Insights into the genome of the De Donno strain of *Xylella fastidiosa*

Annalisa Giampetruzzi
PhD researcher

TOPICS OF PRESENTATION

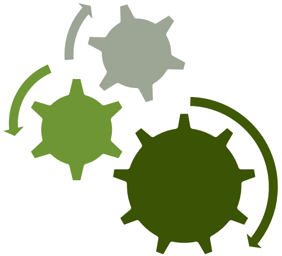
- 1) Whole-genome phylogeny based on single nucleotide polymorphisms (SNPs) and the study of the pan-genome of the 27 public available whole genome sequences of X. fastidiosa in 2016
(Giampetruzzi et al., 2017-Phytopatology)

- 2) Complete Genome Sequence of the Olive-Infecting Strain *Xylella fastidiosa* subsp. *pauca* De Donno
(Giampetruzzi et al., 2017-Genome Announcement)

- 3) Updating of study of Whole-genome phylogeny(SNPs) and of the pan-genome of the 40 currently public available whole genome sequences of *X.fastidiosa* including *Xylella fastidiosa* subsp.*pauca* De Donno (unpublished)

Whole-genome phylogeny based on single nucleotide polymorphisms (SNPs)

In 2016,
27 *X. fastidiosa* genomes
were available in the NCBI genomes database



kSNP 3.02 software,

an alignment-free sequence analysis tool, it identifies the pan-genome SNPs in a set of genome sequences, and estimates phylogenetic trees based upon those SNPs (Gardner et al., 2015)

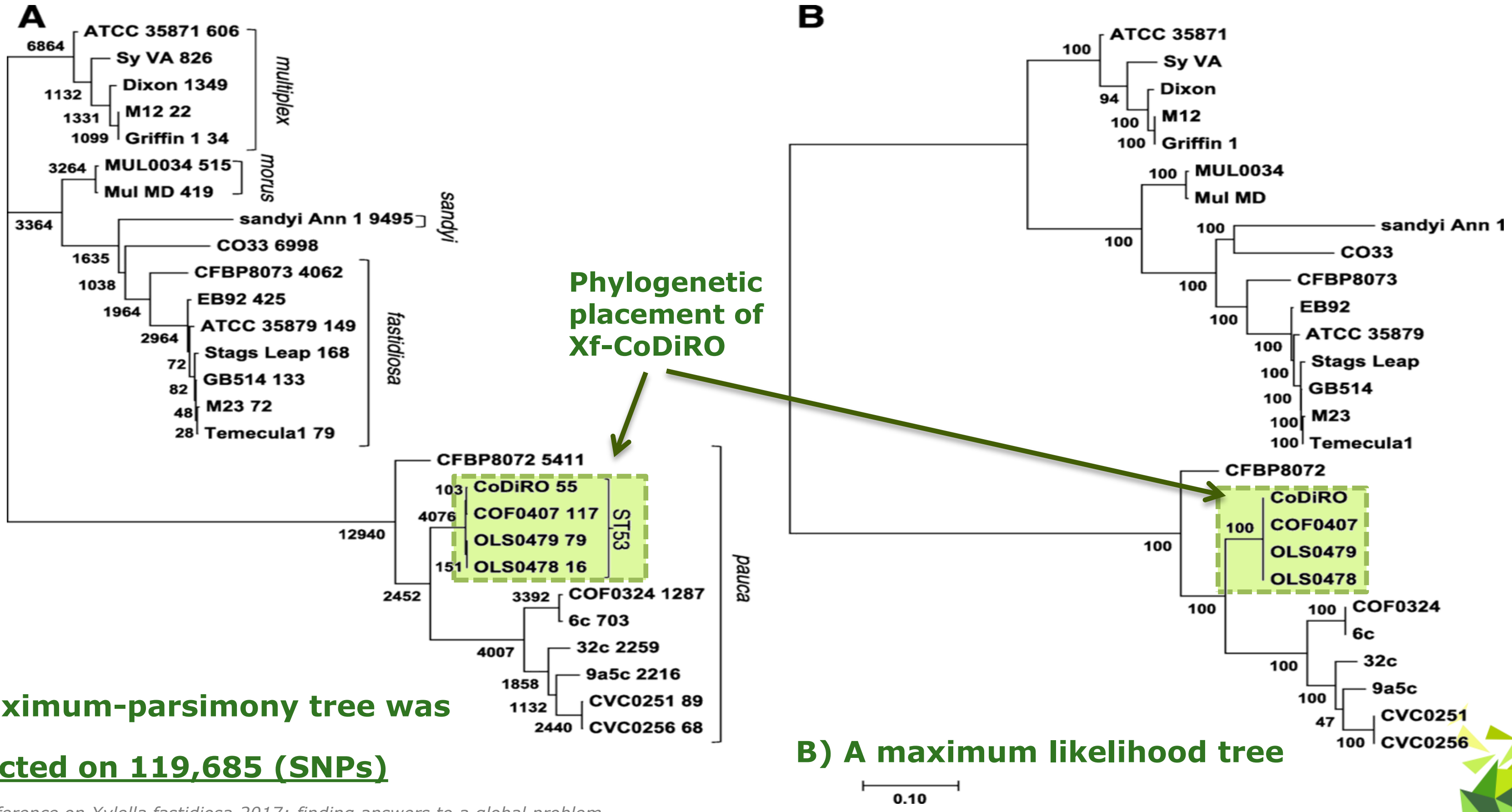
TABLE 1. List and general features of *Xylella fastidiosa* strains used in the study[a]

