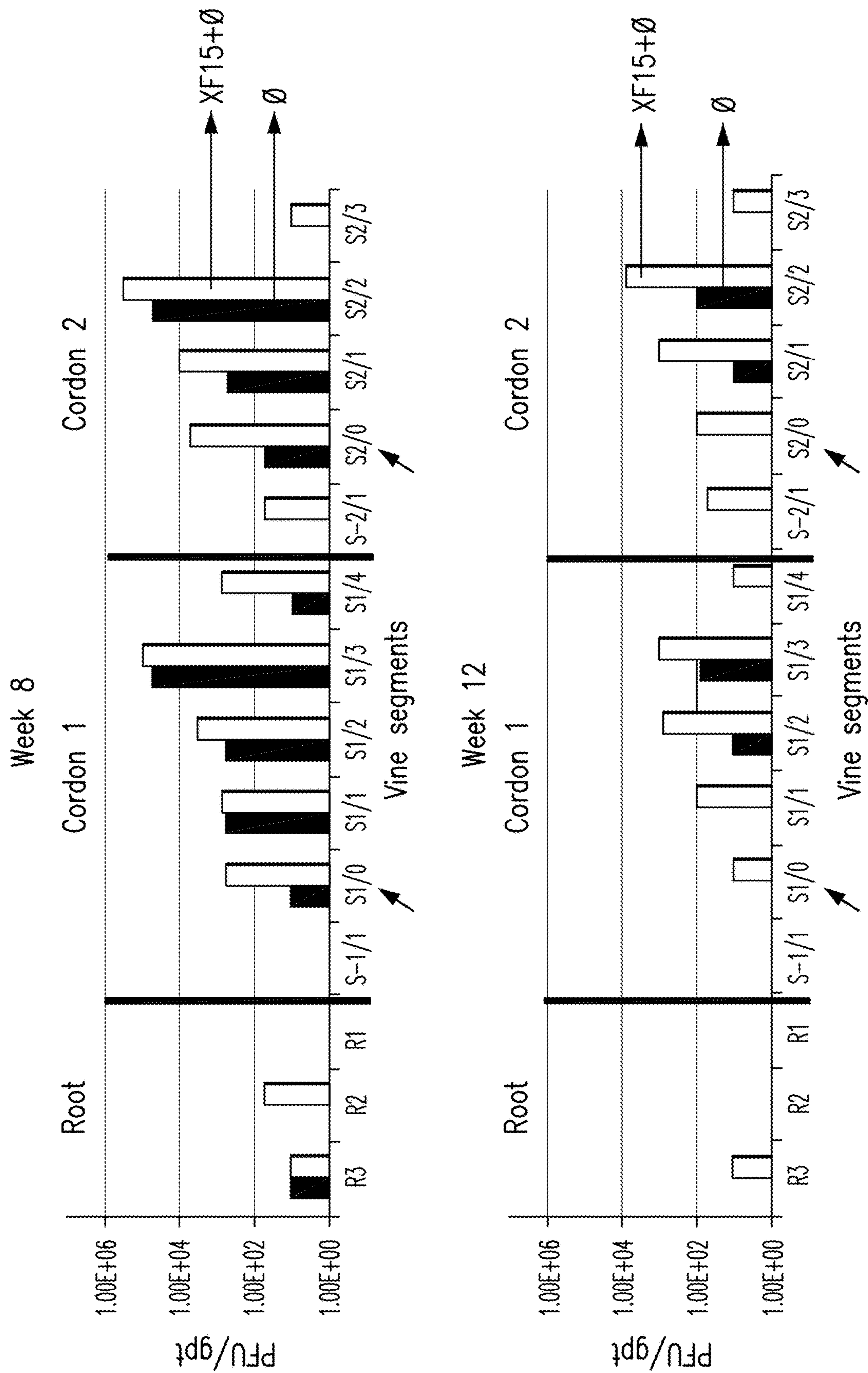


FIG. 10

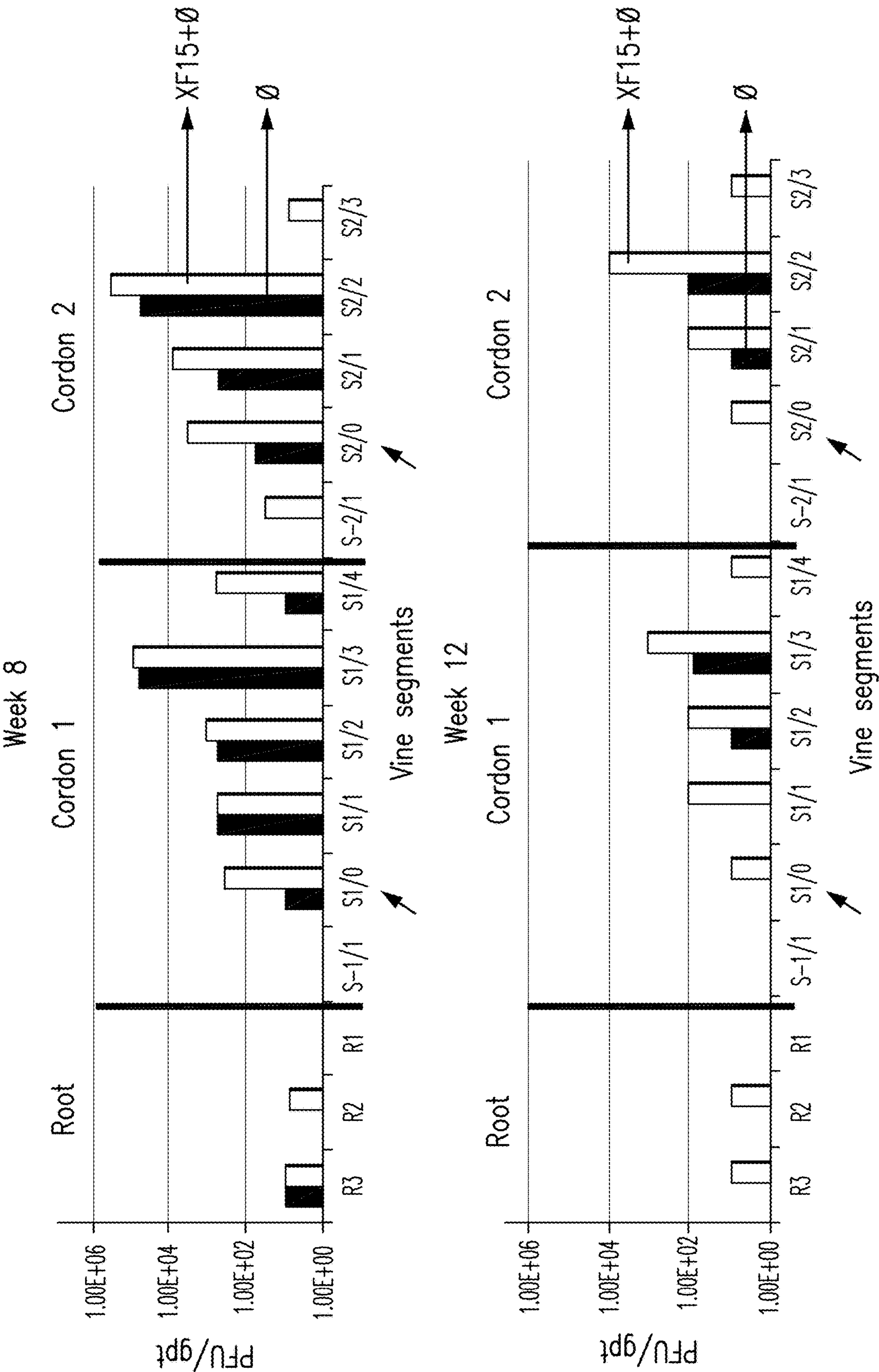
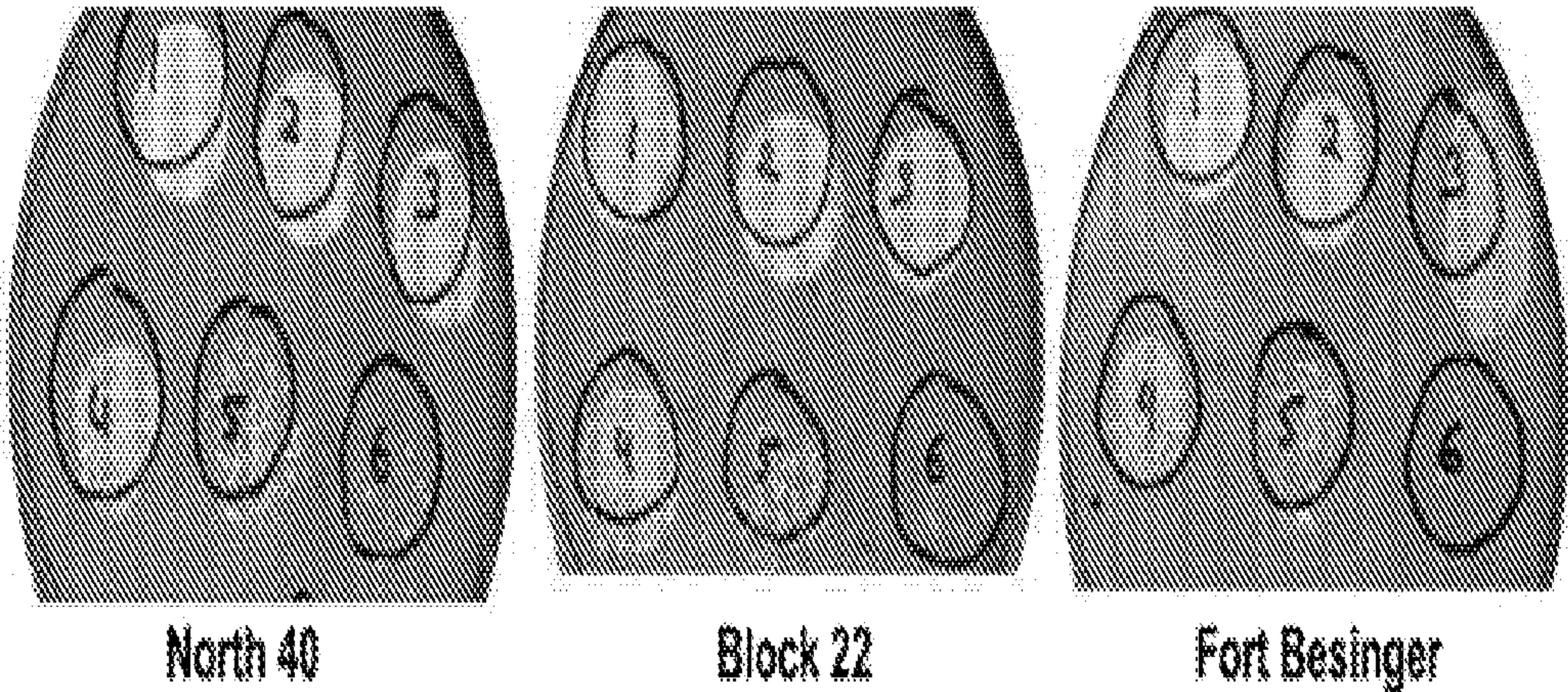


FIG. 11

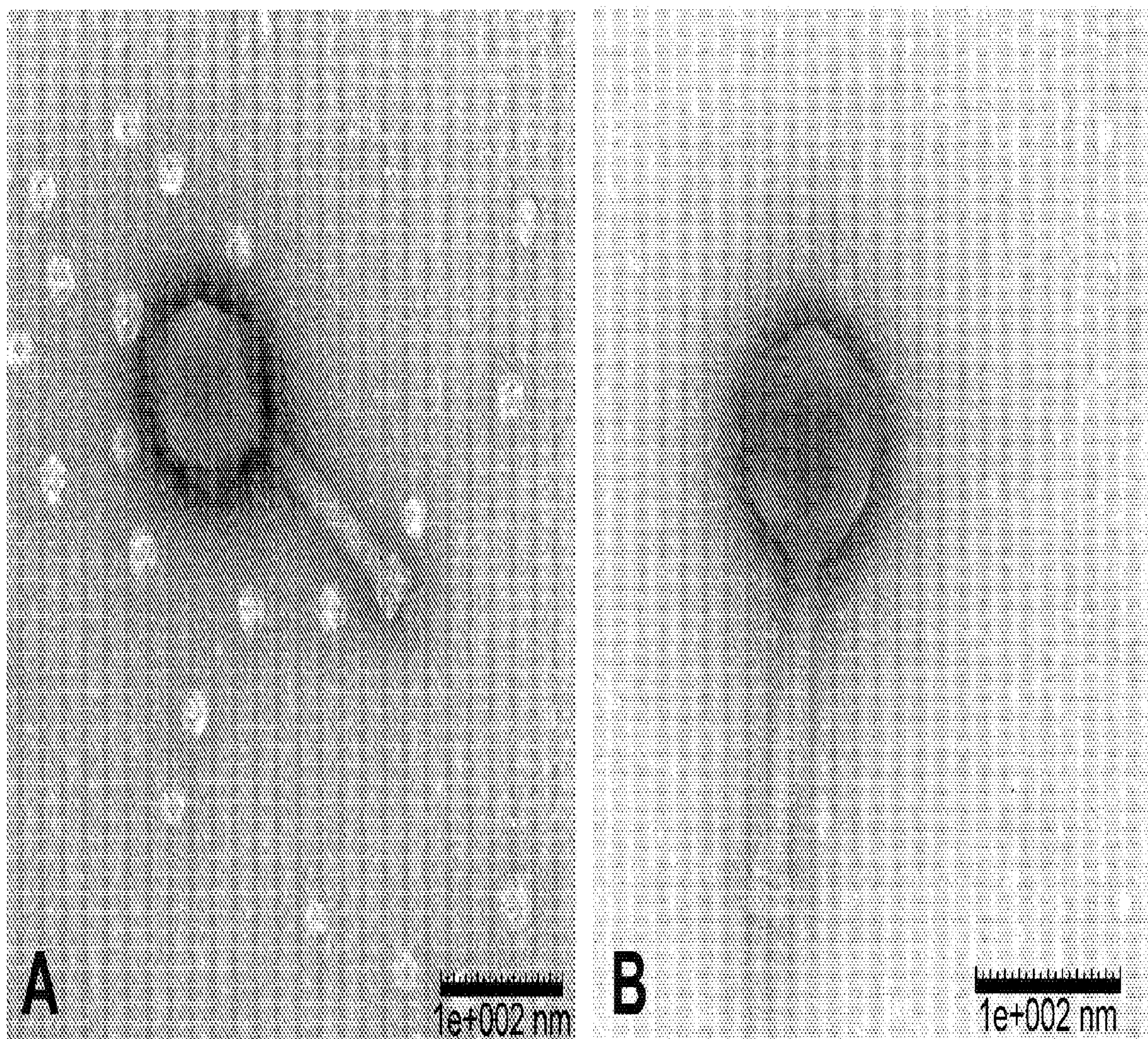
Fig. 12

Phage	<i>XacA</i> North40	<i>XacA</i> Block22	<i>XacA</i> Fort Besinger
Xfas 303	+	+	+



Spot Titration of Phage Xfas303 on *Xac* Strains

Fig. 13



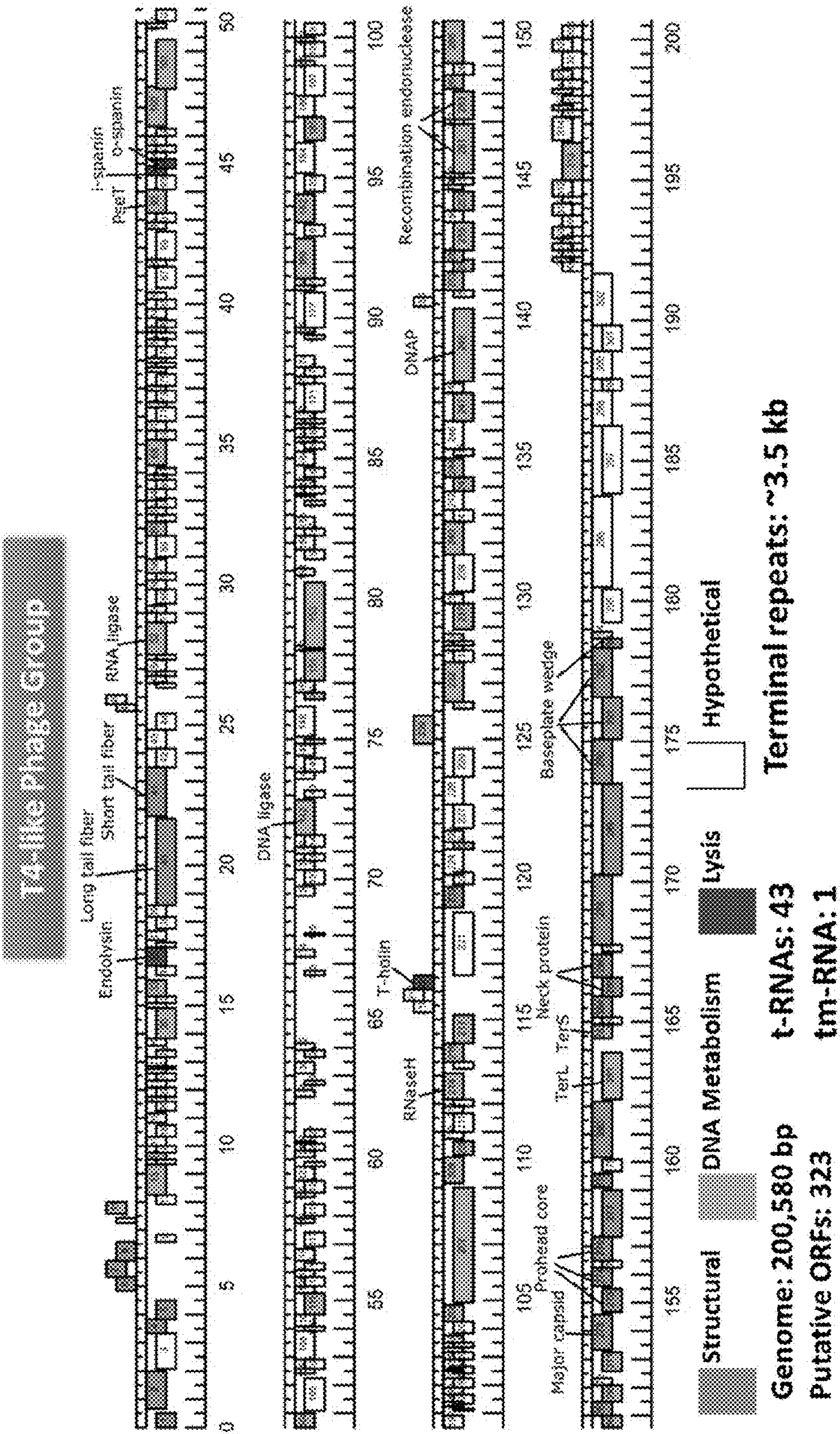
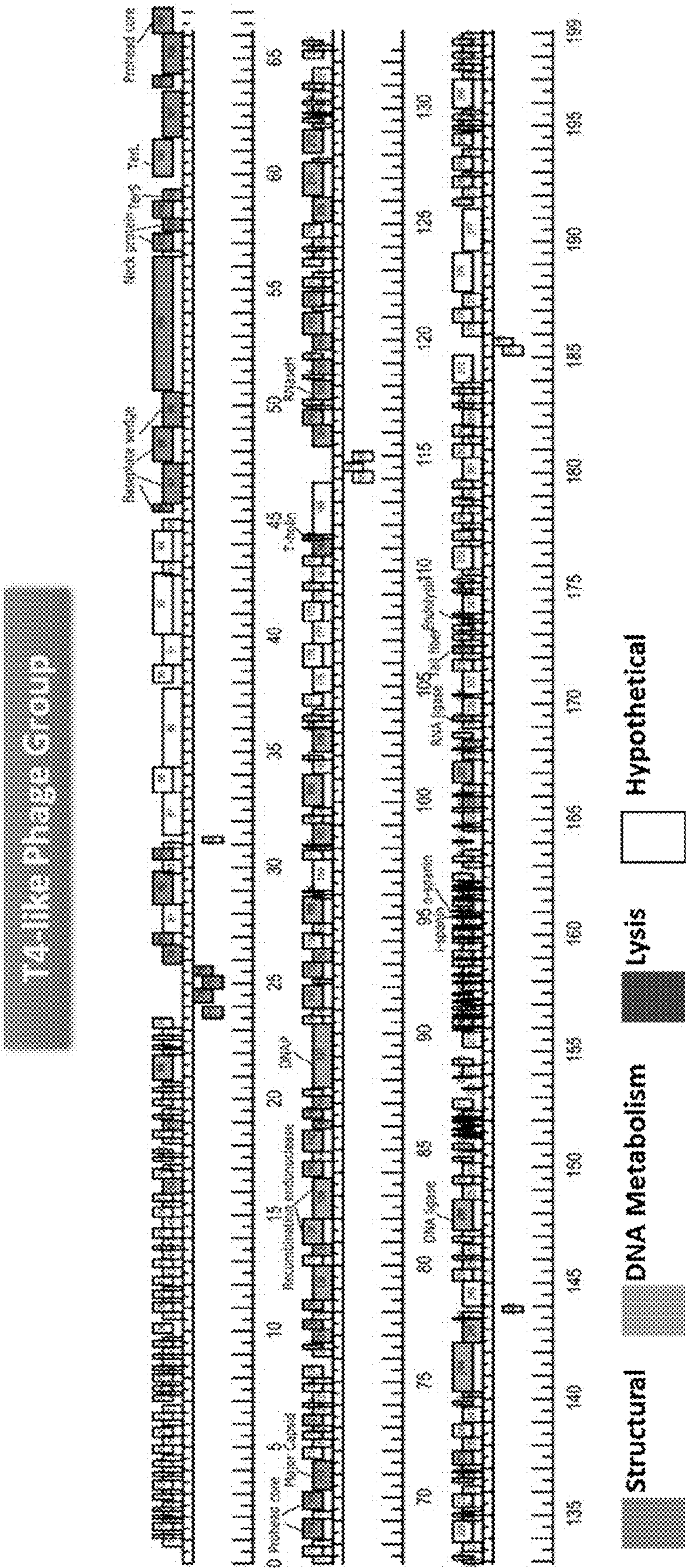


FIG. 14



Terminal repeats: ~7 kb

FIG. 15

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**METHOD FOR TREATMENT AND
CONTROL OF PLANT DISEASE****CROSS REFERENCE TO RELATED
APPLICATIONS**

This application is a continuation of U.S. application Ser. No. 15/174,589, filed Jun. 6, 2016, which application is a continuation-in-part of U.S. application Ser. No. 14/057,851, filed Oct. 18, 2013, now U.S. Pat. No. 9,357,785, which claims the benefit of priority to U.S. Provisional Application No. 61/716,245 filed Oct. 19, 2012, and No. 61/785,535 filed Mar. 14, 2013, the content each of which are herein incorporated by reference in their entireties.

**STATEMENT REGARDING FEDERALLY
SPONSORED RESEARCH**

The U.S. government has certain rights in this invention, pursuant to the following: Animal & Plant Health Inspection Service (APHIS) Cooperative Agreement Award for the Texas Pierce's Disease Research & Education Program, Agreement Number 11-8500-0955-CA, with AgriLife Research; and Otsuka Pharmaceutical Co., LTD, Agreement number 406039, with AgriLife Research.

INCORPORATION OF SEQUENCE LISTING

The sequence listing that is contained in the file named "TAMC019USCP1_ST25.txt," which is 1,710,969 bytes as measured in Microsoft Windows operating system and was created on May 25, 2016, is filed electronically herewith and incorporated herein by reference.

FIELD OF THE INVENTION

The invention relates to the field of plant pathology. More specifically, the invention relates to methods and compositions for isolating bacteriophage and for treatment of plant diseases caused by *Xylella fastidiosa* and *Xanthomonas axonopodis* comprising use of a bacteriophage, a virus of bacteria.

BACKGROUND OF THE INVENTION

Bacteria can cause many diseases in plants, including Pierce's Disease of grapevines, and Citrus Canker of citrus plants. The bacteria infect plant tissues and can cause wilting, poor growth, lesions on fruit, and even plant death. Infection can occur through spreading by wind, rain, contaminated equipment, or vector insects, rapidly spreading to other plants, and resulting in deleterious effects to the plant and massive crop losses. Effective treatment of these diseases requires a method of treating the plant to eliminate the bacteria.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides a method of propagating a virulent bacteriophage (phage) that includes *X. fastidiosa* in its host range, comprising infecting a culture of *Xanthomonas* bacteria with the bacteriophage, allowing the bacteriophage to propagate, and isolating bacteriophage particles from the culture. In another embodiment, the *Xanthomonas* bacteria comprises species strain EC-12. In another embodiment, the bacteriophage infects the cell by binding to a cell surface feature. In another embodiment, the

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cell surface feature is a Type IV pilus. In another embodiment, the bacteriophage comprises a tailed bacteriophage from the group consisting of a podophage, a siphophage, and a myophage. In other embodiments, the bacteriophage is isolated from the environment, a sewage treatment plant, or effluent, a plant, or a surface thereof or from the surrounding soil. In other embodiments of the present invention, a surrogate host is used to enrich for virulent bacteriophage. In still another embodiment, the bacteriophage is virulent in *Xylella fastidiosa*. In other embodiments, agar overlaying is used for growth of the bacteriophage.

In another aspect, the invention provides a method of obtaining a candidate biocontrol agent for Pierce's Disease comprising contacting *X. fastidiosa* and *Xanthomonas* bacteria with a sample comprising a population of virulent bacteriophage and isolating at least a first bacteriophage from the population capable of lysing said *X. fastidiosa* and *Xanthomonas* bacteria. In one embodiment, the bacteriophage infects a cell by binding to a cell surface feature. In another embodiment, the cell surface feature is a Type IV pilus. In still another embodiment, the cell surface feature is required for pathogenesis/virulence of the bacterial host. Other embodiments include contacting a lawn of at least one of *X. fastidiosa* and *Xanthomonas* with the sample, contacting the *X. fastidiosa* and *Xanthomonas* with the sample simultaneously, and contacting the *X. fastidiosa* and *Xanthomonas* with the sample sequentially. In other embodiments, the bacteriophage is isolated from the environment, a sewage treatment plant, or effluent, a plant, or a surface thereof or from the surrounding soil. In another embodiment, the bacteriophage used is virulent in *Xylella fastidiosa*. The method may further comprise detecting lysed bacterial host cells, or plaque formation, after contacting host bacteria with the virulent bacteriophage. In particular embodiments, the method comprises a plate agar overlay or a plate of the bacterial host cells onto which a sample of bacteriophage have been introduced.

In other embodiments, the bacteriophage is prepared by use of a soft agar overlay containing the *X. fastidiosa* and *Xanthomonas*, and in further embodiments, high-titer phage plate lysates are prepared by harvesting one or more overlay plate(s) comprising a *X. fastidiosa* strain or a *Xanthomonas* strain, such as EC-12, exhibiting confluent lysis, followed by maceration and clarification by centrifugation. After being filter sterilized, the resulting lysates may be stored, for instance at 4° C. Subsequently, high-titer phage lysates are purified, for instance by isopycnic CsCl centrifugation, and extracted phage solution are dialyzed. The resulting CsCl-purified bacteriophage typically displays a titer of about 1×10^{11} PFU/ml.

In some embodiments, a ratio of bacteriophage in plant tissue filtrates (PTFs) is about 1 ml of PTF to 20 ml the surrogate host (actively growing culture of selected host) for 4 days for *X. fastidiosa* strain Temecula or for 4 h for *Xanthomonas* strain EC-12.

Another aspect of the invention provides a method of preventing or reducing symptoms or disease associated with *X. fastidiosa* in a plant, comprising contacting a plant with bacteriophage that includes *X. fastidiosa* in its host range, wherein the symptoms or disease associated with *X. fastidiosa* comprise typical Pierce's Disease (PD) symptoms, wherein the leaves display a yellow or red appearance along margins, with eventual leaf margin necrosis. In one embodiment, the bacteriophage particles may be introduced into the plant. In another embodiment, the plant is selected from the group consisting of a grapevine plant, a citrus plant, almond, coffee, alfalfa, *oleander*, oak, sweetgum, redbud, elm,

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peach, apricot, plum, blackberry, mulberry, and *Chitalpa tashkentensis*. In another embodiment, the bacteriophages are introduced into the plant by injection, an insect vector or delivered via the root system by injection. In other embodiments, injection comprises a needle or a needle-free system, a pneumatic air or pressure injection system. In other embodiments, the injection is performed manually, or once, or more than once. In another embodiment, the insect vector is a glassy winged sharpshooter. In another embodiment, the bacteriophage to be introduced into the plant is from 1 to 10^{12} PFU/ml (plaque forming units/ml), 10^4 to 10^{11} PFU/ml, and 10^7 to 10^{10} PFU/ml. In another embodiment, the bacteriophage particles are obtained by a method comprising infecting a culture of *Xanthomonas* bacteria with the bacteriophage, allowing the bacteriophage to propagate, and isolating bacteriophage particles from the culture. In another embodiment, the method comprises contacting a population of plants with the bacteriophage particles to prevent or reduce symptoms associated with *X. fastidiosa*. In still another embodiment, the bacteriophage comprises at least one bacteriophage (phage) of a strain selected from the Xfas100 phage type or the Xfas300 phage type, described below.

In another aspect, the invention provides a plant disease biocontrol composition formulated for delivery to a plant, the composition comprising at least one diluent, adjuvant or surfactant, and at least one bacteriophage from the Xfas100 phage type or the Xfas300 phage type, described below. In one embodiment, the composition is further defined as being formulated for introduction to a plant via injection, spraying, misting, or dusting. In another embodiment, the composition is further defined as being formulated for topical administration to a plant.

In another aspect, the invention provides a method of obtaining a candidate biocontrol agent for citrus canker comprising contacting *Xanthomonas axonopodis* pv. *citri* bacteria with a sample comprising a population of virulent bacteriophage and isolating at least a first bacteriophage from the population capable of lysing said *Xanthomonas axonopodis* bacteria. In one embodiment, the bacteriophage infects a cell by binding to a cell surface feature. In another embodiment, the cell surface feature is a type IV pilus. In still another embodiment, the cell surface feature is required for pathogenesis/virulence of the bacterial host. Other embodiments include contacting a lawn of *Xanthomonas* with the sample. In another embodiment, the bacteriophage used is virulent in *Xanthomonas axonopodis*.

Another aspect of the invention provides a method of preventing or reducing symptoms or disease associated with *Xanthomonas axonopodis* in a plant, comprising contacting a plant with bacteriophage that includes *Xanthomonas axonopodis* in its host range. In one embodiment, the bacteriophage particles may be introduced into the plant. In some embodiments, the plant is a citrus plant selected from the group consisting of a *Citrus* spp., a *Fortunella* spp., a *Poncirus* spp., a lime, a lemon, an orange, a grapefruit, a pomelo, and hybrids of trifoliate orange used for rootstocks. In another embodiment, the bacteriophages are introduced into the plant by injection, by an insect vector, or is delivered via the root system by injection. In some embodiments, injection comprises a needle or a needle-free system, a pneumatic air or pressure injection system. In other embodiments, the injection is performed manually, or once, or more than once. In another embodiment, the insect vector is a glassy winged sharpshooter. In another embodiment, the bacteriophage to be introduced into the plant is at a concentration of from 1 to 10^{12} PFU/ml (plaque forming units/

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ml), 10^4 to 10^{11} PFU/ml, and 10^7 to 10^{10} PFU/ml. In another embodiment, the method comprises contacting a population of plants with the bacteriophage particles to prevent or reduce symptoms associated with *Xanthomonas axonopodis* and pathovars thereof in the population. In still another embodiment, the bacteriophage comprises at least one bacteriophage of a strain selected from the Xfas100 phage type or the Xfas300 phage type, described below.

In another aspect, the invention provides an isolated bacteriophage that is virulent to *Xanthomonas axonopodis* a Xfas303 bacteriophage, wherein a representative sample of said bacteriophage has been deposited under ATCC Accession Number PTA-13099. In yet another aspect, the invention provides an isolated bacteriophage that is virulent to *Xanthomonas axonopodis* and/or *X. fastidiosa* as one of bacteriophage selected from the group consisting of: Xfas101, Xfas102, Xfas103, Xfas104, Xfas105, Xfas106, Xfas107, Xfas108, Xfas109, Xfas110, Xfas301, Xfas302, Xfas304, Xfas305, and Xfas306, wherein representative samples of said bacteriophage Xfas103, Xfas106, Xfas302, Xfas303, Xfas304, and Xfas306 have been deposited under ATCC Accession Number PTA-13095, PTA-13096, PTA-13097, PTA-13098, PTA-13099, and PTA-13100.

In certain embodiments, the invention provides a method of preventing or reducing symptoms or disease associated or caused by *X. fastidiosa* or *Xanthomonas axonopodis* pv. *citri* in a plant comprising a step of contacting said plant with a virulent bacteriophage which includes *X. fastidiosa* and/or *Xanthomonas axonopodis* pv. *citri* in its host range, further wherein the bacteriophage is at least one bacteriophage selected from the group consisting of the Xfas100 phage type, and the Xfas300 phage type.

In some embodiments, the Xfas100 type phage has at least one characteristic selected from the group consisting of (a) the bacteriophage is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by binding to a Type IV pili; (c) the phage belongs to a group of tailed bacteriophage exhibiting long non-contractile tails with capsid ranging from 55-77 nm in diameter, a morphology typical of Siphoviridae family; (d) the genomic size of bacteriophage is about 55500 bp to 56200 bp; and (e) the bacteriophage prevents or reduces symptoms associated with Pierce's Disease in a plant or plants.

In further embodiments, the Xfas300 type phage has at least one characteristic selected from the group consisting of: (a) the bacteriophage is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by binding to a Type IV pilus; (c) the phage belongs to a group of tailed bacteriophage exhibiting short non-contractile tails with capsid ranging from 58-68 nm in diameter, a morphology typical of Podoviridae family; (d) the genomic size of bacteriophage is about 43300 bp to 44600 bp; and (e) the bacteriophage has an activity of preventing or reducing symptoms associated with Pierce's Disease in a plant or plants.

In certain embodiments, a single type of virulent bacteriophage is introduced into a plant; in other embodiments, a combination of 2, 3, 4, 5, 6, or more virulent bacteriophage isolates or types are introduced into a plant, either simultaneously or sequentially. In certain embodiments, the bacteriophage comprise a genome with a DNA sequence selected from the group consisting of SEQ ID NO:11-24, or a DNA sequence at least 90%, 95%, 98%, or 99% identical thereto. Thus, in certain embodiments, the bacteriophage to be introduced into a plant is selected from the group consisting of: Xfas101, Xfas102, Xfas103, Xfas104, Xfas105, Xfas106, Xfas107, Xfas110, Xfas301, Xfas302, Xfas303,

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Xfas304, Xfas305, and Xfas306. Plant disease biocontrol compositions formulated for delivery to a plant, and comprising such Xfas100 and/or Xfas300 type bacteriophage are also contemplated. The biocontrol composition may further comprise a carrier. In some embodiments the carrier may comprise a diluent, a surfactant, and/or a buffer.

In another aspect, the invention provides a method of preventing or reducing symptoms or disease associated with *Xylella fastidiosa* or *Xanthomonas* in a plant, comprising contacting said plant with particles of at least one virulent bacteriophage, wherein *Xylella fastidiosa* and/or *Xanthomonas axonopodis* are hosts of the bacteriophage, wherein the bacteriophage is of the Xfas500 phage type, for example a XfaMija or XfaMijo bacteriophage or variants thereof. In one embodiment, said bacteriophage is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas* bacteria. In other embodiments, said bacteriophage infects a cell by binding to a Type IV pilus. In further embodiments, said bacteriophage comprises a contractile tail with a capsid size ranging from 85 nm to 95 nm in diameter and belongs to the Myoviridae family. In yet further embodiments, the genomic size of said bacteriophage is about 190,000 bp to 230,000 bp.

In certain embodiments, said bacteriophage prevents or reduces symptoms associated with Pierce's Disease in a plant or plants. In other embodiments, contacting comprises introducing the bacteriophage particles into the plant, for example by injection, by an insect vector, via the root system, by spray, by mist, or by dust on the plant. In further embodiments, said plant is selected from the group consisting of a grapevine plant, a citrus plant, almond, coffee, alfalfa, oleander, oak, sweetgum, redbud, elm, peach, apricot, plum, blackberry, mulberry, olive, and *Chitalpa tashkentensis*. In yet further embodiments, said insect vector is a glassy winged sharpshooter. The number of said bacteriophage to be introduced into said plant may be from 1 to 10^{12} PFU/ml, or from 10^4 to 10^{11} PFU/ml, or from 10^7 to 10^{10} PFU/ml. In certain embodiments, said bacteriophage virulent to *Xylella fastidiosa* and *Xanthomonas* species are introduced simultaneously or sequentially to the plant by a combination of two, three, four, five, or six virulent bacteriophage strains.

In certain embodiments, said virulent bacteriophage comprises at least one bacteriophage strain selected from the group consisting of: XfaMija and XfaMijo, wherein representative samples of said phage have been deposited under ATCC Accession Numbers ATCC PTA-122743 and ATCC PTA-122742, respectively (the "Deposited Bacteriophage"). The invention further contemplates variants of the Deposited Bacteriophage, which are bacteriophage having minor variation(s) in the genomic sequence and polypeptides encoded thereby while retaining the same general genotypic, phenotypic characteristics and lytic activity against *Xylella fastidiosa* and/or *Xanthomonas* bacteria as the Deposited Bacteriophage. For example, said bacteriophage may be a XfaMija (Xfas501) type bacteriophage and displays the following characteristics: (a) the bacteriophage is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by binding to a Type IV pilus; (c) the bacteriophage comprises a contractile tail with a capsid size ranging from 85 nm to 95 nm in diameter and belongs to the Myoviridae family; (d) the genomic size of the bacteriophage is about 190,000 bp to 230,000 bp; and (e) the bacteriophage prevents or reduces symptoms associated with Pierce's Disease in a plant or plants. Said bacteriophage may also be a XfaMijo (Xfas502) type bacteriophage and displays the following characteristics: (a) the bacteriophage

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is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by binding to a Type IV pilus; (c) the bacteriophage comprises a contractile tail with a capsid size ranging from 85 nm to 95 nm in diameter and belongs to the Myoviridae family; (d) the genomic size of the bacteriophage is about 190,000 bp to 230,000 bp; and (e) the bacteriophage prevents or reduces symptoms associated with Pierce's Disease in a plant or plants.

In another aspect, the invention provides a plant disease biocontrol composition formulated for delivery to a plant, comprising at least one carrier and at least one virulent bacteriophage selected from the group consisting of: XfaMija and XfaMijo; wherein said bacteriophage is virulent to *Xylella fastidiosa* and *Xanthomonas axonopodis* species. In some embodiments, the carrier is a non-naturally occurring carrier. Plant disease biocontrol compositions of the present invention may increase the virulence of said bacteriophage relative to the same bacteriophage in the absence of said composition, and may maintain the virulence of said bacteriophage for a longer period of time relative to the same bacteriophage in the absence of said composition. Plant disease biocontrol compositions provided by the invention may further comprise at least one additional bacteriophage isolate or type, and may be formulated for introduction to a plant via injection, spraying, misting, or dusting, for example for topical administration to a plant.

In another aspect, the invention provides a method of propagating a virulent bacteriophage that includes *Xylella fastidiosa* or *Xanthomonas axonopodis* in its host range, comprising infecting a culture of Xanthomonadaceae bacteria with at least one virulent bacteriophage selected from the group consisting of: XfaMija and XfaMijo, allowing said bacteriophage to propagate, and isolating virulent bacteriophage particles from the culture. In some embodiments, said virulent bacteriophage is isolated from the environment, for example from a sewage treatment plant or effluent therefrom or from a plant or a surface thereof or from the surrounding soil. In certain embodiments, a surrogate host is used to enrich for said virulent bacteriophage. In further embodiments, agar overlaying is used for growth of said bacteriophage. In yet further embodiments, said virulent bacteriophage is selected from the group consisting of: XfaMija and XfaMijo; wherein representative samples of said phage have been deposited under ATCC Accession Numbers ATCC PTA-122743 and ATCC PTA-122742, respectively.

BRIEF DESCRIPTION OF THE DRAWINGS

For a more complete understanding of the features and advantages of the present invention, reference is now made to the detailed description of the invention along with the accompanying figures and in which:

FIG. 1: Shows a TEM image of phages Xfas302, Xfas303, Xfas304, and Xfas305, with morphology and size characteristic of Podoviridae.

FIG. 2: Shows a TEM image of phages Xfas101, Xfas102, Xfas103, and Xfas104, with morphology and size characteristic of Siphoviridae.

FIG. 3: Shows Podoviridae and Siphoviridae bacteriophages of *X. fastidiosa* isolated from wastewater, able to form plaques on XF15 and EC-12.