Strain	Host plant	Origin	Collection date	Size (Mb)/CDS	GC%	Accession number (chromosomes/WGS)	Plasmids accession number	Citation or release date
9a5c	*Citrus sinensis*	São Paulo, Brazil	1992	2.73175/2,982	52.64	NC002488.3	pXF1.3: NC002489.3; pXF51: NC002490.1	Simpson et al. 2000
Dixon	*Prunus dulcis*	California, USA	na	2.62233/2,914	52	AAAL02	–	7/10/2002
Temecula1	*Vitis vinifera*	California, USA	1998	2.52115/2,757	51.80	NC004556.1	pXFPD1.3: NC004554.1	Van Sluys et al. 2003
M12	*P. dulcis*	California, USA	2003	2.47513/2,706	51.9	NC010513.1	–	Chen et al. 2010
M23	*P. dulcis*	California, USA	2003	2.57399/2,803	51.76	NC010577.1	pXFAS01: NC010579.1	Chen et al. 2010
GB514	*Vitis vinifera*	Texas, USA	na	2.51738/2,835	51.77	NC017562.1	Unnamed: NC017561.1	9/23/2010
EB92.1	*Sambuccus nigra*	USA	1992	2.47543/2,750	51.5	AFDJ01	–	Zhang et al. 2011
ATCC 35871	*P. salicina*	Georgia, USA	na	2.41626/2,676	51.7	AUAJ01	–	7/15/2013
Griffin-1	*Quercus rubra*	Georgia, USA	2006	2.38731/2,724	51.7	AVGA01	–	Chen et al. 2013
32c	*Coffea* sp.	São Paulo, Brazil	na	2.60755/2,915	52.5	AWYH01	–	Alencar et al. 2014
6c	*Coffea* sp.	São Paulo, Brazil	na	2.606/2,916	52.35	AXBS01	pxF6c: NZAXBS01000046.1	Alencar et al. 2014
Mul-MD	*Morus alba*	Maryland, USA	2011	2.52055/2,838	51.6	AXDP01	–	Guan et al. 2014b
Ann-1	*Nerium oleander*	USA	na	2.78091/3,162	52.07	NZCP006696.1	Unnamed1: NZCP006697.1	6/6/2014
MUL0034	*M. alba*	USA	na	2.66658/2,974	51.97	NZCP006740.1	Unnamed2: NZCP006739.1	6/6/2014
Sycamore Sy-VA	*Platanus occidentalis*	Virginia, USA	2002	2.47588/2,758	51.6	JMHP01	–	Guan et al. 2014a
ATCC 35879	*Vitis vinifera*	Florida, USA	1987	2.52233/2758	51.8	JQAP01	–	10/21/2014
CoDiRO	*Olea europaea (Vinca minor)*	Italy	2013	2.54293/2,816	51.96	JUJW01	Unnamed: NZCM003178.1	Giampetruzzi et al. 2015a
CO33	*Coffea arabica*	Costa Rica	2015	2.68193	51.7	LJZW01	–	Giampetruzzi et al. 2015b
CFBP8072	*Coffea arabica*	Ecuador	2012	2.49666/2,763	51.9	LKDK01	–	Jacques et al. 2016
CFBP8073	*Coffea canephora*	Mexico	2012	2.58215/2,840	51.6	LKES01	–	Jacques et al. 2016
OLS0479	*Nerium oleander*	Costa Rica, San Jose Province	2011	2.53996/2,827	51.93	LRVH01	pXF-P1.COF0407: NZCM003743.1; pXF-P4.COF0407: NZCM003744.1; pXF-PS.COF0407: NZCM003745.1; pXF-RC.COF0407: NZCM003746.1	2/5/2016
CVC0256	*Citrus sinensis*	São Paulo, Brazil	1999	2.70214/3,045	52.51	LRVF01	pXF-BHR.CVC0256: NZCM003748.1; pXF-P1.CVC0256: NZCM003749.1; pXF-P4.CVC0256: NZCM003750.1; pXF-PS.CVC0256: NZCM003751.1	2/5/2016
OLS0478	*Nerium oleander*	Costa Rica, San Jose Province	2011	2.55541/2,861	51.91	LRVI01	pXF-P1.OLS0478: NZCM003752.1; pXF-P4.OLS0478: NZCM003753.1	2/5/2016
COF0407	*Coffea* sp.	Costa Rica, San Jose Province	2009	2.53847/2,837	51.84	LRVJ01	pXF-P1.OLS0479: NZCM003762.1; pXF-P4.OLS0479: NZCM003763.1; pXF-PS.OLS0479: NZCM003764.1; pXF-RC.OLS0479: NZCM003765.1	2/5/2016
Stag's Leap	*Vitis vinifera*	California, USA	2005	2.5108/2,755	51.7	LSMJ01	–	Chen et al. 2016