FIG. 4: Shows a genomic map of Siphoviridae Xfas103 and Xfas106.

FIG. 5: Shows a genomic map of Podoviridae Xfas302, Xfas303, Xfas304, and Xfas306.

FIG. 6: Shows a grapevine plant exhibiting symptoms of Pierce's Disease 8 weeks after inoculation with strain XF54 and not challenged with bacteriophage.

FIG. 7: Shows a summary of the grapevine bacteriophage therapeutic and preventative challenge study.

FIG. 8: Shows movement and persistence of individual bacteriophages in inoculated grapevines at 8 (Top) and 12 (Bottom) weeks after phage inoculation. Left panel: phages present in root tissue. Middle panel: phages present in cordon 1 of grapevine. Right panel: phages present in cordon 2 of grapevine.

FIG. 9: Shows levels of XF15 in inoculated grapevines challenged with phage cocktail 3 weeks later. Samples were collected 9 weeks after phage cocktail challenge (12 weeks after bacterial inoculation). Left panel: bacteria present in root tissue. Middle panel: bacteria present in cordon 1 of grapevine. Right panel: bacteria present in cordon 2 of grapevine. Gray bars show XF15 levels in XF15 inoculated vines. Black bars show XF15 levels in XF15 inoculated vines challenged with phage cocktail at week 3-post pathogen inoculation. Arrows show segment with point of inoculation. Each bar is representative of average CFU/gpt (gram plant tissue) of roots and 2 cordons for 3 vines.

FIG. 10: Shows levels of cocktail phages in grapevines initially inoculated with XF15 and challenged with phage cocktail 3 weeks later. Samples were collected 5, 7, and 9 weeks after phage cocktail challenge (8, 10, and 12 weeks after initial bacterial inoculation). Left panel: phages present in root tissue. Middle panel: phages present in cordon 1 of grapevine. Right panel: phages present in cordon 2 of grapevine. Black bar show phage levels in cocktail inoculated plants. Gray bar show phage levels in XF15 inoculated vines challenged with phage cocktail at week 3-post pathogen inoculation. Arrows show segment with point of inoculation. Each bar is representative of the average PFU/gpt (gram plant tissue) of 4 phages in cocktail determined from roots and 2 cordons for 3 vines.

FIG. 11: Shows levels of phages in grapevines initially inoculated with phage cocktail and challenged 3 weeks later with XF15. Samples were collected 5, 7, and 9 weeks after XF15 challenge (8, 10, 12 weeks after initial phage inoculation). Left panel: phages present in root tissue. Middle panel: phages present in cordon 1 of grapevine. Right panel: phages present in cordon 2 of grapevine. Black bars show phage levels in cocktail inoculated vines. Gray bars show phage levels in cocktail inoculated vines challenged with XF15 at week 3-post phage inoculation. Arrows show segment with point of inoculation. Each bar is representative of the average PFU/gpt (gram plant tissue) of 4 phages in cocktail determined from roots and 2 cordons for 3 vines.

FIG. 12: Shows results of spot titration of phage Xfas303 on *Xanthomonas axonopodis* pv. *citri* strains.

FIG. 13: Shows TEM images of (A) phage XfaMija and (B) phage XfaMijo, with morphology characteristic of Myoviridae.

FIG. 14: Shows a genomic map of Myoviridae XfasMija.

FIG. 15: Shows a genomic map of Myoviridae XfasMijo.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

SEQ ID NO:1—The *X. fastidiosa*-specific oligonucleotide forward primer designed for *X. fastidiosa* gyrB.

SEQ ID NO:2—The *X. fastidiosa*-specific oligonucleotide reverse primer designed for *X. fastidiosa* gyrB.

SEQ ID NO:3—The bacteriophage Xfas304-specific oligonucleotide forward primer designed for the bacteriophage DNA primase gene.

5 SEQ ID NO:4—The bacteriophage Xfas304-specific oligonucleotide reverse primer designed for the bacteriophage DNA primase gene.

SEQ ID NO:5—The bacteriophage Xfas303-specific oligonucleotide forward primer designed for the bacteriophage DNA primase gene.

10 SEQ ID NO:6—The bacteriophage Xfas303-specific oligonucleotide reverse primer designed for the bacteriophage DNA primase gene.

15 SEQ ID NO:7—The bacteriophage Xfas103-specific oligonucleotide forward primer designed for the bacteriophage DNA helicase gene.

SEQ ID NO:8—The bacteriophage Xfas103-specific oligonucleotide reverse primer designed for the bacteriophage DNA helicase gene.

20 SEQ ID NO:9—The bacteriophage Xfas106-specific oligonucleotide forward primer designed for the bacteriophage DNA helicase gene.

SEQ ID NO:10—The bacteriophage Xfas106-specific oligonucleotide reverse primer designed for the bacteriophage DNA helicase gene.

25 SEQ ID NO:11—The genomic sequence of bacteriophage Xfas101.

SEQ ID NO:12—The genomic sequence of bacteriophage Xfas102.

30 SEQ ID NO:13—The genomic sequence of bacteriophage Xfas103.

SEQ ID NO:14—The genomic sequence of bacteriophage Xfas104.

35 SEQ ID NO:15—The genomic sequence of bacteriophage Xfas105.

SEQ ID NO:16—The genomic sequence of bacteriophage Xfas106.

SEQ ID NO:17—The genomic sequence of bacteriophage Xfas107.

40 SEQ ID NO:18—The genomic sequence of bacteriophage Xfas110.

SEQ ID NO:19—The genomic sequence of bacteriophage Xfas301.

45 SEQ ID NO:20—The genomic sequence of bacteriophage Xfas302.

SEQ ID NO:21—The genomic sequence of bacteriophage Xfas303.

SEQ ID NO:22—The genomic sequence of bacteriophage Xfas304.

50 SEQ ID NO:23—The genomic sequence of bacteriophage Xfas305.

SEQ ID NO:24—The genomic sequence of bacteriophage Xfas306.

55 SEQ ID NO:25—The bacteriophage Mija-specific oligonucleotide forward primer designed for the bacteriophage DNA primase gene.

SEQ ID NO:26—The bacteriophage Mija-specific oligonucleotide reverse primer designed for the bacteriophage DNA primase gene.

60 SEQ ID NO:27—The bacteriophage Mijo-specific oligonucleotide forward primer designed for the bacteriophage DNA primase gene.

65 SEQ ID NO:28—The bacteriophage Mijo-specific oligonucleotide reverse primer designed for the bacteriophage DNA primase gene.

SEQ ID NO:29—The genomic sequence of bacteriophage Mija.

SEQ ID NO:30—The genomic sequence of bacteriophage Mijo.

DETAILED DESCRIPTION OF THE INVENTION

The following definitions and methods are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the present invention. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art.

The invention provides, for the first time, methods allowing efficient propagation and isolation of bacteriophage (phage) capable of infecting, replicating within, and lysing *X. fastidiosa* and/or *Xanthomonas axonopodis* (Xa) and pathovars thereof. The invention also provides a method for controlling bacterial disease in plants. Plant diseases that may be controlled in accordance with the present invention may include, but are not limited to, Pierce's Disease and citrus canker. Bacterial species useful in accordance with the invention may include, but are not limited, to a *Xylella* species, such as *Xylella fastidiosa*, or a *Xanthomonas* species, such as *Xanthomonas axonopodis* and pathovars thereof, such as *Xanthomonas axonopodis* pv. *citri* (Xac).

As used herein, a "bacteriophage" or "phage" refer to a virus of bacteria. As used herein, "*Xanthomonas axonopodis*" or "Xa" refers to a *Xanthomonas axonopodis* bacterial species or pathovar thereof, which may include *Xanthomonas axonopodis* pv. *citri* (Xac) or any other pathovar of *Xanthomonas axonopodis*. Currently, propagation of bacteriophage capable of lysing *X. fastidiosa* is labor-intensive in the laboratory, using *X. fastidiosa* host cells and complex, expensive media in a solid format. This may require 7-10 days to yield low quantities of bacteriophage. The present invention thus represents a significant advance, providing for propagation of bacteriophage capable of infecting *X. fastidiosa* by growing the bacteriophage in a fast-growing host bacteria such as *Xanthomonas* species EC-12 to rapidly produce bacteriophage; this is designated as the "surrogate host" approach. The technique is fast and cost-effective, capable of use with conventional media components available in the art. The technique is also amenable to scale-up. The ability to produce virulent phages that lyse (kill) *X. fastidiosa* and/or Xa in a surrogate host that can replicate hourly under standard conditions, instead of days using a host that at best replicates daily in a very complex media makes viable for the first time the production and implementation of *X. fastidiosa*- and/or *Xanthomonas axonopodis*-mediated disease control and treatment methods comprising use of virulent phages. Culture of Xa can be performed in nutrient broth with a generation time of approximately 2-3 hours. However, Xa is a permitted pathogen and thus requires a biosafety level of 2 (BL2) to culture. Therefore, similar to *X. fastidiosa*, Xa may not be practical for large-scale production.

Bacteriophage may be isolated by a soft agar overlay method, allowing for isolation of phage from *X. fastidiosa* and/or *Xanthomonas* cells, and in further embodiments, high-titer phage plate lysates are prepared by harvesting one or more overlay plate(s) of a *X. fastidiosa* strain or a *Xanthomonas* strain, such as strain EC-12, exhibiting confluent lysis, followed by maceration, clarification by centrifugation, and filter sterilization. The resulting lysates may be stored at 4° C. Subsequently, high-titer phage lysates may be purified for instance by isopycnic CsCl centrifugation, and extracted phage solution can be dialyzed. Resulting

CsCl-purified bacteriophage having a titer of about 1×10^{11} PFU/ml can thus be obtained. In other embodiments, bacteriophage in plant tissue filtrates (PTFs) may be filtered. A preferred ratio for filtration is 1 ml of PTF to 20 ml of the surrogate host culture (an actively growing culture of a selected host), grown, for instance, for 4 days for *X. fastidiosa* strain Temecula or for 4 h for *Xanthomonas* strain EC-12.

Using methods for the detection and propagation of bacteriophage virulent to *X. fastidiosa* and/or *Xanthomonas axonopodis* ("Xa") pathovars, virulent bacteriophage which are capable of causing lysis of *X. fastidiosa* and/or Xa can be selected from a desired source, such as from the environment, including plants, wastewater, and/or soil water, and propagated according to the invention. Bacteriophages that may be identified in accordance with the present invention may be defined by particular characteristics as described by Casjens et al. (*Research in Microbiology*, 159:340-348, 2008), such as capsid shape and size, genome size, arrangement of genes and/or gene modules, morphology, and life cycle. In one embodiment, bacteriophages of the present invention may be virulent, isometric, with a triangulation number of T=7, a genome size of about 60 kb or within about 15% of 60 kb, may include direct terminal repeats in the genome. The virulent bacteriophage can be used, for example, to control and prevent disease cause by *Xylella* species and subspecies and/or *Xanthomonas* species such as *Xanthomonas axonopodis* and pathovars thereof, such as *citri*.

Currently, five subspecies of *Xylella* are recognized as causing plant disease. Plant species able to be infected by *Xylella* are listed, for example, at cnr.berkeley.edu/xylella/control/hosts, as described in Hernandez-Martinez et al., (*Phytopathology*, 97(7):857-864, 2007) and Nunney et al., (*PLOS ONE*, 5(11):e15488, 2010), and may include commercial crops such as, but not limited to, grapevines, citrus, coffee, almond, peach, alfalfa, apricot, plum, blackberry, mulberry, olive and horticultural plants such as *oleander*, oak, sweetgum, redbud, elm, and *Chitalpa tashkentensis*. In one embodiment of the invention, bacteriophage can be isolated from environments where *X. fastidiosa* is unable to grow because of its unique growth requirements. Further, in accordance with the present invention, plant species able to be infected by a *Xanthomonas axonopodis* pathovar may include, but are not limited to, a *Citrus* spp., a *Fortunella* spp., a *Poncirus* spp., a lime, a lemon, an orange, a grapefruit, a pomelo, and hybrids of trifoliate orange used for rootstocks.

The invention thus provides methods for development of bacteriophage-based treatments for the control of plant diseases caused by *X. fastidiosa*, which is a xylem-limited, insect vectored, Gram-negative bacterium that causes disease in many plants. Most notably, *X. fastidiosa* is the causal agent of Pierce's Disease (PD) of grapes, which is currently a limiting factor in the cultivation of high quality wine grapes in areas of the U.S., including Texas and California. One important plant disease caused by *X. fastidiosa* is Pierce's Disease of grape, which causes visible symptoms including yellowed leaves, or leaves with red along margins. Eventually drying and necrosis of leaf margins and leaves may occur. Insect vectors such as the leafhopper Glassy Winged Sharpshooter ("GWSS") may spread the disease, as well as phage which infect the disease-causing bacteria and which may be useful for biocontrol efficacy.

Presently, there are no effective control measures for PD short of aggressive culling of the infected vines. The current invention permits treatment of such diseases by providing,

for the first time, a viable system for generating sufficient bacteriophage quantities in a cost-effective manner to permit plant treatments. The invention also provides methods for development of bacteriophage-based treatments for the control of plant diseases caused by Xa, including Xac, which is the causal agent of citrus canker. In a particular embodiment, the invention provides a method for controlling disease of Xa in a plant.

As used herein, the term “virulent” refers to a virus, particularly a bacteriophage, that is able to infect, replicate within, and lyse (kill) a host cell. The term “temperate” refers to a bacteriophage that can integrate into the host genome (lysogenize) or lyse the host cell. In one embodiment of the invention, phages are propagated in a suitable host, as is described herein. The term “host” refers to a bacterial cell that can be used to produce large quantities of bacteriophage. One step in the development of a bacteriophage-based control strategy provided herein is the identification and propagation of virulent phages that recognize particular bacterial receptor sites. Production and delivery of bacteriophage virulent to disease-causing bacteria must be economical to represent a viable biocontrol option.

Phages infect a host cell via recognition of receptors, which can include, but are not limited to, surface proteins such as Omp A and OmpF, the core and O-chain of the bacterial LPS in Gram-negative bacteria, sex and type IV pili (e.g. Roine et al., *Mol. Plant Microbe Interact.*, 11:1048-1056 (1998)), and flagella. Without being limited to any given theory, it is believed that bacteriophage may infect *X. fastidiosa* and Xa cells via type IV pili. Thus, in one embodiment, a host according to the present disclosure may be any type of bacteria, and particularly any bacterial species that a virulent temperate bacteriophage, or a derivative thereof, such as a passaged phage, is able to adsorb to and infect via a surface receptor that is required for virulence and/or pathogenicity, such as a type IV pili or a TonB-like protein. By “passaged phage” is meant a phage population which has been propagated by one or more periods of growth in cultured host cells. Typical hosts used in the present invention may be bacterial cells, particularly bacterial species of the family Xanthomonadaceae, which includes both *Xylella* and *Xanthomonas*. In some embodiments, strains of *X. fastidiosa* which may be useful in practicing this invention may include Temecula1 (ATCC 700964); Ann-1 (ATCC 700598); Dixon (ATCC 700965); XF53, XF54, and XF95 (Whitehorn et al., *Science*, 336: 351-352 (2012)); XF134, XF136, XF140, XF141, XF15-1, XF15-1-1, TM1 (Jones, et al., *Ann. Rev. Phytopathol.*, 45:245-262 (2007)); and tonB1 (Summer et al., *J. Bacteriol.* 192:179-190 (2010)). Exemplary strains of *Xanthomonas*, which are susceptible to one or more of the disclosed bacteriophage isolates, and which may be useful for this invention include EC12, Pres-4, or Jal-4 and Xac isolates such as North 40, Ft. Basinger, and Block22, among others. Other Xanthomonad bacteria may also be utilized in view of their susceptibility to Xfas100 and/or Xfas300 bacteriophage.

As used herein, the term “isolation” is defined as separation and identification of an organism from a solution containing a mixed culture of organisms. Organisms able to be isolated can include viruses, bacteria, plant cells, or the like. Bacteriophage can be isolated as described herein and known in the art. In one embodiment, general laboratory methods for isolating bacteriophage may include but are not limited to growth in cultured cells, bacteriophage assay, double agar method, and plaque assay, among others. The present invention provides a method of isolating bacterio-

phage by a method involving overlaying at least a first sample comprising different strains of bacterial host cells together in order to isolate bacteriophage able to infect and propagate within both host cell types.

The invention also provides a method of propagating a virus (bacteriophage) virulent to *Xylella fastidiosa* and/or Xa. Methods of propagating bacteriophages are known in the art, and can encompass any method capable of producing quantities of bacteriophage sufficient for treating plant diseases. In one embodiment, propagating bacteriophage virulent to *X. fastidiosa* and/or Xac can comprise growing bacteriophage in *Xanthomonas* bacteria, allowing the bacteriophage to propagate, and isolating bacteriophage particles from the culture.

Bacteriophage virulent to *X. fastidiosa* may be prepared using a soft agar overlay method. High-titer phage plate lysates may be prepared, for instance, by harvesting an overlay plate of *X. fastidiosa* strain Temecula or *Xanthomonas* strain EC-12 exhibiting confluent lysis, followed by maceration and clarification by centrifugation. After being filter sterilized, the resulting lysates can be stored at 4° C. Subsequently, high-titer phage lysates may be purified by isopycnic CsCl centrifugation, and extracted phage solution are dialyzed. CsCl-purified bacteriophage having a titer of, for instance, 1×10^{11} PFU/ml can be obtained.

A preferred ratio of bacteriophage in plant tissue filtrates (PTFs) for enrichment is, for instance, 1 ml of PTF to 20 ml of the surrogate host culture (actively growing culture of selected host), grown for 4 days for *X. fastidiosa* strain Temecula or for 4 hours for *Xanthomonas* strain EC-12.

The invention also provides a method of treating or reducing symptoms associated with *X. fastidiosa* and/or Xa pathovars in a plant or plants. Typical Pierce’s Disease symptoms include leaves becoming slightly yellow or red along margins, respectively; eventually leaf margins may dry or die in its zones

One embodiment of the contemplated methods involves administering, to a plant infected with *X. fastidiosa* and/or Xa, bacteriophage(s) virulent to *X. fastidiosa* and/or Xa in a manner that will result in treatment of the plant. Treatment of plants for infection may be done by spraying, misting, dusting, injection, or any other method known in the art. Methods for formulating compositions for such applications are also well known in the art. For example, *X. fastidiosa* infects the vascular tissues of plants, and thus the invention as described herein may comprise introducing via injection a purified population of bacteriophage particles virulent to *X. fastidiosa* to a plant infected with *X. fastidiosa* such that the bacteriophage is able to infect and lyse the *X. fastidiosa* cells thereby treating the plant infection. However, one skilled in the art will recognize that other methods may successfully be used, as well. Xa is a foliar pathogen and infects plant leaves, stems, and fruit naturally by rain splashing directly through leaf stomata, or by way of wounds produced during strong winds or by insects. Thus, in one embodiment, the present invention may comprise introducing by spraying a composition comprising a purified population of bacteriophage particles virulent to Xa to a plant infected with Xa.

As used herein, the terms “treatment,” “treating,” and “treat” are defined as acting upon a disease, disorder, or condition with an agent to reduce or ameliorate the physiologic effects of the disease, disorder, or condition and/or its symptoms. “Treatment,” as used herein, covers any treatment of a disease in a host (e.g., a plant species, including those of agricultural interest, such as edible plants or those used to produce edible products, as well as ornamental plant

species), and includes: (a) reducing the risk of occurrence of the disease in a plant, (b) impeding the development of the disease, and (c) relieving the disease, i.e., causing regression of the disease and/or relieving one or more disease symptoms. "Treatment" is also meant to encompass delivery of an inhibiting agent to provide an effect, even in the absence of a disease or condition. For example, "treatment" encompasses delivery of a disease or pathogen inhibiting agent that provides for enhanced or desirable effects in the plant (e.g., reduction of pathogen load, reduction of disease symptoms, etc.).

The invention also provides a plant disease biocontrol composition formulated for delivery to a plant, the composition comprising at least one carrier, and at least one bacteriophage that is virulent to *Xylella fastidiosa* and *Xanthomonas* species such as Xa.

The virulent bacteriophage to *Xylella fastidiosa* and/or *Xanthomonas* species such as Xa as an active ingredient in the composition of the present invention is also provided as one of bacteriophage selected from the group consisting of the Xfas100 phage type, such as Xfas101, Xfas102, Xfas103, Xfas104, Xfas105, Xfas106, Xfas107, Xfas108, Xfas109, and Xfas110, and/or the Xfas300 phage type, such as Xfas301, Xfas302, Xfas303, Xfas304, Xfas305, and Xfas306, wherein said phage type of the Xfas103, Xfas106, Xfas302, Xfas303, Xfas304, and Xfas306, which have been deposited under ATCC Accession Numbers PTA-13096, PTA-13095, PTA-13098, PTA-13099, PTA-13100, and PTA-13097, respectively. The virulent bacteriophage to *Xylella fastidiosa* and/or *Xanthomonas* species such as Xa as an active ingredient in the composition of the present invention is also provided as one of bacteriophage selected from the group consisting of the XfaMija or XfaMijo phage type, which have been deposited under ATCC Accession Numbers ATCC PTA-122743 and ATCC PTA-122742, respectively or variants thereof.

The virulent bacteriophage of the Xfas100 phage type as an active ingredient in the present invention displays at least one of the following characteristics: (a) the bacteriophage has an activity of the capable of lysing said *Xylella fastidiosa* and *Xanthomonas* bacteria, (b) the bacteriophage infects a cell by binding to a Type IV pilus, (c) the tailed bacteriophage exhibits long non-contractile tails with capsid ranging from 55-77 nm in diameter, a morphology typical of Siphoviridae family, (d) the genomic size of bacteriophage is about 55500 bp to 56200 bp and (e) the bacteriophage has an activity of preventing or reducing symptoms associated with Pierce's Disease in a plant or plants.

The virulent bacteriophage of the Xfas300 phage type as an active ingredient in the present invention has at least one of the characteristics, wherein said characteristics is; (a) the bacteriophage has an activity of the capable of lysing said *Xylella fastidiosa* and *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by binding to a Type IV pilus; (c) the group of a tailed bacteriophage exhibits short non-contractile tails with capsid ranging from 58-68 nm in diameter, a morphology typical of Podoviridae family; (d) the genomic size of the bacteriophage is about 43300 bp to 44600 bp; and (e) the bacteriophage has an activity of preventing or reducing symptoms associated with Pierce's Disease in a plant or plants. Virulent bacteriophage as an active ingredient in compositions of the present invention further comprises at least one bacteriophage selected from the Xfas100 phage type and/or the Xfas300 phage type, wherein said Xfas100 phage type is Xfas103 and Xfas106 and/or said Xfas300 phage type is Xfas302, Xfas303, Xfas304, and Xfas306.

The virulent bacteriophage of the Xfas500 phage type (for example XfasMija and XfasMijo) as an active ingredient in the present invention has at least one of the characteristics: (a) the bacteriophage has an activity of the capable of lysing said *Xylella fastidiosa* and *Xanthomonas* bacteria; (b) the bacteriophage infects a cell by adsorbing to a Type IV pilus; (c) the group of a tailed bacteriophage exhibits contractile tails (ranging from 198-207 nm in length) with capsid (87-91 nm in diameter), a morphology typical of Myoviridae family; (d) the genomic size of the bacteriophage is about 190,000 bp to 230,000 bp; and (e) the bacteriophage has an activity of preventing or reducing symptoms associated with Pierce's Disease in a plant or plants. Virulent bacteriophage as an active ingredient in compositions of the present invention further comprises at least one bacteriophage selected from the Xfas500 phage type, wherein said Xfas500 phage type is Xfas501 (Mija) and Xfas502 (Mijo).

Bacteriophage virulent to *Xylella fastidiosa* and *Xanthomonas* species, such as Xa, used as an active ingredient in the composition of the present invention is also provided by a combination of phage, such as a cocktail of two, three, four, five, six, or more virulent bacteriophage isolates or types, which may be provided simultaneously or sequentially, including with a carrier. The term "carrier" refers to a diluent, adjuvant, surfactant, excipient, or vehicle with which the phage is administered. Such carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Saline solutions, including phosphate solution such as sodium monohydrogen phosphate, potassium dihydrogen phosphate and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable excipients may include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene glycol, water, ethanol, and the like.

A plant disease biocontrol composition, if desired, may also contain minor amounts of wetting or emulsifying agents, or pH buffering agents.

Protective agents such as, but not limited to, casein based formulations, flour-based formulations, sucrose, Congo red, N-propyl-gallate, and lignin-based formulations, can be added to a plant disease biocontrol composition.

Phage concentration required for efficient disease control is not limited, but for example can be from 1×10^1 to 1×10^{12} PFU/ml, 1×10^4 to 1×10^{11} PFU/ml or 1×10^7 to 1×10^{10} PFU/ml.

Depending growing age of tree, the thickness of the stem, the size of the root, the dosage is adjusted appropriately. A plant disease biocontrol composition can be a dry product, a substantially dry product, a liquid product, or a substantially liquid product. In some embodiments, a dry or substantially dry product can be reconstituted in a liquid (e.g., water, etc.), and then applied to a plant. In other embodiments, such a composition can be applied in dry or substantially dry form, where liquid that is already present on the plant, is concurrently applied to the plant, or that subsequently appears on the plant (e.g., by application, condensation, etc.) facilitates exposure of the bacteriophage to target bacteria. In another embodiment, such a composition can be applied by spray, mist, or dust on the plant.

A plant disease biocontrol composition can take the form of a solution, a suspension, an emulsion, a powder, a tablet, and the like.

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The timing of application of a plant disease biocontrol composition is not limited, but may for instance be daily, weekly, or twice-weekly, monthly, bimonthly, or quarterly.

The present invention also provides an isolated bacteriophage that is virulent to *Xylella fastidiosa* and *Xanthomonas* species, such as Xa and pathovars thereof.

The invention also provides an isolated bacteriophage as one of bacteriophage selected from the group consisting of the Xfas100 phage type, such as Xfas101-Xfas110, and/or the Xfas300 phage type, such as Xfas301-Xfas306, and wherein Xfas103, Xfas106, Xfas302, Xfas303, Xfas304, and Xfas306, which have been deposited under ATCC Accession Numbers PTA-13096, PTA-13095, PTA-13098, PTA-13099, PTA-13100, and PTA-13097, respectively. The invention further provides an isolated bacteriophage as one of bacteriophage selected from the group consisting of XfaMija or XfaMijo phage type, which have been deposited under ATCC Accession Numbers ATCC PTA-122743 and ATCC PTA-122742, respectively or variants thereof.

Such a bacteriophage can be detected by confirming the capability of forming plaques on *Xylella fastidiosa* and/or *Xanthomonas* species.

DEPOSIT INFORMATION

A deposit of representative bacteriophage of each of strains Xfas103, Xfas106, Xfas302, Xfas303, Xfas304, and Xfas306, and a deposit of representative bacteria of *X. anopodis* EC-12, which are disclosed herein above and referenced in the claims, was made with the ATCC, located at P. O. Box 1549, Manassas, Va. 20108, USA. The date of deposit for the accessions was Jul. 24, 2012 and the accession numbers for the deposited strains are PTA-13096, PTA-13095, PTA-13098, PTA-13099, PTA13100, PTA13097, and PTA-13101, respectively. All restrictions upon the deposit will be removed upon the granting of a patent, and the deposit is intended to meet all of the requirements of 37 C.F.R. § 1.801-1.809. The deposit will be maintained in the depository for a period of 30 years, or 5 years after the last request, or for the effective life of the patent, whichever is longer, and will be replaced if necessary during that period.

A deposit of representative bacteriophage of each of strains XfaMija and XfaMijo, which are disclosed herein above and referenced in the claims, was made with the ATCC, located at P. O. Box 1549, Manassas, Va. 20108, USA. The date of deposit for the accessions was Jan. 13, 2016, and the accession numbers for the deposited strains are ATCC PTA-122743 and ATCC PTA-122742, respectively. All restrictions upon the deposit will be removed upon the granting of a patent, and the deposit is intended to meet all of the requirements of 37 C.F.R. § 1.801-1.809. The deposit will be maintained in the depository for a period of 30 years, or 5 years after the last request, or for the effective life of the patent, whichever is longer, and will be replaced if necessary during that period.

EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate

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that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

Media, Culture Conditions and Bacterial Strains

This example describes the isolation, propagation, and the morphological and genomic characterization of bacteriophage virulent to *X. fastidiosa* and *Xanthomonas* species. The medium used in this study differs from standard medium used to grow *X. fastidiosa*, which allows rapid growth but affects the ability of the bacteriophage to infect. PW broth medium as modified by Sherald et al. (*Plant Disease* 67:849-852, 1983) designated PW-M, was used for growth of *X. fastidiosa* isolates, except that the final bovine serum albumin content was 0.3% as modified by Hill and Purcell (*Phytopathology* 85(12):1368-1372, 1995). For solid medium (PW-MA) and soft agar, the PW-M broth was amended with 15 g/l and 7.5 g/l, respectively, of Plant Cell Culture Tested agar (Sigma). The complex medium TN broth (TNB) was used for routine maintenance of non-*X. fastidiosa* cultures. Solid medium (TNA) was identical, with the exception that it lacked KNO₃ and was supplemented with 20 g/L agar. For soft agar overlays, TN medium was amended with 7.5 g/L of agar (TNSA). For plating of plant extracts to obtain total bacterial counts, TNA medium was amended with cycloheximide (40 µg/ml; TNAC). All cultures were grown at 28° C. and liquid cultures were monitored at λ=600 nm using Nephelo flasks. California *X. fastidiosa* isolates included in the study were Temecula (XF15), which is representative of *X. fastidiosa* subspecies *fastidiosa*, Ann1 (XF108), representative of *X. fastidiosa* subspecies *sandyi*, and Dixon (XF102), representative of *X. fastidiosa* subspecies *multiplex* (Hendson et al., *Applied and Environmental Microbiology* 67(2):895-903, 2001). Texas *X. fastidiosa* isolates included one each from *Platanus occidentalis* (XF1), *Helianthus annuus* (XF5), *Iva annua* (XF18), *Ambrosia psilostachya* (XF23), *Ratibida columbifera* (XF37), *Vitis aestivalis* (XF39), *Vitis mustangensis* (XF41), three isolates from *Ambrosia trifida* var. *texana* (XF16, 40, and 43), two from *Nerium oleander* (XF93 and 95), and 15 from *Vitis vinifera* (XF48, 50, 52, 53, 54, 56, 58, 59, 60, 66, 67, 70, 71, 76, and 78). All isolates were single-colony purified by the streak isolation method, and stored at -80° C. after amending PW-M broth cultures to a final concentration of 20% glycerol (v/v). *X. fastidiosa* isolates were confirmed at the species and subspecies level using polymerase chain reaction (PCR) analysis as previously described (Hernandez-Martinez et al., *Plant Disease* 90(11):1382-1388, 2006). The MIDI Sherlock® Microbial Identification System that analyzes fatty acid methyl esters by gas chromatography (GC-FAME) was used to identify *Xanthomonas* species.

Example 2

Processing of Plant Samples and Isolation of Bacteria

Plant samples of *Vitis vinifera*, *V. mustangensis*, and weeds were obtained from vineyards in Brazos County and Washington County, Texas. Rice (*Oryza sativa*) plant tissue and weeds from rice fields were obtained from Jefferson County and Wharton County, Texas. Rice seed samples were obtained from the Texas AgriLife Research Center in Beau-

mont, Tex. Samples from rose plants (*Rosa* spp.; Knock Out) and jalapeno (TAM-mild; *Capsicum annuum*) were obtained in Brazos County, Texas. To obtain plant extracts, 10 g of plant tissue were ground using a mortar and pestle in 50 ml bacteriophage buffer (P-buffer; 50 mM Tris-HCl pH 7.5, 100 mM NaCl, 8 mM MgSO₄), vortexed, and strained through a double-layer of cheesecloth to remove large particles. The extract was then dilution plated to both PW-M and TNAC for the isolation of *X. fastidiosa* and non-*X. fastidiosa* bacteria, respectively, and incubated at 28° C. Plates were evaluated for growth daily for up to 10 days.

Example 3

Isolation, Purification and Titration of Bacteriophage from Plant Samples

To obtain plant tissue filtrates (PTFs) the clarified plant extract was centrifuged (10,000×g, 10 min at 4° C.), twice and the tissue extract were filtered through a 0.22 µm filter (Supor, Pall Life Sciences). The presence of bacteriophage in PTFs was directly determined by spotting 10 µl of a 10-fold dilution series on overlays of a panel of *X. fastidiosa* and *Xanthomonas* species hosts and observing for zone or plaque formation after lawn development (6-7 days for *X. fastidiosa* isolates and 18 h for *Xanthomonas* species isolates). Alternatively, bacteriophage were enriched from the PTFs by adding 1 ml of each filtrate to 20 ml of an actively growing culture of an *X. fastidiosa* isolate (4 day culture; A₆₀₀=0.30) or an A₆₀₀=0.25 (4 h) culture of a *Xanthomonas* species host. After 3-4 days or 24 h of growth for the *X. fastidiosa* or *Xanthomonas* species enrichment, respectively, the cultures were centrifuged (10,000×g, 10 min at 4° C.) and filter sterilized (0.22-µm filter). To determine the presence of bacteriophage in the enriched supernatants, 10 µl of a 10-fold dilution series was spotted on overlays of a panel of *X. fastidiosa* and *Xanthomonas* species hosts and observed for zone or plaque formation. Five-day-old cultures of *X. fastidiosa* isolates grown on PW-MA were used to make host suspensions in PW-M broth (A₆₀₀=0.5), whereas 18-h cultures of *Xanthomonas* species isolates grown on medium TNA were used to make suspensions in TN broth (A₆₀₀=0.5), and used to make overlays. Soft agar overlays used to survey bacterial supernatants for bacteriophage activity were made by mixing 100 µl of the bacterial suspension with 7 ml of molten PW-M or TN soft agar, pouring the mixture on PW-MA or TNA plates, and allowing it to solidify and dry. Spotted overlays showing either plaques or cleared zones formation were further investigated by plating as above, except that the PTF dilutions were directly mixed with individual host indicator suspensions before overlaying. Individual plaques formed on either *X. fastidiosa* or *Xanthomonas* species host overlays were excised, suspended in P-buffer and titered. This procedure was repeated three times to obtain a single plaque isolate. High-titer lysates (1×10¹⁰ PFU/ml) were prepared by harvesting overlays of plates exhibiting confluent lysis with 5 ml of P-buffer, macerating the soft agar overlay, clearing the lysate by centrifugation (10,000×g, 15 min at 4° C.) and filter sterilizing through a 0.22-µm filter. Lysates were stored at 4° C.

Plant extracts were plated to both PW-M and to TNAC for selection of *X. fastidiosa* and to obtain total bacterial counts, respectively. Plant extracts from all plants assayed did not yield any evidence of *X. fastidiosa* isolates. However, the non-selective plating did yield a large variety of bacterial colony types. Representative single colonies of yellow pig-

mented bacteria were picked from plates and streak purified to obtain stocks. The stocks were used to make overlays to which the PTFs were spotted to observe for zone or plaque formation. Bacterial isolates Presidio-4, Jal-4, and EC-12 obtained from extracts of rice seed, jalapeno leaves, and rice tissue, respectively, were all identified as *Xanthomonas* species using fatty acid methyl ester analysis by gas chromatography (GC-FAME) and were used as hosts for evaluation of PTFs. Other Xa strains may be utilized as well, in view of the virulence of one or more disclosed bacteriophage on such strains.

Dilutions of several PTFs produced plaques on isolates XF15, XF53, XF54, XF95, after 5 to 6 days of incubation, indicating that bacteriophage able to form plaques on these hosts were present in the plant tissue. Initial titers observed from extracts ranged from 5×10¹ to 7×10⁵ PFU/gram of tissue. Since all PTFs showed the same pattern of production on XF15, XF53, XF54, and XF95, strain XF15 was used as the host for plaque purification and production. The high titer found in this non-enriched PTF indicates that natural bacterial hosts associated with the plant tissue can serve as host for bacteriophage, which can produce plaques on overlays of *X. fastidiosa*. Serial plating of the PTF yielded individual plaques that were uniform in size. Individual plaques were excised and plaque-purified three times using XF15 as the host to obtain clonal isolates. A culture dish of bacteriophage Xfas302 purified and increased using *Xylella fastidiosa* host strain Temecula (1×10⁹ PFU (Plaque Forming Units/ml)) and titered on *Xanthomonas* species isolate Pres-4 and EC-12 (both of 5×10⁷ CFU (Colony Forming Units/ml)), indicating that Bacteriophage Xfas302 propagated on *X. fastidiosa* strain XF15 (Jones et al., 2007) or *X. fastidiosa* Temecula strain (ATCC 700964) was able to form plaques on *Xanthomonas* species strain Pres-4 and EC12 (EC12 deposited under ATCC Accession Number PTA-13101) providing evidence that bacteriophage propagated on *X. fastidiosa* can adsorb, replicate, and form plaques on *Xanthomonas* strains. Host range studies presented below further substantiate these results.

Phages Xfas101-Xfas105 all produced small clear plaques on XF15 lawns, whereas phages Xfas301-Xfas305, produced large clear plaques on the same host. TEM images of Xfas 302-Xfas305 and Xfas101-Xfas104 are shown in FIG. 1 and FIG. 2, respectively. High titer lysates produced using XF15 were used to obtain CsCl-purified preparations of each bacteriophage, which were used to conduct transmission electron microscopy (TEM) studies. Phages Xfas101-Xfas105 all exhibited long non-contractile tails with capsids ranging from 55-64 nm in diameter, and thus were determined to belong to the Siphoviridae family. Xfas301-Xfas305 all exhibited short non-contractile tails with capsids ranging from 58-65 nm in diameter, morphology typical of Podoviridae.

Example 4

Enrichment of Bacteriophage from Wastewater

Clarified wastewater samples were obtained from treatment facilities in the Bryan, Tex. area. Samples were obtained from the Still Creek, Carter Creek, Turkey Creek, and Burton Creek facilities (Brazos County, Texas). Samples were centrifuged (10,000×g, 10 min at 4° C.) twice and the tissue extracts were filtered through a 0.22-µm filter. Phages were enriched by adding 1 ml of each filtrate to 20 ml of an actively growing culture of selected hosts as described above. After 72 and 24 h of growth for the *X. fastidiosa* or

Xanthomonas species enrichment, respectively, the cultures were centrifuged and filter sterilized. The enriched filtrates were spotted to titer on overlays as described above.

Phages Xfas106-109 and Xfas306 were isolated from individually enriched samples obtained from the four wastewater treatment plants using host EC-12 as the host. TEM studies of purified bacteriophage concentrates morphologically identified bacteriophage Xfas306 as Podoviridae by a short non-contractile tail with a capsid of 68 nm in diameter (FIG. 3), whereas phages Xfas106-109 isolated exhibited long non-contractile tails with capsids of ~77 nm in diameter (FIG. 3) characteristic of Siphoviridae. Bacteriophage Xfas306 produced large clear plaques on both hosts EC-12 and XF15, whereas phages Xfas106-109 produced small clear plaques on the same hosts (FIG. 3). Therefore, the method used in this experiment enabled isolation of *X. fastidiosa* bacteriophage from environmental samples.

Example 5

CsCl-Purification

Filter-sterilized bacteriophage suspensions were concentrated by centrifugation (90,000×g for 2.5 h at 5° C.) using a Type 60Ti rotor in a Beckman L8-70M ultracentrifuge. Pellets were resuspended in P-buffer and treated with DNase I and RNase A (Sigma) at a final concentration of 1 µg/ml at 25° C. for 2 h. CsCl was added to the bacteriophage suspension at a final concentration of 0.75 g/ml and centrifuged (300,000×g for 18 h at 5° C.) in a VTi 65.2 rotor. The visible bacteriophage band was extracted using an 18-gauge syringe needle and dialyzed against P-buffer amended to 1 M NaCl overnight at 4° C. and twice for 4 h at 25° C. against P-buffer to obtain a suspension of 1×10¹¹ PFU/ml. The CsCl-purified bacteriophage was stored at 4° C.

Example 6

Transmission Electron Microscopy

Electron microscopy of CsCl-purified bacteriophage (1×10¹¹ PFU/ml) was performed by diluting with P-buffer and applying 5 µl onto a freshly glow-discharged formvar-carbon coated grid for 1 min. Grids were then washed briefly on de-ionized water drops and stained with 2% (w/v) aqueous uranyl acetate. Specimens were observed on a JEOL 1200EX transmission electron microscope operating at an acceleration voltage of 100 KV.

Example 7

Efficiency of Plating and Host Range

The efficiency of plating (EOP) was obtained by calculating the ratio of the bacteriophage plaque titer obtained with the heterologous (non-propagating) host to that obtained on the homologous (propagating) host. Bacteriophage stocks were titered on either *X. fastidiosa* or *Xanthomonas* species host using the appropriate medium by mixing 100 µl bacteriophage stock dilutions with individual host indicator suspensions ($A_{600}=0.5$) in soft agar (7 ml) before overlaying on solid medium.