[a] The coding sequence (CDS) number was obtained by RAST. Priority was given to citation, when existing, alternatively the release date is reported. na, not available.

SNP analysis of 27 *X. fastidiosa* genomes

Genetic relationships among ST53 isolates and *Xylella fastidiosa* subspecies



A) A maximum-parsimony tree was constructed on 119,685 (SNPs)

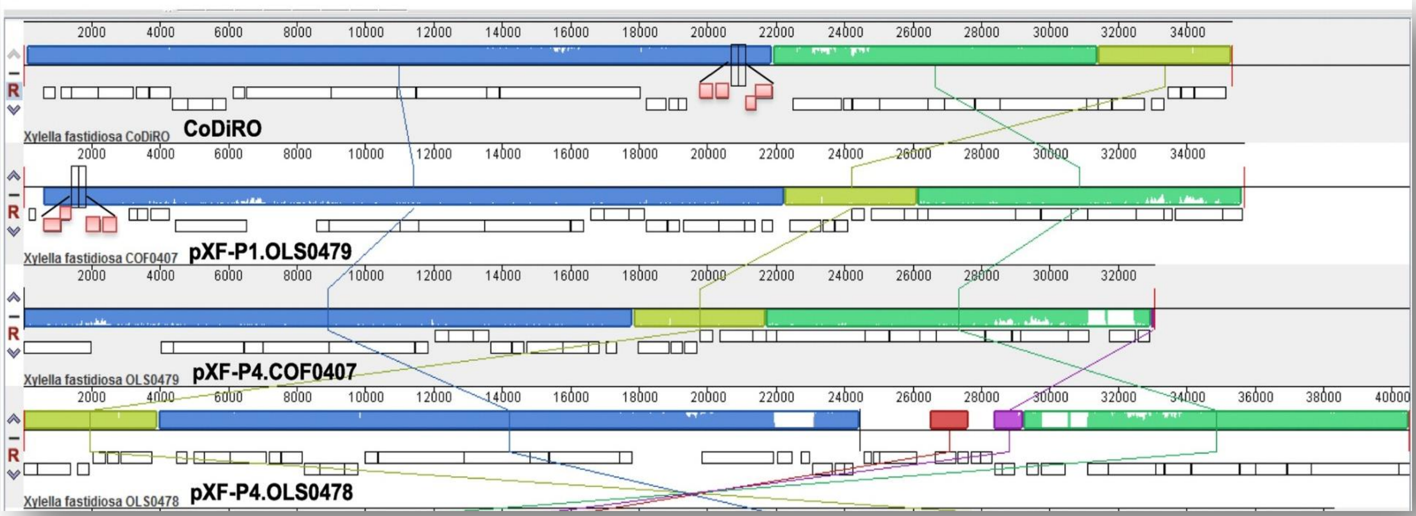
B) A maximum likelihood tree

Genomic elements characterizing CoDiRO and Costa Rican isolates: a conjugative plasmid (35kb)