Studies comparing the EOP of Xfas phages are shown in Table 1. The EOP for phages isolated from plant samples propagated using *Xanthomonas* species strain EC-12 and then titered using *X. fastidiosa* strain XF15 as the host, ranged from 1×10⁻¹ to 1×10⁻³, with similar results seen

when bacteriophage propagated using strain XF15 were then titered using EC-12 as the host. Similar studies with phages isolated from wastewater filtrates and propagated on strain EC-12 exhibited EOPs ranging from 1×10⁻¹ to 5×10⁻¹. EOPs of 1×10⁻¹ to 3×10⁻¹ were obtained when phages Xfas106-109 were propagated on strain XF15 and plated on host EC-12, indicating that, while DNA restriction and modification barriers may exist, phages propagated in fast-growing strain EC-12, in one day, can adsorb, replicate and form plaques on *X. fastidiosa*, a process which can take up to 10 days on *X. fastidiosa* alone.

TABLE 1

Efficiency of Plating for Xfas Phages Propagated on <i>X. fastidiosa</i> or <i>Xanthomonas</i> species hosts			
Bacteriophage Designation	Propagated → Plated XF15 → EC-12	Propagated → Plated EC-12 → XF15	
Xfas101	3.00E-02	5.00E-02	
Xfas102	3.33E-02	5.00E-02	
Xfas103	1.00E-02	3.33E-03	
Xfas104	4.00E-01	5.00E-02	
Xfas105	1.00E-01	1.00E-01	
Xfas106	1.00E-01	2.50E-01	
Xfas301	5.00E-03	1.00E-02	
Xfas302	1.00E-01	5.00E-04	
Xfas303	2.67E-03	1.00E-03	
Xfas304	1.00E-02	5.00E-03	
Xfas305	1.00E-02	5.00E-02	
Xfas306	3.33E-01	3.00E-01	

Lawns of the host were made by overlaying plates of the appropriate medium, PW-M (for XF15) or TNA (for EC-12) with the homologous soft agar seed with individual host. High titer lysates (1×10⁹ PFU/ml) of individual bacteriophage preparations were then spot titered on to the individual lawns by spotting 10 µl of a 10-fold dilution series on overlays of the *X. fastidiosa* or *Xanthomonas* species hosts. After incubation of plates at 28° C. for the appropriate times, (24 h for EC-12 or 5-7 days for XF15) plates were evaluated for zones and plaque formation.

Initial host range studies shown in Table 2 indicate that all phages which were able to form plaques on *X. fastidiosa* host XF15 also formed plaques on host EC-12, whereas hosts Jal-4 and Pres 4 exhibited insensitivity to most of the siphophages. Reasons for resistance range from lack of adsorption or other post adsorption mechanism such as bacteriophage-genome uptake blocks, superinfection immunity, restriction modification, and clustered regularly interspaced short palindromic repeats (CRISPRs).

TABLE 2

Host Range of Xfas phages*						
Phages	Temecula (XF15)	Hosts EC-12	Jal 4-1	Pres 4	Ann1 (XF108)	Dixon (XF102)
Xfas101	S	S	S	R	S	S
Xfas102	S	S	S	R	S	S
Xfas103	S	S	R	R	S	S
Xfas104	S	S	R	R	S	S
Xfas105	S	S	S	R	S	S
Xfas106	S	S	R	R	S	S
Xfas107	S	S	R	R	S	S
Xfas108	S	S	R	R	S	S
Xfas109	S	S	R	R	S	S
Xfas301	S	S	R	R	S	S
Xfas302	S	S	S	S	S	S
Xfas303	S	S	S	S	S	S
Xfas304	S	S	S	S	S	S

TABLE 2-continued

Host Range of Xfas phages*						
Phages	Temecula (XF15)	Hosts EC-12	Jal 4-1	Pres 4	Ann1 (XF108)	Dixon (XF102)
Xfas305	S	S	S	S	S	S
Xfas306	S	S	R	R	S	S

*EC-12 host for propagation of phage used in testing.
S = ability to form clear plaques on indicated host;
R = not able to form plaques on indicated host.

Example 8

Preliminary Identification of Xfas Adsorption Sites

Based on the observation that *X. fastidiosa* phages obtained or enriched from either plant tissue or wastewater samples formed plaques on *X. fastidiosa* it was of interest to determine if cell surface components could serve as adsorption sites. Known adsorption sites for phages include surface proteins such as OmpA and OmpF, the core and O-chain of the bacterial LPS in Gram-negative bacteria, sex and type IV pili, and flagella. The wild type and a derivative mutant with a deletion of the pilA, resulting in a derivative devoid of type IV pili, were evaluated as hosts for Xfas phages. All bacteriophages tested formed plaques on the XF15 wild type strain but not the XF15ΔpilA mutant. Results suggested that type IV pili may be a primary site of attachment for Xfas phages.

Based on results obtained with XF15-ΔpilA it was of interest to determine if pilA deletion mutants of *Xanthomonas* species strain EC-12 would become insensitive to Xfas phages Xfas103, Xfas106 Xfas302, Xfas303 Xfas304 and Xfas306. Strain EC-12Δ pilA was insensitive to the phages in plate titer assays, and in an adsorption experiment with phage Xfas303 no adsorption to the host was observed. The EC-12ΔpilA-complemented in trans for the pilA was sensitive to all tested phages. This further demonstrated that type IV pili are a primary site of attachment for phages as observed for *X. fastidiosa*.

Example 9

Bacteriophage DNA Isolation and Genome Sequencing

Bacteriophage genomic DNA was prepared from 10-20 ml of filter-sterilized, high-titer (>1×10⁹ PFU/ml) CsCl-purified bacteriophage lysates using a modified form of the Promega Wizard DNA clean-up kit (Promega). Briefly, 10-20 ml of bacteriophage lysate was digested with 10 μg/ml each of DNase I and RNase A (Sigma) at 37° C. for 30 min and precipitated in the presence of 10% (w/v) polyethylene glycol 8000 and 1 M NaCl for 16-20 h at 4° C. The

precipitate was centrifuged at 10,000×g, 4° C. for 10 min and the pellet resuspended in 0.5 ml of P-buffer. One ml of the DNA purification resin supplied with the Wizard kit was added to the resuspended bacteriophage, loaded onto a minicolumn and washed with 2 ml of 80% (v/v) isopropanol. DNA was eluted from the resin by addition of 100 μl of water pre-heated to 80° C. followed immediately by centrifugation of the minicolumn. DNA integrity was verified by running on a 0.8% agarose gel and staining with ethidium bromide and DNA was quantified by band densitometry. Bacteriophage genome size was estimated by pulsed-field gel electrophoresis (PFGE) analysis of genomic DNA on a 1% agarose gel (Pulsed-Field agarose, BioRad) and comparison to a size marker (MidRange Marker I, NEB).

Phages were sequenced using “454” pyrosequencing (Roche/454 Life Sciences, Branford, Conn., USA, at Emory GRA Genomics Core: Emory Univ., Atlanta, Ga.). Bacteriophage genomic DNA was prepared from bacteriophage isolates as described above and mixed in equimolar amounts to a final concentration of ca. 100 ng/μl. The pooled DNA was sheared, ligated with a multiplex identifier (MID) tag specific for each of the four pools and sequenced by pyrosequencing using a full-plate reaction on a Roche FLX Titanium sequencer according to the manufacturer’s protocols. The pooled bacteriophage DNA was present in two sequencing reactions. The reaction contained genomic DNA representing 39 genomic elements totaling ca. 3,331 kb of genomic sequence, and the sequencing run yielded 987,815 reads with an average length of 405 bp, providing a total of 120-fold coverage for the entire pool. The trimmed FLX Titanium flowgram outputs corresponding to each of the four pools were assembled individually using the Newbler assembler version 2.5.3 (454 Life Sciences) by adjusting settings to include only reads containing a single MID identifier per assembly. The identity of individual contigs was determined by PCR using primers generated against contig sequences and individual bacteriophage genomic DNA preparations as template; the generation of the expected size product from a bacteriophage DNA template was used to match individual phages to their contigs. Sequencher (Gene Codes Corporation) was used for sequence assembly and editing. Protein coding regions were predicted using Genemark (opal.biology.gatech.edu/Genemark/gmhmm2_prok.cgi) and manually edited in Artemis (www.sanger.ac.uk/Software/Artemis/) (Lukashin et al., *Nucleic Acids Research* 26(4):1107-1115, 1998; Rutherford et al., *Bioinformatics* 16(10):944-945, 2000). DotPlots were generated using DOTTER (Brodie et al., *Bioinformatics* 20(2): 279-281, 2004). Predicted proteins were compared to proteins in the GenBank database using BLAST (www.ncbi.nlm.nih.gov/blast/Blast.cgi). Conserved domains, lipoprotein processing signals and transmembrane domains (TMDs) were identified with InterProScan (www.ebi.ac.uk/Tools/webservices/services/interproscan), LipoP (www.cbs.dtu.dk/services/LipoP/), and TMHMM (www.cbs.dtu.dk/services/TMHMM/), respectively.

TABLE 3

Genomic size of Xfas Phages.						
Family of Morphology	Phage	SEQ ID	ATCC Accession Numbers	Genomic Size (bp)	Identity (bp)	Dice score (% identity over entire genome of Xfas103)
Xfas100 Types	Xfas101	11		56, 132	56, 144	100.01
	Xfas102	12		56, 132	56, 144	100.01

TABLE 3-continued

Genomic size of Xfas Phages.							
		Xfas103	13	PTA-13096	56, 147	56, 147	100.00
		Xfas104	14		56, 144	56, 144	100.00
		Xfas105	15		56, 144	56, 144	100.00
		Xfas106	16	PTA-13095	55, 601	31, 026	55.53
		Xfas107	17				
		Xfas110	18		56, 134	56, 144	100.01
	Family of Morphology	Phage	SEQ ID	ATCC Accession Numbers	Genomic Size (bp)	Identity (bp)	Dice score (% identity over entire genome of Xfas303)
Xfas300 Types	Podoviridae	Xfas301	19		44, 443	33, 254	75.25
		Xfas302	20	PTA-13098	44, 521	33, 347	75.39
		Xfas303	21	PTA13099	43, 940	43, 940	100.00
		Xfas304	22	PTA-13100	43, 869	1, 933	4.40
		Xfas305	23		43, 324	43, 940	100.71
		Xfas306	24	PTA-13097	43, 745	32, 886	75.01

Dice Score = $((2 \times \text{identity}) / (\text{Sequence length of both phages})) \times 100$

Example 10

Genomic Analysis of Xfas Phages and Description of the Xfas100 and Xfas300 Phage Types

The phages isolated for their ability to attack *Xanthomonas* EC-12 and *X. fastidiosa* and subspecies that all require the type IV pili for infection and are all virulent, in that no lysogenic colonies can be isolated from infections and no genes associated with temperate life style (repressor, integrase) are found in the genome sequences. The phages can be further classified in two phage types, as defined by Casjens et al. (*Research in Microbiology*, 159:340-348, 2008).

(1) Xfas100 phage type: The Xfas100 phage type is comprised of virulent Siphophages (ICTV Siphoviridae) of *Xanthomonas* and *Xylella*, the prototypes of which are the phages Xfas101, Xfas102, Xfas103, Xfas104, Xfas105, Xfas106, Xfas107, Xfas108, Xfas109, and Xfas110 (Table 12) and further examples of which are listed in Table 3 as any phage designated "Xfas1nn," where n is any number (referred to as the Xfas 100 series). This flexible nomenclature system is necessary because it is anticipated that further variants of the Xfas1nn phage type will be isolated. Xfas100-type phages are siphophages, are virulent in life-style, and require the type IV pili for infection of *Xylella* and *Xanthomonas* species. Xfas100-type phages have icosahedral capsid heads measuring approximately 55-77 nm in diameter and flexible tails of approximately 200-262 nm in length; both dimensional values are as determined within the standard precision of negative-stain electron microscopy (see FIGS. 2 and 3). The Xfas100 series viral DNA has cohesive (cos) ends characterized by single-stranded DNA overhangs (Casjens, et al., *Methods Mol Biol* 502:91-111, 2009), which is important for phages to be used in antibacterial applications because cos DNA packaging avoids the generation of generalized transducing particles that would potentiate the transfer of pathogenesis determinants. The Xfas100 genome has a characteristic overall organization (see FIG. 4) with the genes arrayed in two divergent gene clusters, A_L and A_R and B_L and B_R . The Xfas100 phage type is further distinguished by the fact that the essential structural and lysis genes of the phage are grouped in rightward gene cluster B_L . The Xfas100 series phage type is also distinguished by encoding its own single-molecule DNA polymerase (Xfas103gp71 and Xfas106gp66), primase

(Xfas103gp76 and Xfas106gp71) and helicase (Xfas103gp69 and Xfas106gp64).

(2) Xfas300 phage type: The Xfas300 phage type is comprised of virulent podophages (ICTV Podoviridae) of *Xanthomonas* and *Xylella*, the prototypes of which are the phages Xfas301, Xfas302, Xfas303, Xfas304, Xfas305, and Xfas306, and further examples of which are listed in Table 3, and refers to any phage with the designation "Xfas3nn" where n is any number (referred as Xfas300 series). This flexible nomenclature system is necessary because it is anticipated that further variants of the Xfas300 phage type will be isolated. Xfas300-type phages have icosahedral capsid heads measuring approximately 58-68 nm in diameter; this dimensional value is as determined within the standard precision of negative-stain electron microscopy (see FIGS. 1 and 3). The Xfas302-306 genome encodes a single-subunit RNA polymerase located adjacent to the structural protein region. The Xfas300 series genome has a characteristic overall organization (see FIG. 5) with the genes arrayed on one strand, including the replication, structural and lysis genes of the phage. The Xfas300 phage type is also distinguished by encoding its own single-molecule DNA polymerase (Xfas302gp18, Xfas303gp17, Xfas304gp17 and Xfas306gp17), single-subunit RNA polymerase (Xfas302gp31, Xfas303gp28, Xfas304gp27 and Xfas306gp30, respectively and helicase (Xfas302gp15, Xfas303gp14, Xfas304gp15 and Xfas306gp14 (see FIG. 5 for schematic of phage genome).

Example 11

Movement, Challenged and Protection Studies in Grapevines Using Bacteriophage Xfas304

Bacteriophage Xfas304, is a member of the family Podoviridae, isolated from environmental samples that has a host range that includes both *X. fastidiosa* and *Xanthomonas* species. In the studies presented here, the movement and persistence of Xfas304 was determined in grapevines in the absence of a sensitive host, in order to determine whether treatment of a plant with bacteriophage may prevent subsequent infection by *X. fastidiosa*. Additionally, grapevines that were first inoculated with *X. fastidiosa* were then challenged 4 weeks post-pathogen-inoculation with bacte-

riophage Xfas304, to determine if the bacteriophage could control the development of Pierce's Disease therapeutically.

For the preventative studies, grapevines were inoculated with 40 μ l of a bacteriophage Xfas304 suspension (1×10^{10} PFU/ml) and then challenged 4 weeks post-bacteriophage-inoculation with *X. fastidiosa*. Bacterial *X. fastidiosa* sus-
 5 pensions used for inoculation were adjusted spectrophotometrically ($A_{600}=0.4$; 1×10^9 CFU/ml). Individual cordons were inoculated between the second and third node on opposite sites (two points/cordon) with 40 μ l of the bacterial suspension using the needle inoculation technique as described by Hopkins (*Plant Dis.* 89:1348-1352, 2005). Control vines were mock inoculated with phosphate buffer at the same point of inoculation of the above.

The results indicated that bacteriophage Xfas304 can be used to treat and prevent Pierce's Disease caused by *X. fastidiosa* subspecies *fastidiosa* in grapevines. Thus, bacteriophage Xfas304 and other virulent *Xylella-Xanthomonas* phages identified from these studies have potential use in the protection and treatment of plants against diseases caused by other *X. fastidiosa* subspecies and *Xanthomonas* species.

Bacteria used in the study included *X. fastidiosa* strains Temecula (XF15) and XF54, associated with Pierce's Disease of grapevines in California and in Texas, respectively. Cultures of *X. fastidiosa* were maintained on PW-M agar medium (Summer et al., *J Bacteriol* 192(1): 179-190, 2010) at 28° C. for 5-7 days. Five-day-old cultures of the *X. fastidiosa* isolates grown on PW-MA were used to make bacterial suspensions in phosphate buffer (0.125 M, pH 7.1) for vine inoculations.

Dormant *V. vinifera* cv. Cabernet Sauvignon clone 08 on 1103P rootstock were purchased from Vintage Nurseries (Wasco, Calif., USA). Vines were planted in 7-gallon pots using 101 Sunshine Mix 1 (Sun Gro Horticulture, Vancouver, British Columbia, Canada). Plants were grown in a greenhouse on a 16-h light (26° C., 300-400 μ E/m²·s)/8-h dark (18° C.) cycle supplemented with illumination from sodium vapor lamps. Plants were irrigated every other day with tap water. Every 15 days, the vines were fertilized with Peter's General Purpose 20-20-20 fertilizer and micronutrients. Plants were progressively pruned to provide uniform plants as follows: upon producing two unbranched solitary shoots of 100-150 cm, two shoots were pruned to 80 cm. Lateral shoots and buds were removed. Two cordons were staked and allowed to grow until each cordon was ~2.5-2.75 m in length before vines were used for the above-experiments.

Standard qRT-PCR line plots were obtained for *X. fastidiosa* strains XF15 and XF54, as well as for bacteriophage Xfas304, all of which had R² values of greater than 0.9 and efficiencies of 157%, 130%, and 123%, respectively. Quantitative assessment of duplicate cordons from triplicate samples of XF15 and XF54 showed distribution of the pathogens throughout all segments assayed, with typical Pierce's Disease (PD) symptoms visible, such as leaves become slightly yellow or red along margins, respectively, and eventually leaf margins dry or die in its zones by week 8 post-inoculation (FIG. 6). In vines inoculated with bacteriophage Xfas304, in the absence of a permissive host, a progression in the distribution of bacteriophage at weeks at 2, 4, and 6 weeks post-inoculation was observed, with a decline between weeks 8-12 and no vine symptoms.

Example 12

Grapevine Inoculation with Bacteria and Bacteriophage

For therapeutic evaluation of bacteriophage treatment, 15 vines (two cordons each) were inoculated with *X. fastidiosa*

strains XF15 or XF54. Bacterial suspensions used for inoculation were adjusted spectrophotometrically ($A_{600}=0.4$; 1×10^9 CFU/ml). Average of qRT-PCR results from three segments (e.g. 1/1a, 1/1b, 1/1c) with similar locations from triplicate vines was used to determine the CFU/gram plant tissue (gpt) and PFU/gpt. Individual cordons were inoculated between the second and third node on opposite sites (two points/cordon) with 40 μ l of the bacterial suspension using the needle inoculation technique as described by Hopkins (*Plant Dis.* 89:1348-1352, 2005). Control vines were mock inoculated with phosphate buffer following the same protocol. Four week post-inoculation with the patho-
 10 gen, the 15 vines from each treatment were challenged with 40 μ l of a bacteriophage Xfas304 suspension (1×10^{10} PFU/ml) using the same inoculation protocol and technique. Vines were scored for symptom development twice weekly for 12 weeks and assayed in triplicate for *X. fastidiosa* and bacteriophage at the time of inoculation, and at 8, 10, and 12 weeks, as described below. To determine if bacteriophage could act in a preventative manner, nine vines (two cordons each) were inoculated with 40 μ l bacteriophage Xfas304 using the same inoculation protocol and inoculation technique as the above. At four weeks post-bacteriophage inoculation, the vines were challenged with 40 μ l ($A_{600}=0.4$; 1×10^9 CFU/ml) of strain XF15 using the same inoculation protocols as the above.

To evaluate the bacterial and bacteriophage movement in the grapevine, 15 vines each were inoculated with either XF15 or XF54 and 24 vines were inoculated with only bacteriophage Xfas304 using the same inoculation protocols as the above. Vines inoculated with XF15 or XF54 were assayed in triplicate immediately after inoculation and at weeks 8, 10, and 12 post-inoculation. Vines inoculated with bacteriophage were assayed in triplicate immediately after inoculation and every two weeks for 12 weeks. Methods for assay are described below.