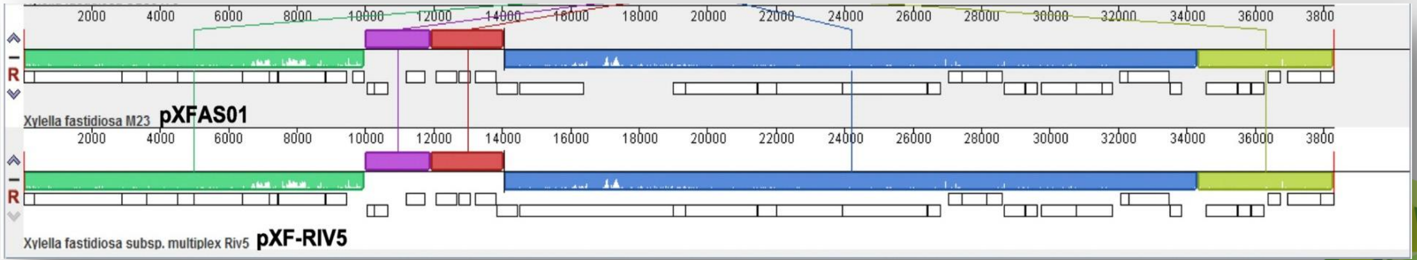
Progressive Mauve multiple alignment of plasmids

The **four ST53 isolates**

The **ParD/ParE** containing sequence was additionally present in **CoDiRO** and pXF.P1.OLS0479 (***Xf* strain COF0407**) and indicated by pink boxes.



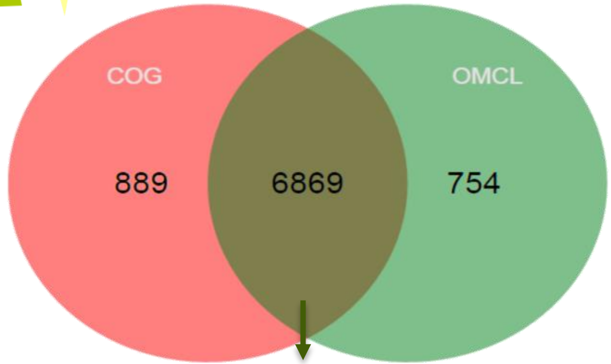
The same type of conjugative plasmid (35kb) shared by the four ST53 isolates was already described in the *Xf* multiplex strain: **pXFAS01, and pXF-RIV5**.