To determine how bacteriophage would affect pathogen populations and disease development in vines, *X. fastidiosa* inoculated vines were challenged with bacteriophage Xfas304 at four weeks post-pathogen inoculation. At 8 weeks post inoculation with XF15, vines challenged with Xfas304 at week 4 showed no PD symptoms and the bacterial populations were one to three logs lower in bacteriophage challenged vines as compared to non-challenged vines. The non-bacteriophage challenged plants showed PD symptoms (FIG. 7, column 2), whereas the bacteriophage challenged vines showed no PD symptoms after week 5 (FIG. 7, column 6). During weeks 8 through 12 post-XF15 inoculation (weeks 4 through 8 post-Xfas304 challenge), no PD symptoms were observed in bacteriophage-challenged vines and XF15 populations continued to decline to almost non-detectable levels as compared to non-bacteriophage challenged vines.

A quantitative evaluation of the bacteriophage population in the presence and absence of an introduced host (XF15) indicated that the bacteriophage were able to replicate in sensitive hosts growing in the vines and declined in the absence of a sensitive hosts. Experiments with strain XF54 challenged with Xfas304 at 4 weeks post-pathogen inoculation showed similar results to that observed for XF15 challenged vines. The XF54 population in vine extracts, as measured by CFU/ml of extract, declined from weeks 8 through 12 in bacteriophage challenged vines as compared to that observed in non-bacteriophage-challenged vines. At weeks 8 through 12 post XF54 inoculation (weeks 4 through 8, post-Xfas304 challenge), no PD symptoms were observed in bacteriophage-challenged vines (FIG. 7, column 7). The

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bacteriophage population increased over the post challenge period in the presences of XF54 and decreased in the absence of a host, again indicating that the bacteriophage was able to replicate in sensitive hosts when present in vines. A summary of the challenge study is presented in FIG. 7, showing that in XF15 or XF54 inoculated vines challenged with bacteriophage Xfas304 (week 4 post-pathogen inoculation) no additional PD symptoms were observed after week 5 (FIG. 7, columns 6 and 7), whereas symptom developed through week 9 and 10 in non-bacteriophage challenged vines inoculated with strain XF15 or XF54, respectively (FIG. 7, columns 2 and 3).

Additional studies were conducted with vines inoculated with bacteriophage Xfas304 and then challenged with XF15 at week 4 post-bacteriophage inoculation to determine the protective (prophylactic) potential of the bacteriophage treatment. At weeks 4 and 8 post-challenge with XF15 vines showed no PD symptoms (FIG. 7, column 8), whereas non-phage treated vines developed symptoms (FIG. 7, column 2). The bacteriophage population increased from week 8 to 12 post challenge period in the presences of XF15 and decreased in the absence of a host.

These results confirm that bacteriophage treatment prevents or reduces PD symptoms by *X. fastidiosa* in a plant and that phage treatment causes no adverse effects to a plant.

Example 13

Sample Collection and Processing

Duplicate cordons from each vine were divided into 5-6 segments and segments were numbered from bottom to top. Each segment was homogenized using a PRO250 homogenizer with 20×115 mm generator (PRO Scientific, CT, USA) in 15 ml of P-buffer (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 8 mM MgSO₄), filtered through sterile cheesecloth (Fisher Scientific, USA) to remove plant tissue debris. For assaying bacteriophage, the filtrate was centrifuged (10,000×g for 15 min) and filter sterilized. The filtrate was used for bacteriophage DNA extraction. The same protocol was used for bacterial assays, except the pellet was resuspended into 1 ml of Milli-Q water for bacterial DNA extraction.

Example 14

Propidium Monoazide (PMA) Treatment of Samples

The PMA protocol as described by Nocker (*J Microbiol Meth* 67:310-20, 2006) was used to exclude dead cells of *X. fastidiosa* from assays used to develop standard curves for assays and for assaying of vine tissue extracts. Briefly, PMA (Biotium Inc., Hayward, Calif.) was dissolved in 20% dimethyl sulfoxide (Sigma-Aldrich, Germany) to yield a stock solution of 20 mM and stored in the dark at -20° C. A volume of 1.25 µl of the PMA stock solution was added to 500 µl *X. fastidiosa* cell suspensions ($A_{600}=0.4$; 1×10^9 CFU/ml) or extracts from control and inoculated vines. Preparations were incubated in clear microcentrifuge tubes in the dark for 5 min with repeated inversion. Following incubation, the microcentrifuge tubes were placed on ice and exposed to a 650-W halogen light source (Ushio, USA) at a distance of 20 cm for 1 min. The tubes were swirled briefly by hand every 15 s and inverted after 30 s of illumination to ensure complete cross-linking of the available DNA and the conversion of free PMA to hydroxylamino propidium. After

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photo-induced cross-linking, viable cells were collected by centrifugation at (12000×g for 2 min at 25° C.) and washed with 500 µl sterile distilled water and resuspended Mili-Q water for DNA extraction.

Bacterial DNA was extracted from PMA treated cell preparations and vine extracts using a ZR Fungal/Bacterial DNA Miniprep (Zymo Research, USA) as per the manufacturer's instructions.

Bacteriophage DNA from control preparations and from plant extracts was extracted using Wizard DNA Clean-up system (Promega, WI, USA) with modifications as described by Summer (*Methods Mol. Biol.* 502:27-46, 2009).

Example 15

Detection of *X. fastidiosa* and Bacteriophage Xfas304 Using Real Time-PCR

A SYBR-green based Real Time-PCR (RTPCR) was performed on the 7500 Real-Time PCR System (Applied Biosystems, CA, USA) using the *X. fastidiosa*-specific primers INF2 5'-GTTTGATTGATGAACGTGGTGAG-3' (SEQ ID NO:1) and INR1 5'-CATTGTTTCTTGGTAGG-CATCAG-3' (SEQ ID NO:2) designed for the gyr B (Bextine and Child, *FEMS Microbiology Letters* 276: 48-54, 2007), and bacteriophage Xfas304-specific primers 304-PrimF 5'-AAGAAGCGTGGTTTGTTC-3' (SEQ ID NO:3) and 304-PrimR 5'-CTACCGGCTTCCCTAACTCC-3' (SEQ ID NO:4) designed for the DNA primase gene. A master mix was made using 10 µl of Express SYBR GreenER SuperMix (Invitrogen), 0.4 µl of both primers (at a concentration of 10 µM), 8.56 µl of sterile molecular grade water, 0.04 µl of ROX reference dye (Invitrogen), and 1 µl DNA template per reaction. Standardized conditions were used for all reactions with an initial denaturing step of 3 min at 95° C., followed by 40 cycles of the following parameters: 95° C. for 30 s, 55° C. for 30 s, and 72° C. for 30 s. At the end of the PCR, the temperature was increased from 72 to 99° C. at a rate of 0.5° C./10 s, and the fluorescence was measured every 10 s. Each DNA sample was analyzed in triplicate. As a positive control, DNA was extracted from *X. fastidiosa* cells and from bacteriophage Xfas304 lysates using methods described the above. Cycle threshold (Ct) values, describing the PCR cycle number at which fluorescence rises above the base line, were determined using the software package provided by the Applied Biosystems.

To determine the Standard curve for absolute quantification, 1-ml volumes of XF15 and XF54 cell suspensions of 1×10^8 CFU/ml were treated using the PMA protocol. Bacterial DNA was extracted as described above, serially diluted from 1×10^{-1} to 1×10^{-5} and subjected to the real-time PCR assay described above. Similarly, bacteriophage DNA was extracted from 1 ml volume of 1×10^9 PFU/ml bacteriophage Xfas304 as described above, diluted from 1×10^{-1} to 1×10^{-6} and subjected to the real-time PCR assay. Three replicates of each sample for *X. fastidiosa* and bacteriophage Xfas304 were used to produce the standard curves. Standard curves were constructed by plotting Ct values generated from real-time PCR against *X. fastidiosa* DNA concentrations (Log DNA conc./µl as determined by A_{260}). The efficiency (E) was calculated as follows: $E=10^{(-1/slope)}-1$ (Klein et al., *Electrophoresis* 20:291-299, 1999).

Example 16

Lysogen Formation Assay Studies

To assay for phage lysogen-formation, survivors of phage infection were tested for the presence of prophages. For each

phage, bacteria were infected with at an input MOI of ~3 and plated in a soft agar overlay. Plates were monitored for colony growth (10-15 days for *X. fastidiosa* strain Temecula and 2-3 days for *Xanthomonas* strain EC-12). Individual colonies that emerged were picked, purified (three times) and re-tested for phage sensitivity by spotting dilutions of the same phage in a soft agar overlay. Primer pairs specific to the Xfas 103 and Xfas 106 helicase gene, or Xfas 303 and Xfas 304 primase gene (Table 5) were then used to test for the presence of prophage sequences in the phage-insensitive isolates. Wild type bacterial DNA was used as negative control and wild type bacterial DNA spiked with phage DNA served as positive controls.

To test whether evidence could be found for abortive lysogeny (i.e., the establishment of repression), the procedure of Gill et. al (Gill J. J., et al., *J. Bacteriol.*, 193:5300-5313 (2011)) was followed, except reversibly bound phage were removed by three successive washes. Liquid cultures of logarithmically growing *Xanthomonas* strain EC-12 were cultured to an OD600 of ~0.3-0.5. One ml aliquots were pelleted by centrifugation and resuspended in 0.20 ml of phage lysate (harvested in TNB) or sterile TNB. After a 30 min incubation at 25° C. cell-phage mixtures were centrifuged and the supernatant removed and titered to determine adsorbed phage. In preliminary experiments it was determined that phage were reversibly bound, which affected the MOI_{actual} calculation (Kasman, L. M., et al., *J. Virol.*, 76:5557-5564 (2002)). To circumvent this problem and to obtain an accurate MOI_{actual}, cells were resuspended in sterile TNB, allowed to incubate for 5 min at 25° C., centrifuged and supernatants removed. This procedure was repeated three times to remove unbound phage. Each supernatant was titered to determine PFU. Cell pellets were resuspended in 0.20 ml of sterile TNB, serially diluted and plated to enumerate the bacterial survivors remaining following phage exposure. From these data, the MOI_{actual}, i.e., the ratio of the number of adsorbed phage to the number of CFU in the phage-free controls) was calculated. These MOI_{actual} values were used to calculate the predicted proportion of uninfected cells using the Poisson distribution. This experiment was replicated three times, using both Xfas 103 and Xfas 303.

Lysogeny

To examine the potential for lysogeny, 40 phage-insensitive isolates of *X. fastidiosa* strain Temecula and *Xanthomonas* strain EC-12 each were recovered following a challenge by phage Xfas 103, Xfas 106, Xfas 303 or Xfas 304. PCR using phage specific primers did not detect the presence of phage lysogens in resistant isolates, indicating resistance was not due to lysogeny. Additionally, the potential for abortive lysogeny was examined using infection at a high MOI and measuring survival (Gill et. al (2011)). As shown in Table 4, following infection, there was no significant difference between predicted and actual survivors, indicating phage infection at a high MOI did not lead to the establishment of repression. Together, these results indicate there is no evidence for lysogeny or repression, supporting the conclusion that the four phages are virulent.

TABLE 4

Predicted bacterial survivors based on MOI _{actual} compared to measured bacterial survivors of <i>Xanthomonas</i> strain EC-12 following exposure to phage Xfas 103 or Xfas 303a.					
	Replicate No.	MOI _{actual}	Predicted % surviving cells	Measured % surviving cells	Fold excess of survivors vs. prediction
Xfas 103	1	6.51	0.15	0.12	0.8
	2	5.57	0.38	0.25	0.65
	3	5.99	0.30	0.24	0.80
Xfas 303	1	5.40	0.45	0.38	0.80
	2	5.39	0.45	0.49	1.08
	3	5.52	0.40	0.37	0.92

a Predicted survivors were calculated from the Poisson distribution for the measured MOI_{actual}. Data shown are from three independent replicate experiments.

Example 17

Phage Cocktail Protection and Prevention Studies

Bacterial Strains, Phages, and Inoculum Preparation:

Bacterial isolates used in the study were *X. fastidiosa* strains Temecula (XF15) and XF54 (see Example 3). Cultures of *X. fastidiosa* were maintained on PW-M as described in Example 1. XF15 and XF54 inocula were prepared as described in Example 11. High-titer phage lysates of Xfas303, Xfas304, Xfas103 and Xfas106 (1×10^{10} PFU/ml) were prepared and titered as described in Example 3. The phage cocktail was prepared by mixing each of the four phages to obtain a final concentration of 1×10^{10} PFU/ml for each phage in the cocktail.

Grapevine Inoculation with Bacteria and Phage Cocktail:

Grapevines were inoculated with either *X. fastidiosa* strain XF15 or XF54 to evaluate bacterial movement in the grapevine. Grapevines were assayed in triplicate immediately after inoculation (0 min) and at 8 and 12 weeks post-inoculation. Additionally, grapevines inoculated with XF15 or XF54 were challenged 3 weeks post-inoculation with the phage cocktail to evaluate therapeutic efficacy. Phage cocktail-inoculated grapevines were challenged at week 3 post-phage inoculation with either XF15 or XF54 to evaluate preventative efficacy of the cocktail. Grapevines from each treatment were scored for symptom development twice weekly. To determine distribution of individual phages comprising the cocktail, grapevines were assayed at weeks 0, 2, 4, 6, 8, 10, and 12 post-inoculation as described below. Grapevines inoculated in either phage or pathogen challenge studies were assayed for phage and/or *X. fastidiosa* infection at weeks 0, 6, 8, 10, and 12 as described below. Control grapevines were assayed at 0, 8, and 12 weeks post inoculation to monitor pathogen distribution and disease development. All grapevine assays were conducted in triplicate with vines containing two cordons. Each cordon (e.g. Cordon1=S1, or Cordon2=S2) was divided into 5-6 (5 inch) segments. Vine segments were numbered from point of inoculation (0) and numbered as below (–) or above (+) the point of inoculation in 5 inch segments. The root portion was divided into three segments: R1, R2, or R3.

Sample Collection and Processing:

For quantification of cocktail phages and pathogens, samples were obtained as described in Example 13. For assaying of phages, the filtrate was centrifuged ($10,000 \times g$ at 4° C. for 15 min) and filter sterilized. The filtrate was used for phage DNA extraction to accomplish quantitative real-time PCR (qRT-PCR) (See below). The same protocol was

used for bacterial assays except the pellet was resuspended into 1 ml of Milli-Q water for isolation of bacterial DNA used in qRTPCR. Average of qRTPCR results from three segments (e.g. 0a,0b,0c) with similar locations from tripli-
cate vines was used to determine the CFU and PFU. To
determine if phage-resistant *X. fastidiosa* would develop as
a result of phage challenge experiments, samples collected
from grapevines at week 12 post-pathogen inoculation were
processed as described in Example 13. Briefly, 100 µl of a
suspension of the pellet in 1 ml Milli-Q was plated on
PW-MA (Example 1) supplemented with 40 µg/ml cyclo-
heximide (PW-MAC) and incubated at 28° C. After 10-12
days, individual colonies were picked and streak-purified 3
times on PW-MAC. Representative individual colonies (20
colonies total) from each grapevine sample were confirmed
at the species and subspecies level using PCR analysis as
described by Hernandez-Martinez et al. (Example 1). Phage
sensitivity of confirmed isolates was determined by the
serial dilution spot assay on overlays and soft agar overlay
method as described in Example 3.

PMA Treatment and qRTPCR:

PMA treatment and SYBR-green based qRTPCR proto-
cols were conducted as described in Example 15 using *X.*
fastidiosa-specific primers INF2 (SEQ ID NO:1) and INR1
(SEQ ID NO:2) and bacteriophage-Xfas303 specific primers
303-PrimF (SEQ ID NO:5) and 303-PrimR (SEQ ID NO:6),
Xfas304 specific primers 304-PrimF (SEQ ID NO:3) and
304-PrimR (SEQ ID NO:4), Xfas103-specific primers 103-
HelF (SEQ ID NO:7) and 103-HelR (SEQ ID NO:8); and
Xfas106-specific primers 106-HelF (SEQ ID NO:9), and
106-HelR (SEQ ID NO:10) listed in Table 5.

TABLE 5

Primers used for qRT PCR (SEQ ID NOs. 1-10) .			
Primer Set	Sequence	Specific organism and gene	Reference
INF2	GTTTGATTGATGAACGTGGTGAG	<i>Xyella fastidiosa</i> , B extine and gyr B	Child, 2007
INR1	CATTGTTTCTTGGTAGGCATCAG		
303-PrimF	AACTACCTGACAGCGACT	Xfas303, primase	This work
303-PrimR	CGTACTAGCTTGGCTTCTA		
304-PrimF	AAGAAGCGTGGTTTGTTC	Xfas304, primase	This work
304-PrimR	CTACCGGCTCCCTAACTCCA		
103-HelF	AACCTGATCTGGTACGAC	Xfas103, helicase	This work
103-HelR	GGACATTTTTCAGTTCTCTC		
106-HelF	CAACCTCATCTGGTATGAC	Xfas106, helicase	This work
106-HelR	GTCTTGGGTAATTCTTTCT		

*All PCR reactions were conducted for 40 cycles with denaturation at 95° C. for 30 sec, annealing at 55° C. for 30 sec and extension at 72° C. for 30 sec.

Movement of *X. fastidiosa* and Disease Development in Grapevines:

Quantitative assessment of duplicate cordons from tripli-
cate samples of XF15 or XF54 inoculated grapevines
showed pathogen distribution in grapevine segments
assayed. qRTPCR detected the presence of an average of
1×10⁴ and 1×10⁵ CFU/gm of plant tissue (gpt) of XF15 in
segment (Seg) S1/1 (cordon 1, 5 inch segment 1 above the
point of inoculation) and S2/1 respectively, and an average
of 1×10⁴ CFU/gpt of XF54 in S1/2 and S2/2 at week 8-post
inoculation. Typical Pierce's Disease symptoms were vis-
ible, such as leaves becoming slightly yellow or red along
margins, and leaf margins dried or necrotic by week 8,
post-inoculation in non-cocktail challenge grapevines. At

week 12 post-inoculation, an average of 1×10⁴ and 1×10⁶
CFU/gpt of XF15 was detected in S1/3 and S2/2, respec-
tively. At the same assay interval, an average of 1×10⁵ and
1×10⁴ CFU/gpt of XF54 was detected in S1/3 and S2/1,
respectively, at week 12 post inoculation, with grapevines
exhibiting PD symptoms. Both pathogens (XF15 and XF54)
were detected in the root system of grapevines at weeks 8
and 12 post pathogen inoculation at an average of 1×10¹-
1×10² CFU/gpt.

Phage Movement and Persistence in Grapevines:

Standard qRTPCR line plots were obtained for phage
Xfas303, Xfas304, Xfas103, and Xfas106 that had R2
values of greater than 0.9 and efficiencies of 127%, 123%,
129%, and 120%, respectively. Quantitative assessment of
duplicate cordons from triplicate samples of grapevines
inoculated with phage cocktail (Xfas303, Xfas304, Xfas103,
and Xfas106) showed distribution of all phages individually
within grapevine segments assayed at weeks 2-8 post-
cocktail inoculation (FIG. 8). By weeks 8 and 12, individual
phages were no longer detectable in roots and had declined
to an average of 1×10¹-1×10² PFU/gpt by week 12 in
segments assayed with no grapevine symptoms observed
(FIG. 8).

Therapeutic Efficacy of Phage Against *X. fastidiosa* in Grapevines:

Grapevines inoculated with XF15 were challenged with
the phage cocktail at three weeks post pathogen inoculation.
At 8 weeks (5 weeks post cocktail challenge), the XF15
population was an average of 2-3 logs higher in non-
challenged grapevines compared to challenged grapevines.
Non-therapeutically treated grapevines showed typical PD

symptoms, whereas challenged grapevines did not. At week
12 post-XF15 inoculation (9 weeks post-cocktail challenge),
bacterial populations were an average of 2-3 logs higher in
non-challenged grapevines when compared to phage cock-
tail challenged grapevines (FIG. 9). PD symptoms were not
observed in phage challenged grapevines throughout the
trial (12 weeks), whereas non-cocktail treated grapevines
exhibited symptoms as early as 4 weeks, which progressed
through week 12. Similarly, the bacterial population in
grapevines challenged with XF54-inoculated cocktail
declined significantly from weeks 8 through 12 compared to
non-challenged grapevines, with no symptoms observed in
cocktail-challenged grapevines. Plating of plant extracts
from 12-week cocktail-challenged grapevines yielded an

average of 1×10^2 CFU/gpt. Representative isolates (20 ea) confirmed as *X. fastidiosa* from each cordon of each of three grapevines were all sensitive to the four phages that composed the cocktail.

Prophylactic Efficacy of Cocktail Treatment for the Prevention of PD in Grapevines:

Prophylactic efficacy of the phage cocktail was evaluated by first inoculating grapevines with the cocktail and then challenging with *X. fastidiosa* strain XF15 or XF54 at week 3 post-cocktail inoculation. Grapevines treated prophylactically showed no PD symptoms at weeks 8 and 12 post-cocktail inoculation. In cocktail-inoculated grapevines that were challenged with XF15, pathogen populations reached a maximum of an average of 1×10^3 CFU/gpt in the segments of the grapevines examined at weeks 8 and 12, and as high as an average of 1×10^6 CFU/gpt in non-prophylactically treated grapevines. Similar results were observed in grapevines treated prophylactically with cocktail and then challenged with XF54 at week 3 post phage cocktail inoculation. Plating of plant extracts from 12-week cocktail challenged-grapevines yielded an average of 3×10^2 CFU/gpt. Representative isolates (20 ea) confirmed as *X. fastidiosa* from each cordon from each of three grapevines were all sensitive to the four phages that composed the cocktail.

Persistence and Replication of Phages in Grapevines:

It was of interest to determine phage populations in grapevines in the presence or absence of introduced hosts (XF15 and XF54). Quantitation of phage populations in the presence or absence of hosts confirmed that the cocktail phages were able to replicate and maintain higher populations if sensitive hosts were present in grapevines and then declined in the absence of a sensitive host in both the therapeutic and prophylactic studies (FIGS. 10 & 11). Phage populations in non-host containing grapevines decreased during weeks 8-12, whereas phage populations increased an average of 1-2 logs during the same period in grapevines inoculated with XF15 or XF54 and challenged (therapeutic treatment) with phage cocktail (FIG. 10). Similar results were obtained in prophylactic study, with phage populations increasing an average of 1-2 logs over that observed in non-host containing grapevines (FIG. 11). These results confirmed that bacteriophage treatment prevents or reduces PD symptoms by *X. fastidiosa* in a plant and demonstrates no adverse effect to a treated plant.

Example 18

Transmission of *X. fastidiosa* by the Glassy-Winged Sharpshooter

The glassy-winged sharpshooter (GWSS), *Homalodisca vitripennis*, is a xylem-feeding leafhopper that transmits *X. fastidiosa* subsp. *fastidiosa* (Xff). The GWSS is prevalent throughout grape growing regions of southern California and Texas. Laboratory-reared Xff-free GWSSs were fed on cowpea (*Vigna unguiculata* subsp. *unguiculata*) plants harboring either *X. fastidiosa* or virulent phage Xfas304 for 48 h in three trials to examine the uptake of Xff or phage by GWSS. To determine the ability of GWSSs to transmit bacteria or phage to plants, GWSSs harboring bacteria or phage were fed on bacteria and phage-free plants. A subset of bacteria harboring GWSSs were challenged by feeding them on plants harboring phage for 48 or 96 h. GWSSs and plants were assayed individually in all experiments to evaluate uptake, transmission or persistence of bacteria and/or phage using qRT-PCR. GWSSs were able to uptake and transfer Xff and/or phage. In GWSSs harboring Xff and

challenged with phage, the titer of phage Xfas304 increased two-fold, as compared to that observed in Xff-free GWSSs. A two-fold decline in bacterial population was observed in GWSSs when challenged with phage Xfas304, as compared to non-challenged. GWSSs transmitted Xff and/or phage to plants.

Bacterial Strains, Phages and Inoculum Preparation:

X. fastidiosa strain XF54 (See Example 1) and phage Xfas304 (See Example 3) were used in this study. Culture of XF54 was grown on PW-M as described in Example 1. Five-day-old culture of XF54 grown on PW-MA was used to make bacterial suspensions in phosphate buffer (0.125 M, pH 7.1). High-titer phage lysate of Xfas304 (1×10^{10} PFU/ml) was prepared and titered as described in Example 3 in sterile deionized water (SDW).

Plant growth conditions and preparation:

Cowpea (*Vigna unguiculata* subsp. *unguiculata*) plants were used as host for GWSSs. Cowpea seeds were planted using 101 Sunshine Mix 1 (Sun Gro Horticulture, Vancouver, British Columbia, Canada). Cowpea were grown in a growth chamber on a 16 h light (26° C., 300-400 μ Em-2 s-1)/8 h dark (18° C.) cycle supplemented with illumination from sodium vapor lamps. Cowpea were watered every other day with tap water and fertilized with Peter's General Purpose 20-20-20 fertilizer and micronutrients every 15 days.

Glassy-winged sharpshooter:

Insects used in experiments were laboratory-reared, young adults (<3 week old), which were initially obtained from the rearing facility at the California Department of Food Agriculture (CDFA) Field Station, Arvin, Calif. The laboratory colony was originally collected mainly from citrus orchards in Ventura County, CA. At the CDFA rearing facility, the laboratory colonies of *H. vitripennis* were reared from egg stage on multiple host plants under greenhouse conditions at $31 \pm 4^\circ$ C., under high-intensity sodium lighting with a photoperiod of 16:8 (L:D) h. The CDFA *H. vitripennis* colonies were maintained on several host plants including cowpea *Vigna unguiculata* [L.] Walp), sunflower (*Helianthus annuus* L.), Japanese euonymus (*Euonymus japonica* Thunb.), and sorghum (*Sorghum bicolor* [L.] Moench). The *H. vitripennis* laboratory colony was replenished by introducing eggs laid by field-collected females as needed. Adult insects were overnight express shipped from Arvin, Calif. to College Station, Tex. in plastic containers containing cowpea and basil placed in Styrofoam shipping containing a frozen cold pack. The GWSSs used in this study were young adults with an approximate sex ratio of 55% males. The GWSSs were housed in the Biological Control Facility, Department of Entomology at Texas A&M University. After receiving, insects were fed on cowpea plants, maintained at 24° C. to 29° C. (16 and 8 h of light and dark, respectively), for two days to allow for adaption to chamber conditions. Prior to use, three GWSSs from each lot were processed to insure the absence of Xff and phage using qRT-PCR. The GWSSs were housed in the Biological Control Facility, Department of Entomology at Texas A&M University. After receiving, insects were fed on cowpea plants, maintained at 24° C. to 29° C. (16 and 8 h of light and dark, respectively), for two days to allow for adaption to chamber conditions. Prior to use, three GWSSs from each lot were processed to insure the absence of Xff and phage using qRT-PCR.

Experimental Design:

Each experimental unit (i.e., cage) contained a 15-cm-long stem of cowpea at the 3-4 leaf stage and a 50 ml flat-bottom tube with a 50-ml suspension of phage or

bacteria in SDW as appropriate. Cowpea stems with attached leaves at the 3-4 leaf stage (cut stem) were collected from two- or three-week-old plants inserted through a hole in the cap and anchored in place with Parafilm (cut stem anchored). GWSSs (3 GWSS/cut stem/cage) were placed in cages and allowed to feed as appropriate.

Uptake of *X. fastidiosa* and Phage by GWSSs:

To determine uptake of *X. fastidiosa* and/or phage by GWSSs, cowpea cut stems with attached leaves were anchored in a tube filled with an Xff (1×10^9 CFU/ml) or phage Xfas304 (1×10^{10} PFU/ml) suspension for 4 h to allow for capillary uptake of Xff or phage. Control cut stems were placed in SDW. After allowing cut stems to uptake the appropriate suspension for 4 h, a subset (3 cut stems) was assayed to quantify *X. fastidiosa* or Xfas304. After the 4-h uptake period, GWSSs (3 GWSSs/cut stem/cage) were allowed to feed on cut stems. Each experimental set was done in triplicate (1 cut stem \times 3 GWSSs \times 3 cages). After 48 h, all cowpea cut stems and GWSSs were assayed to quantify the presence of Xff and/or phage by qRT-PCR. Water uptake controls were conducted for all experiments under the same conditions and assayed for Xff and phage.

Initial experiments were designed to determine if GWSSs could acquire Xff or phage from cut stems that harbored the pathogen or phage, and if so, whether they could transfer the Xff or phage to other cut stems. After 48 h, cut stems and GWSSs harbored an average of $2 \times 10^8 \pm 1 \times 10^8$ CFU/g of plant tissue (gpt) and $1 \times 10^6 \pm 0.7 \times 10^6$ CFU/GWSS, respectively confirming that GWSSs could acquire *X. fastidiosa* as previously reported (Bextine et al., *Biotechniques* 38:184, 186, 2005). In a parallel experiment to determine if phage could be acquired by GWSSs from feeding on cut stems, GWSSs assayed after 48 h harbored an average of $2 \times 10^6 \pm 0.9 \times 10^6$ PFU/GWSS that was acquired from cut stems containing $2 \times 10^8 \pm 1 \times 10^8$ PFU/gpt. The results showed that GWSSs could acquire phage by feeding on cut stems.

Uptake and Transfer of Phage by GWSSs:

To determine phage uptake and transfer by GWSSs, cowpea cut stems (9) were anchored in 50-ml tubes filled with phage Xfas304 suspension (1×10^{10} PFU/ml). Controls (3 cut stems) were placed in SDW. Both sets of cut stems were allowed to uptake respective medium. After 4 h, three of the cut stems allowed to uptake phage were assayed to determine phage concentration. The remaining 6 cut stems were each placed in individual cages with GWSSs (3 GWSSs/cut stem/cage). After 48 h, 9 GWSSs and their respective 3 cut stems were assayed for phage content and the remaining 9 GWSSs were transferred to fresh cowpea cut stems anchored in SDW (3 GWSSs/cut stem \times 3 cages) and allowed to feed for an additional 48 h to determine phage transfer to cut stems. Cut stems (3) and GWSSs (9) were assayed for phage after the designated period. Water uptake controls were conducted for all experiments under the same conditions and assayed for phage.

Having determined that both phage and bacteria could be acquired by GWSSs, it was of interest to determine if GWSSs that acquired phage from cut stems could transfer phage and/or bacteria to another cut stem. A subset of phage-harboring GWSSs were transferred to fresh cowpea cut stems in SDW and allowed to feed. After 48 h, the cut stems and GWSSs harbored an average of $3 \times 10^2 \pm 2.5 \times 10^2$ PFU/gpt and $3 \times 10^3 \pm 1.6 \times 10^3$ PFU/GWSSs, respectively, indicating that GWSSs could transfer phage.

Phage Challenge of *X. fastidiosa* Harboring GWSSs:

To determine if phage could affect the *X. fastidiosa* population in GWSSs, GWSSs harboring Xff were challenged with phage. Briefly, using methods described above

with triplicate replicates, GWSSs fed on Xff-containing cut stems, verified to contain Xff, were transferred to cowpea cut stems uptaking phage Xfas304 and allowed to feed. After 48 or 96 h of feeding, the cut stems and GWSSs were assayed for phage and/or Xff. For uptake of Xff, cowpea cut stems (15) were placed in a XF54 suspension (1×10^9 CFU/ml) for 4 h before introducing GWSSs. At 4 h, 3 cut stems were assayed for Xff. Each of the 12 remaining cut stems were placed in cages with 3 GWSSs/cut stem and the GWSSs allowed to feed for 48 h on the Xff containing cut stems. After 48 h, the Xff-fed GWSSs and host cut stems were subdivided into 3 groups: Group 1 was assayed for Xff (3 cut stems and 9 GWSSs); Group 2 (9 GWSSs) was transferred to fresh cowpea cut stems (3) placed in SDW and allowed to feed for 48 h before GWSSs and cut stems were assayed for Xff; Group 3 (18 GWSSs) was transferred to cowpea cut stems (3) placed in a Xfas304 suspension (1×10^{10} PFU/ml) and allowed to feed for 48 or 96 h before the GWSSs and cut stems were assayed for Xff and phage. Water uptake controls were conducted for all experiments under the same conditions and assayed for both *X. fastidiosa* and phage.

36 GWSSs were allowed to feed on cowpea cut stems in a Xff suspension and then assayed to determine Xff uptake, Xff and/or phage transfer, and effect on phage and/or Xff in GWSSs. GWSSs (Group 1) allowed to feed on cut stems for 48 h that had been placed in a suspension of the Xff strain XF54 (3×10^9 CFU/ml) were determined to harbor on the average $1 \times 10^6 \pm 0.7 \times 10^6$ CFU/GWSSs and the host feeding cut stems were determined to harbor an average of $2 \times 10^8 \pm 1 \times 10^8$ CFU/gpt. After GWSSs harboring Xff (Group 2; $1 \times 10^6 \pm 0.7 \times 10^6$ CFU/GWSS) were allowed to feed on fresh cut stems in SDW for 48 h, the cut stems showed an average of $1 \times 10^3 \pm 1.3 \times 10^3$ CFU/gpt and the GWSSs an average of $2 \times 10^3 \pm 1 \times 10^3$ CFU/GWSSs residual Xff; reconfirming previous results of Xff transfer by GWSSs. Group 3 of the Xff harboring GWSSs transferred to cut stems in an Xfas304 suspension (2×10^{10} PFU/ml) and allowed to feed for 48 h, showed uptake of phage and persistence of Xff. The assayed GWSSs, at 48 h of feeding, harbored an average of $3 \times 10^4 \pm 1.8 \times 10^4$ PFU/GWSS of Xfas304 and retained $2 \times 10^3 \pm 1.1 \times 10^3$ CFU/GWSSs of XF54. The cut stems assayed at the same time interval contained an average of $3 \times 10^8 \pm 2 \times 10^8$ PFU/gpt and $2 \times 10^3 \pm 0.6 \times 10^3$ CFU/gpt. The GWSSs allowed to feed for 96 h harbored an average of $2 \times 10^5 \pm 1.2 \times 10^5$ PFU/GWSS of Xfas304 and $1 \times 10^2 \pm 0.9 \times 10^2$ CFU/GWSS of XF54, indicating a reduction in XF54 and an average 6-fold increase in Xfas304.

Collection and Assay of Cowpea Cut Stems and GWSSs:

GWSSs were sacrificed by freezing at -20° C. for 5 min and cowpea cut stems were collected by cutting at the junction of the tube cap with sterile razor. Each GWSS of each triplicate was placed into 1.5-ml micro-centrifuge tube with 0.5 ml of P-buffer (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 8 mM MgSO_4), homogenized using a sterile plastic micro-pestle (Fisher), and filtered through sterile cheesecloth (Fisher Scientific, USA) to remove tissue debris. Each cut stem of each of triplicate was weighed and commuted using a sterile razor blade and homogenized in 1 ml of P-buffer using a mortar and pestle and filtered through sterile cheesecloth (Fisher Scientific, USA) to remove tissue debris. For assaying phage, the filtrate was centrifuged (10,000 \times g for 15 min) and filter sterilized. A portion of filtrate was used for phage DNA extraction as in Example 9, followed by qRT-PCR as described below. The remaining portion of the filtrate was used to titer phage as described in Example 3. The same protocol was used for bacterial assays (CFUs), except the pellet was resuspended into 0.5 ml of sterile

Milli-Q water for PMA treatment, bacterial DNA extraction, and qRT-PCR as described below.

PMA Treatment and qRT-PCR:

PMA treatment and SYBR-green based qRT-PCR protocols were conducted as described in Example 17 using *X. fastidiosa*- and phage-specific primers.

Example 19

Phage Activity Against *Xanthomonas axonopodis* pv. *Citri*

Although previous studies have evaluated the use of phage for the control of citrus canker, no conclusive data confirmed the virulent nature of the phages (Balogh et al., *Plant Disease*, 92:1048-1052, 2008). Only virulent, non-transducing phage should be used to evaluate and implement a sustainable phage biocontrol system. The sensitivity of three Xac field strains (North 40, Block 22, Fort Basinger) obtained from Florida, to two fully characterized virulent phages representative of the Podoviridae (Xfas303) and the Siphoviridae (Xfas103), respectively, was tested. Results indicate that the three Xac strains tested were only sensitive to phage Xfas303 (FIG. 12). Phage Xfas303 was able to form clear plaques on three Xac strains tested. 454 pyrosequencing was performed of the Xfas303 genome and predicted genes were fully annotated. The presence of a single subunit RNA Polymerase (SSRNAP) was found, which is indicative of virulent phages such as T7 and KMV (Dunn et al., *J. Mol. Biol.* 166:477-53521, 1983; Lavigne et al., *Virology* 312:49-59, 2003). Additionally, it was determined that the type IV pili of *Xanthomonas* spp. strain EC-12 is the primary receptor site for the phage Xfas303 by making in-frame deletion mutants of *pilA* in the bacteria. Both phages Xfas303 and Xfas103 adsorb and form clear plaques on the strain EC-12, but not the Δ *pilA* derivative, showing results only for plating of phage Xfas303 on EC-12 or EC-12 Δ *pilA*. It was also determined that type IV pili are the primary receptor site for phage Xfas303; thus this phage may have a different secondary receptor site requirement for infection or that phage DNA was restricted. Results indicate that the developed non-Xac dependent procedure may be used to isolate virulent phage for Xac with no loss in efficiency of plating (EOP of 0.75).

Example 20

Evidence for Expression of Type IV Pili in Xac

Reports in the literature are conflicting as to the expression and role of type IV pili in the infection process and pathogenesis of Xac (Brunings et al., *Mol. Plant. Pathol.* 4:141-57, 2003; Li et al., *PLoS ONE* 6:e21804, 2011; Yang et al., *Curr. Microbiol.* 48:251-61, 2004). The results presented above indicate that all three Xac strains tested expressed functional type IV pili, as the pili must be retracted to facilitate adsorption and infection of a phage. Using light microscopy studies the three Xac strains were evaluated for twitching motility, an indicator of functional type IV pili. *Pseudomonas aeruginosa* strain PAO1 and *Xanthomonas* ssp. strain EC-12 were used as positive controls and EC-12 Δ *pilA* was used as a negative control. The three Xac strains (North 40, Block 22 and Fort Basinger) were evaluated for twitching motility. The PAO1, EC-12, and three Xac strains exhibited twitching motility, whereas the EC-12 Δ *pilA* did not. Microscopy studies corroborate results obtained with phage sensitivity testing and indicated that three Xac strain have functional type IV pili that act as an adsorption site for phage Xfas303. Results corroborate the observations of others (Brunings et al., *Mol. Plant. Pathol.* 4:141-57, 2003; Li et al., *PLoS ONE* 6:e21804, 2011; Yang et al., *Curr. Microbiol.* 48:251-61, 2004) that type IV pili are expressed by Xac.

Example 21

Isolation and Characterization of XfaMija and XfaMijo

Bacterial Strains and Culture Conditions.

Bacterial strains used are listed in Table 6. *X. fastidiosa* strains were cultured and maintained in PW-M broth (PW-MB) or on PW-M agar (PW-MA) plates and PW-M soft agar (PW-MSA) (PW-MB with 7.5 g/liter plant cell culture-tested agar) was used for overlays. *Xanthomonas* strain was cultured at 28° C. in tryptone nutrient broth (TNB) or tryptone nutrient agar (TNA) (TNB lacking KNO₃ with 20 g/liter agar). TNA soft agar (TNSA) (TNB lacking KNO₃ with 7.5 g/liter agar) was used for overlays. Plant extracts were plated onto PW-MA or TNA supplemented with cycloheximide (40 µg/ml), designated PW-MC and TNAC, respectively.