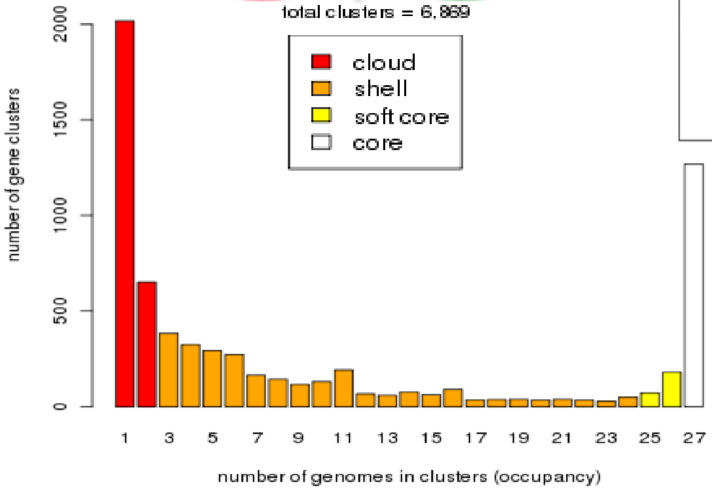


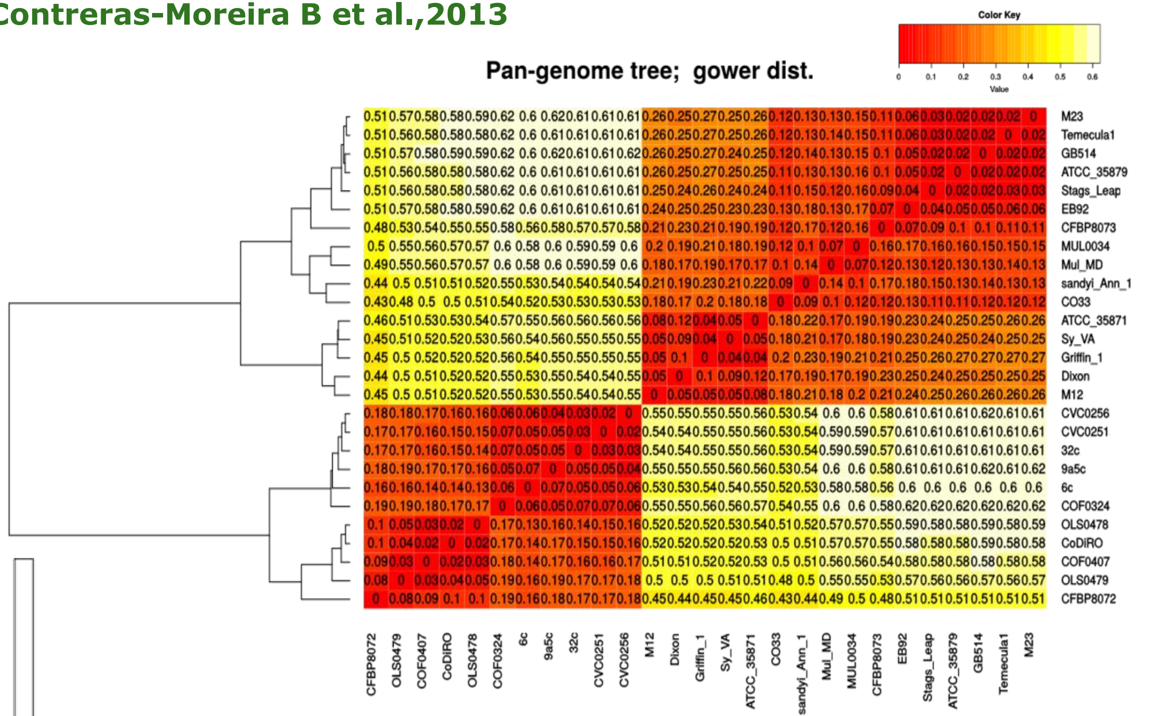
PANGENOME ANALYSIS OF *XYLELLA FASTIDIOSA*

(GET_HOMOLOGUES software)

Contreras-Moreira B et al.,2013



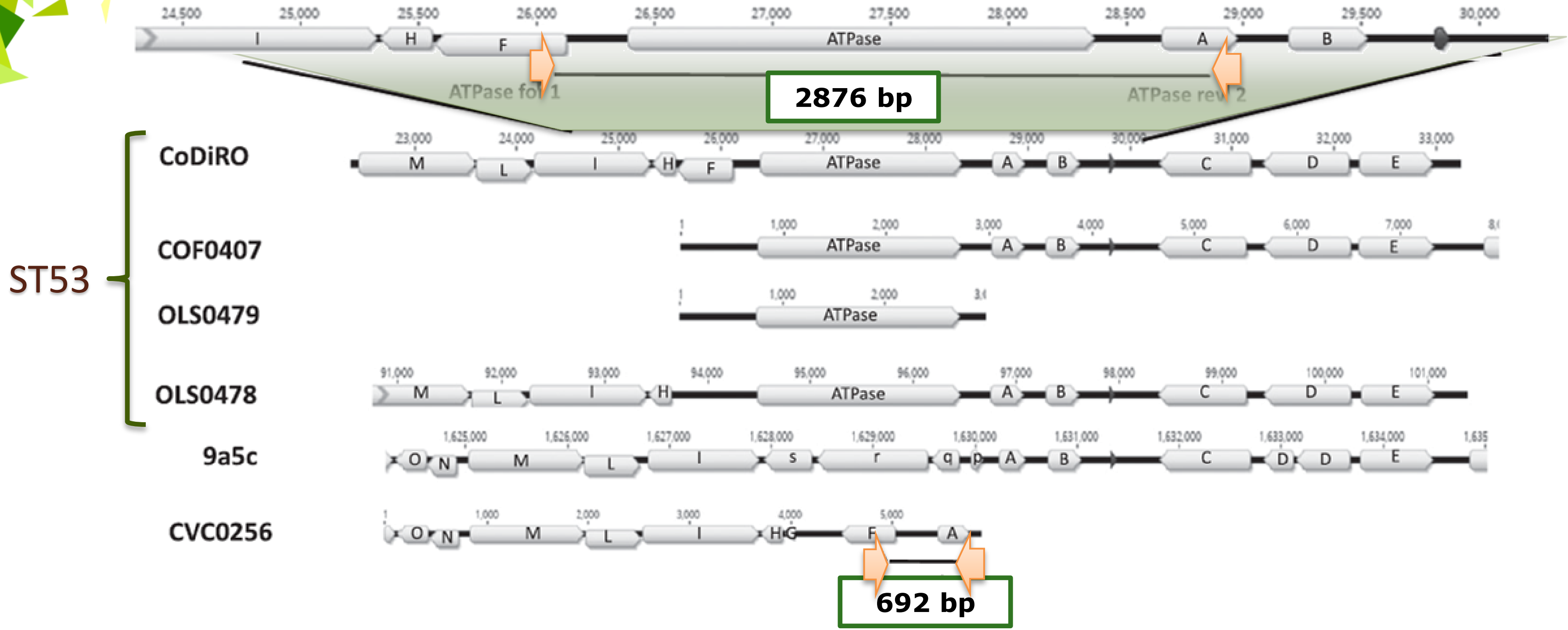




2668 cloud in 1-2 genomes
2680 shell in 3-24 genomes
1521 soft core in 25-26 genomes
1269 core in all 27 genomes

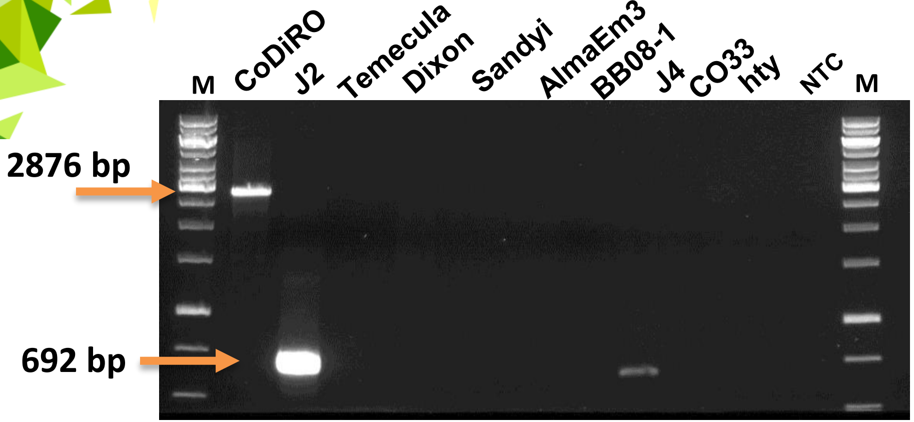
Heatmap and dendrogram obtained from the average nucleotide identity matrix based on the CDSs composition