TABLE 6

Bacterial strains used for phage isolation and characterization.		
Strain	Genotype or relevant characteristics	Reference or source
<i>Xylella fastidiosa</i>		
Temecula 1	<i>X. fastidiosa</i> subsp. <i>fastidiosa</i> , Wild-type Pierce's Disease isolate, ATCC 700964, twitching motility ⁺	Van Sluys, J Bacteriol. 185: 1018, 2003
XF15-1	Temecula 1; Δ <i>pilA</i> ::Km ^r , twitching motility ⁻	Ahern, J Bacteriol. 196: 459, 2014
Ann-1	<i>X. fastidiosa</i> subsp. <i>sandyi</i> , oleander isolate, ATCC 700598, twitching motility ⁺	Bhattacharyya, Genome Res. 12: 1556, 2002
Dixon	<i>X. fastidiosa</i> subsp. <i>multiplex</i> , almond isolate, ATCC 700965, twitching motility ⁺	Bhattacharyya, Genome Res. 12: 1556, 2002

TABLE 6-continued

Bacterial strains used for phage isolation and characterization.		
Strain	Genotype or relevant characteristics	Reference or source
XF53	Grape isolate (subsp. <i>fastidiosa</i>)	Ahern, J Bacteriol. 196: 459, 2014
XF54	Grape isolate (subsp. <i>fastidiosa</i>)	Ahern, J Bacteriol. 196: 459, 2014
XF95	Oleander isolate (subsp. <i>sandyi</i>)	Ahern, J Bacteriol. 196: 459, 2014
XF15.7	<i>X. fastidiosa</i> Temecula 1 Salvo ^{a,R} , twitching motility ⁺	This work
XF15.11	<i>X. fastidiosa</i> Temecula 1 Sano ^{a,R} , twitching motility ⁺	This work
XF15.12	<i>X. fastidiosa</i> Temecula 1 Prado ^{a,R} , twitching motility ⁺	This work
XF15.16	<i>X. fastidiosa</i> Temecula 1 Sano ^{a,R} , twitching motility ⁺	This work
XF15.28	<i>X. fastidiosa</i> Temecula 1 Salvo ^{a,R} , twitching motility ⁺	This work
XF15.37	<i>X. fastidiosa</i> Temecula 1 Paz ^{a,R} , twitching motility ⁺	This work
XF15.38	<i>X. fastidiosa</i> Temecula 1 Paz ^{a,R} , twitching motility ⁺	This work
XF15.51	<i>X. fastidiosa</i> Temecula 1 Prado ^{a,R} , twitching motility ⁻	This work
XF134-155, 161-163	<i>X. fastidiosa</i> isolate from <i>V. vinifera</i> , Santa Clara County, CA	This work
XF156-160, 164, 165	<i>X. fastidiosa</i> isolate from <i>V. vinifera</i> , Sonoma County, CA	This work
XF166-173	<i>X. fastidiosa</i> isolate from <i>V. vinifera</i> , Napa County, CA	This work
XF174-183	<i>X. fastidiosa</i> isolate from <i>V. vinifera</i> , Uvalde County, TX	This work
<i>Xanthomonas</i>		
EC-12	<i>Xanthomonas</i> sp., rice isolate (ATCC PTA-13101)	Ahern J Bacteriol. 196: 459, 2014
Jal-4	<i>X. euvesicatoria</i> , jalapeno isolate	Ahern J Bacteriol. 196: 459, 2014
Presidio-4	<i>Xanthomonas</i> sp., rice isolate	Ahern J Bacteriol. 196: 459, 2014
EC-12-1	EC-12, unmarked deletion of pilA	Ahern J Bacteriol. 196: 459, 2014

Km^r = Kanamycin resistant.
^a= phage used for selection of phage resistant mutant.
^R= Resistant to phages Sano, Salvo, Prado and Paz.
⁺= Present
⁻= Absent

Bacteriophage Isolation and Purification.

Plant and ditch water samples were assayed for the presence of phage able to form plaques on *X. fastidiosa* strain Temecula 1. Plant extracts were prepared by macerating 10 g of plant tissue in 50 ml of P-buffer (1) using a mortar and pestle, strained through a sterile double layer of cheese cloth to remove large particles, and filter sterilized. Water sample was centrifuged twice and filter sterilized. Plant and water filtrates were directly screened for phage activity using the spot test and soft agar overlay method on *Xanthomonas* strain EC-12 as described by Ahern, et al., 2014. Individual plaques formed on overlays of *Xanthomonas* strain EC-12 were excised, suspended in P-buffer, and filter sterilized, and titers were determined. This procedure was repeated three times to obtain single plaque isolates. Purified phages were tested for activity on *X. fastidiosa* strain Temecula 1. High-titer phage plate lysates (1×10¹⁰ PFU/ml) were prepared by harvesting overlay plates of *X. fastidiosa* strain Temecula 1 or *Xanthomonas* strain EC-12 exhibiting confluent lysis. After being flooded with 5 ml of P-buffer, the soft agar overlay was macerated, clarified by centrifugation, and filter sterilized. The resulting lysates were stored at 4° C.

Phage DNA Isolation and Genome Sequencing.

DNA was isolated from high-titer phage suspensions. Phage DNA was sequenced in an Illumina MiSeq 250-bp paired-end run with a 550-bp insert library. Quality-controlled, trimmed reads were assembled to a single contig of circular assembly at 30.9-fold coverage using SPAdes version 3.5.0. The contig was confirmed to be completed by PCR using primers that face the upstream and downstream ends of the contig. Products from the PCR amplification of the junctions of concatemeric molecules were sequenced by Sanger sequencing (Eton Bioscience, San Diego, Calif., USA). Genome termini was determined by restriction enzyme digestion profile. Genes were predicted using GeneMarkS and corrected using software tools available on the Center for Phage Technology (CPT) Galaxy. Protein-coding regions were initially predicted by using GeneMark.hmm, Glimmer3 and MetaGeneAnnotator refined by manual analysis in Artemis, and analyzed by using BLAST (E value cutoff of 0.005). Proteins of particular interest were additionally analyzed by InterProScan, HHpred searches.

Transmission Electron Microscopy.

Electron microscopy of high titer phage (1×10¹⁰ PFU/ml) was performed by diluting stock with 1/5th dilution of P-buffer. Phages were applied onto thin 400-mesh carbon

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coated Formvar grids, stained with 2% (wt/vol) uranyl acetate, and air dried. Specimens were observed on a JEOL 1200EX transmission electron microscope operating at an acceleration voltage of 100 kV. Five virions of each phage were measured to calculate mean values and standard deviations for dimensions of capsid and tail.

Host range and efficiency of plating.

Host ranges of purified phages (propagated on *X. fastidiosa* strain Temecula 1) were determined by the serial dilution spot test method, as described by Ahern, et al., 2014. A panel of *X. fastidiosa* and *Xanthomonas* isolates were used as indicator hosts. Phage sensitivities of type IV pilus mutants and complements were tested similarly. Efficiency of plating (EOP) was determined by calculating the ratio of the phage plaque titer obtained with a heterologous (non-propagating) host to that obtained with a homologous (propagating) host. All experiments were done in triplicate.

One-Step Growth Curve.

One-step growth curves were used to determine the burst size and latent period of the phages. Liquid cultures of logarithmically growing *Xanthomonas* strain EC-12 were infected with individual phages at a multiplicity of infection (MOI) of ~3 and allowed to adsorb at 28° C. for 5 min. To stop further phage adsorption, cultures were diluted 1,000-fold in TNB. Infected centers were incubated at 28° C. with constant shaking (150 rpm). Samples were taken at 3-min intervals, immediately filter sterilized, and plated in soft agar lawns of *Xanthomonas* strain EC-12. All experiments were done in triplicate.

Bacteriophage Adsorption.

Liquid cultures of logarithmically growing cells (*X. fastidiosa* strain Temecula 1 or *Xanthomonas* strain EC-12) were infected with individual phages (propagated on homologous hosts) at an MOI of ~0.1. The mixture was incubated at 28° C. with shaking (150 rpm). Samples were taken (2-h intervals for *X. fastidiosa* strain Temecula 1 and 2-min intervals for *Xanthomonas* strain EC-12) and immediately filter sterilized, and titers were determined. The rate of phage particle disappearance is defined as $dP/dt = -kBP$, where B is the concentration of bacteria, P is the concentration of free phage at any time (t), and k is the adsorption rate constant in $ml\ cell^{-1}\ min^{-1}$. All experiments were done in triplicate.

Lysogen Formation Assay.

To assay for phage lysogen formation, survivors of phage infection were tested for the presence of prophages. For each phage, bacteria were infected at an input MOI of ~3 and plated in a soft agar overlay. Plates were monitored for colony growth (10 to 15 days for *X. fastidiosa* strain Temecula 1 and 2 to 3 days for *Xanthomonas* strain EC-12). Individual colonies that emerged were picked, purified (three times), and retested for phage sensitivity by spotting dilutions of the same phage in a soft agar overlay. Primer pairs specific to Mija and Mijo primase genes (Table 7) were then used to test for the presence of prophage sequences in the phage-insensitive isolates. Wild-type bacterial DNA was used as the negative control, and wild-type bacterial DNA spiked with phage DNA served as the positive control. Phages Mija and Mijo have been shown to be useful in lysogen formation.

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TABLE 7

Primers for Mija and Mijo			
Primer Name*	Sequence (5'-3')	SEQ ID NO.	Amplicon size (bp)
Mija-PrimF	TCCCAAGAGTGATTGTATCC	25	221
Mija-PrimR	CTGCGATACAGTTCTCAACA	26	
Mijo-PrimF	CAAAATCGTCATCTACGACA	27	193
Mijo-PrimR	CTTTTGTGTTGGTTTTGCTT	28	

*All PCR reactions were conducted for 40 cycles with denaturation at 95° C. for 30 sec, annealing at 55° C. for 30 sec and extension at 72° C. for 30 sec.

Test for Abortive Lysogeny.

To test whether evidence for abortive lysogeny (i.e., the establishment of repression) could be found, a procedure described previously by Gill J. *Bacteriol.* 193:5300-5313, 2011 and Ahern, et al., 2014, was followed. This was performed using *Xanthomonas* strain EC-12 and replicated three times. Phages Mija and Mijo have been shown to be useful in the establishment of lysogens.

Nomenclature.

Novel phages of the Xfas500 phage type were given the names XfaMija (Xfas501) and XfaMijo (Xfas502) for mnemonic purposes. Names were checked for uniqueness by literature searching and were prefixed with Xfa, which is the ReBase species acronym for *X. fastidiosa*. Phages XfaMija and XfaMijo were deposited in the ATCC under accession numbers ATCC PTA-122743 and ATCC PTA-122742, respectively. For simplicity, the phage names may be used without the Xfa prefix.

Phage Isolation and Characterization.

Samples from both plant tissues and ditch, creek or sewage were screened in the laboratory against both *X. fastidiosa* strain Temecula 1 and *Xanthomonas* strain EC-12. Of the phages isolated, Mija and Mijo are representative. Phage Mija was isolated from Duck salad weed (*Heteranthera limosa*) collected from rice fields in El Campo (Wharton County), Texas. Phage Mijo was isolated from water sample collected from a ditch in Weslaco (Hidalgo County), Texas. The physical and host range properties of the two representative phages are summarized in Tables 8, 9, and 10, and FIG. 13. Phages Mija and Mijo exhibit Myoviridae morphology, with isometric heads (average diameter of ~89 nm) and contractile tails (~202 nm) (FIGS. 13A and B, respectively). Both phages formed small clear plaques on both *X. fastidiosa* and *Xanthomonas* hosts, with differences in host range (Table 9). Sensitivity of a collection of 10 Texas and 40 California *X. fastidiosa* isolates representative of 20 SSR typing groups with both phages determined their broad host range activity individually (Table 10). Both phages cannot form plaques on *X. fastidiosa* type IV pilus mutant (Table 9). Phages Mija and Mijo, propagated on *Xanthomonas* strain EC-12, showed a 1- to 2-log reduction in efficiency on *X. fastidiosa* strain Temecula 1 (Table 11).

TABLE 8

General, physiological and structural characteristics of phages Mija and Mijo.		
Feature	Phage	
	Mija	Mijo
Isolation host	EC-12	EC-12
Capsid width (nm) ^a	89 (±2.1)	89 (±0.8)
Tail length (nm) ^a	202 (±2.3)	202 (±4.2)
Adsorption rate k (ml cell ⁻¹ min ⁻¹) ^{bc}		
Temecula	(2.13 ± 0.24) × 10 ⁻¹⁰	(1.82 ± 0.18) × 10 ⁻¹⁰
EC-12	(5.68 ± 0.31) × 10 ⁻⁹	(1.29 ± 0.21) × 10 ⁻⁹
Burst size (PFU/cell) ^d	122 (±8.4)	117 (±6.8)
^a Phage physical dimensions are the means of measurements of five virions, bracketed values after each dimension indicate standard deviations. ^b Phage adsorption rate constants k are the means of three independent experiments, bracketed values indicate standard deviations. ^c Phage stocks propagated on homologous host. ^d Phage burst are the means of three independent experiments, bracketed values indicate standard deviations. <i>Xanthomonas</i> strain EC-12 was used as host.		

TABLE 9

Phage host range.		
Strain	Phage	
	Mija	Mijo
<i>X. fastidiosa</i>		
Temecula 1	+ ^a	+
XF15-1	-	-
XF15-1-1	+	+
Ann-1	+	+
Dixon	+	+
XF53	+	+
XF54	+	+
XF95	+	+
<i>Xanthomonas</i>		
EC-12	+	+
Jal-4	+	+
Presidio-4	+	-
EC-12-1	-	-

^aAbility to form individual plaques.

TABLE 10

Phage sensitivity of <i>X. fastidiosa</i> SSR types.			
Isolates	Phages		SSR
	Mija	Mijo	Type
XF134	+	+	G-1
XF135	+	+	G-2
XF136	+	+	G-3
XF137	+	+	G-2
XF138	+	+	G-4
XF139	+	+	G-5
XF140	+	+	G-6
XF141	+	+	G-7
XF142	+	+	G-6
XF143	+	+	G-8
XF144	+	-	G-9
XF145	+	+	G-10
XF146	+	+	G-11
XF147	+	+	G-10
XF148	+	+	G-12
XF149	+	+	G-2
XF150	+	+	G-2
XF151	+	+	G-3
XF152	+	+	G-13

TABLE 10-continued

Phage sensitivity of <i>X. fastidiosa</i> SSR types.			
Isolates	Phages		SSR
	Mija	Mijo	Type
XF153	+	+	G-3
XF154	+	+	G-14
XF155	+	+	G-15
XF156	+	+	G-16
XF157	+	+	G-17
XF158	+	+	G-18
XF159	+	+	G-3
XF160	+	+	G-9
XF161	+	+	G-19
XF162	+	+	G-2
XF163	+	+	G-2
XF164	+	+	G-5
XF165	+	+	G-10
XF166	+	+	G-5
XF167	+	+	G-8
XF168	+	+	G-9
XF169	+	+	G-20
XF170	+	+	G-20
XF171	+	+	G-5
XF172	+	+	G-5
XF173	+	+	G-20

(+) = phage form plaques on isolate using spot dilution series (10¹-10⁴);
(-) = no phage form plaques on isolate

TABLE 11

Influence of production host on efficiency of plating. ^a			
Production	Indicator	Phage	
host	host	Mija	Mijo
Temecula	Temecula	1.0	1.0
Temecula	EC-12	(9.76 ± 0.5) × 10 ⁻¹	(3.32 ± 0.3) × 10 ⁻²
EC-12	EC-12	1.0	1.0
EC-12	Temecula	(1.07 ± 0.2) × 10 ⁻¹	(2.67 ± 0.7) × 10 ⁻²

^a Data shown are the means of triplicate independent experiments ± SD.

Adsorption rate constants for Mija and Mijo on *X. fastidiosa* strain Temecula 1 were on the order of ~2×10⁻¹⁰ ml cell⁻¹ min^d, which is 100-fold higher than those for phages previously reported. In contrast, the rate constants for *Xanthomonas* strain EC-12 were ~10-fold higher, at ~3×10⁻¹⁰ ml cell⁻¹ min^d. The burst sizes of Mija and Mijo phages were ~122 PFU/cell at 32 min and ~117 PFU/cell at 30 min with *Xanthomonas* strain EC-12 as the host (Table 8). The extremely slow adsorption to *X. fastidiosa* strain Temecula 1 made it unfeasible to determine burst size with this host.

Genomics of Mija and Mijo.

The general characteristics of the phage genomes are summarized in Table 12, and complete annotations with supporting evidence are provided in Table S2 in the supplemental material. The genomes of Mija and Mijo were found to be 200.5 and 198.9 kb, encoding 325 and 360 genes, respectively. Both phages are T4-like with circularly permuted genome. For annotation purposes, due to absence of rIIa or rIIb gene homologs, Mija and Mijo were opened in a transcriptional break upstream to terminase large subunit

(TerL). Mija and Mijo have 44.3% and 43.8% nucleotide sequence identity with T4 across the genome, respectively, whereas both phages share 47.3% sequence identity at nucleotide level, as determined by Emboss Stretcher (European Molecular Biology Open Software Suite).

TABLE 12

General features of Mija and Mijo phage genomes.		
Feature	Phage	
	Mija	Mijo
Genome size (bp)	200,580	198,991
GC content (%)	50.2	52

TABLE 12-continued

General features of Mija and Mijo phage genomes.		
Feature	Phage	
	Mija	Mijo
Predicted No. of genes	325	360
Coding density (%)	91.3	91.7

SEQUENCE LISTING

The patent contains a lengthy sequence listing. A copy of the sequence listing is available in electronic form from the USPTO web site (<https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US11788052B2>). An electronic copy of the sequence listing will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

- What is claimed is:
1. A method of preventing or reducing symptoms or disease associated with *Xylella fastidiosa* or *Xanthomonas* in a plant, comprising contacting said plant with particles of at least one virulent bacteriophage, wherein *Xylella fastidiosa* and/or *Xanthomonas axonopodis* are hosts of the bacteriophage, selected from the group consisting of bacteriophages of the Xfas100 phage type, bacteriophages of the Xfas300 phage type, and bacteriophages of the Xfas500 type; wherein the Xfas100 phage type comprises a genome with a DNA sequence 90% or more identical to a sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:18; the Xfas300 phage type comprises a genome with a DNA sequence 90% or more identical to a sequence selected from the group consisting of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ.ID 22, SEQ ID NO:23, and SEQ ID NO:24; and wherein the Xfas500 phage type comprises a DNA sequence selected from the group consisting of SEQ ID NO:25-28.

2. The method of claim 1, wherein said bacteriophage is capable of lysing said *Xylella fastidiosa* and/or *Xanthomonas axonopodis* bacteria.

3. The method of claim 1, wherein said bacteriophage infects a cell by binding to a Type IV pilus.

4. The method of claim 1, wherein contacting comprises introducing the bacteriophage particles into the plant.

5. The method of claim 1, wherein the plant is selected from the group consisting of a grapevine plant, a citrus plant, almond, coffee, alfalfa, *oleander*, oak, sweetgum, redbud, elm, peach, apricot, plum, blackberry, mulberry, olive, and *Chitalpa tashkentensis*.

6. The method of claim 4, wherein the bacteriophage particles are introduced into the plant by injection, by an insect vector, via the root system, by spray, by mist, or by dust on the plant.

7. The method of claim 6, wherein the insect vector is a glassy winged sharpshooter.

8. The method of claim 4, wherein the number of said bacteriophage particles to be introduced into said plant is from 1 to 10¹² PFU/ml.

9. The method of claim 4, wherein said bacteriophage particles are introduced simultaneously or sequentially to the plant by a combination of two, three, four, five, or six virulent bacteriophage strains.

10. The method of claim 1 for preventing or reducing symptoms or disease associated with *Xylella fastidiosa* or *Xanthomonas* in a plant, comprising contacting said plant with particles of at least one virulent bacteriophage, wherein *Xylella fastidiosa* and/or *Xanthomonas axonopodis* are hosts of the bacteriophage; wherein the Xfas500 phage type bacteriophage have been deposited under ATCC Accession Numbers ATCC PTA-122743 and ATCC PTA-122742, or variants thereof; wherein the Xfas100 phage type is at least one bacteriophage selected from the group consisting of: Xfas103, and Xfas106; and the Xfas300 phage type is at least one bacteriophage selected from the group consisting of: Xfas302, Xfas303, Xfas304, and Xfas306; wherein said phage of the Xfas100 and Xfas300 phage types have been deposited under ATCC Accession Numbers PTA-13096, PTA-13095, PTA-13098, PTA-13099, PTA-13100, and PTA-13097, respectively, for phages Xfas103, Xfas106, Xfas302, Xfas303, Xfas304, and Xfas306.

11. The method of claim 1, wherein the Xfas100 phage type comprises a genome with a DNA sequence 95% or more identical to a sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:18; and the Xfas300 phage type comprises a genome with a DNA sequence 95% or more identical to a sequence selected from the group consisting of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ.ID 22, SEQ ID NO:23, and SEQ ID NO:24.

12. The method of claim 1, wherein the Xfas 100 phage
type comprises a genome with a DNA sequence 98% or
more identical to a sequence selected from the group con-
sisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID 5
NO:17, and SEQ ID NO:18; and the Xfas300 phage type
comprises a genome with a DNA sequence 98% or more
identical to a sequence selected from the group consisting of
SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ.ID
22, SEQ ID NO:23, and SEQ ID NO:24. 10

13. The method of claim 1, wherein the Xfas 100 phage
type comprises a genome with a DNA sequence 99% or
more identical to a sequence selected from the group con-
sisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID 15
NO:17, and SEQ ID NO:18; and the Xfas300 phage type
comprises a genome with a DNA sequence 99% or more
identical to a sequence selected from the group consisting of
SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ.ID
22, SEQ ID NO:23, and SEQ ID NO:24. 20

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