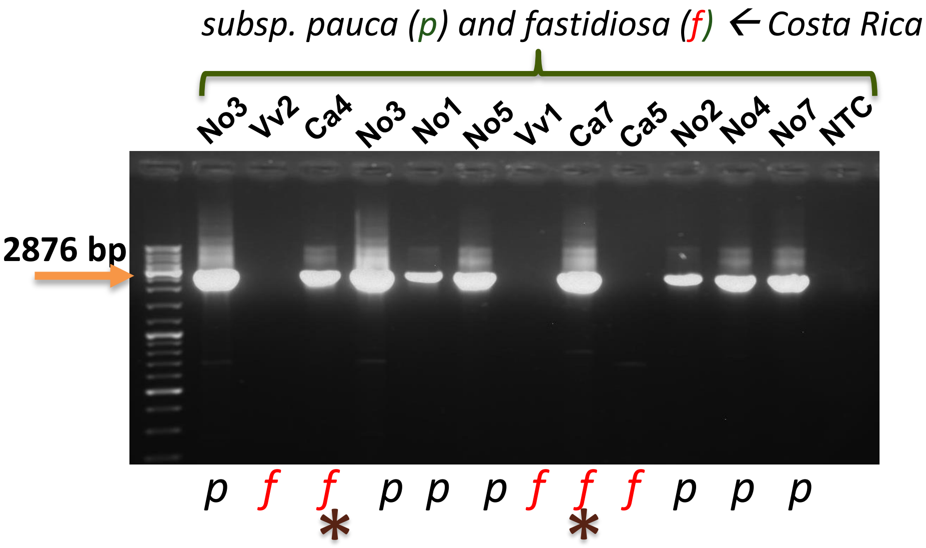
GENES UNIQUE TO THE ST53 CLADE

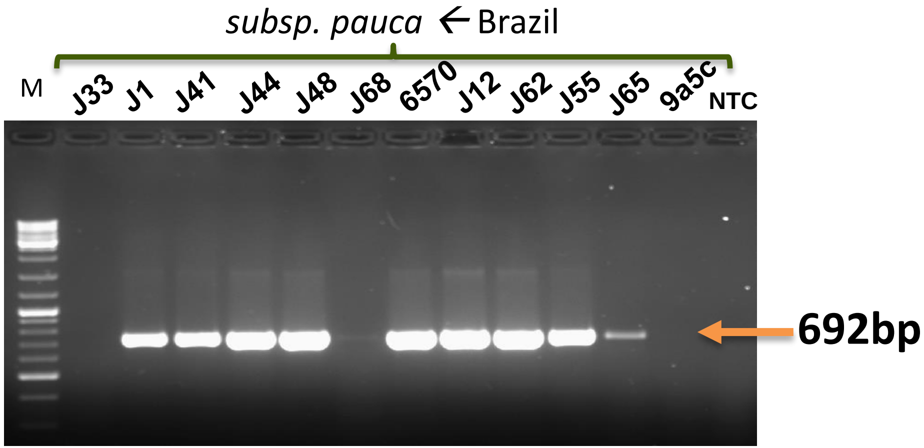


In silico identification of a gene encoding a putative histidine kinase-like ATPase,

"*IN VITRO*" DETECTION OF GENE CODING A PUTATIVE ATPase







"*In vitro*" detection on different isolates of *Xf* confirmed the *in silico* detection of ATPase in the four ST53, moreover ATPase was detected in two (*) ST21 isolates (coffee plants) of the subspecies fastidiosa from Costa Rica

1) CONCLUSIONS

➢Maximum-parsimony and maximum likelihood trees constructed using the SNPs and the pan-genome data distinguished the subsp. fastidiosa, multiplex, pauca, sandyi, and morus and **groups the Italian and three Costa Rican ST53 isolates in a compact clade** that diverges from the South American pauca isolates.

➢Gene encoding a putative histidine kinase-like **ATPase was identified** only in the clade of **the Italian and three Costa Rican ST53 isolates**, and it will be further characterized …

➢The work described, represented a great opportunity of exchanging experiences, materials and methods among institutions of different countries involved in the EU projects,

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Bacteriology

e-Xtra*

Genome-Wide Analysis Provides Evidence on the Genetic Relatedness of the Emergent *Xylella fastidiosa* Genotype in Italy to Isolates from Central America

Annalisa Giampetruzzi, Maria Saponari, Giuliana Loconsole, Donato Boscia, Vito Nicola Savino, Rodrigo P. P. Almeida, Stefania Zicca, Blanca B. Landa, Carlos Chacón-Diaz, and Pasquale Saldarelli

DISSPA-UNIBA
CNR-IPSP Bari
University of California, Berkeley
CSIC-Córdoba, Spain
CIET, Universidad de Costa Rica

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COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

January 2014

“De Donno” olive tree
(40.011389 N 18.048056 E)

October 2015

Isolate from the De Donno tree was used for the assembling of the first version of the **Draft** Genome released in the 2015:

genomeA
Journals.ASM.org

Draft Genome Sequence of the *Xylella fastidiosa* CoDiRO Strain

Annalisa Giampetruzzi,[a] Michela Chiumenti,[a] Maria Saponari,[a] Giacinto Donvito,[b] Alessandro Italiano,[b] Giuliana Loconsole,[a] Donato Boscia,[a] Corrado Cariddi,[c] Giovanni Paolo Martelli,[c] Pasquale Saldarelli[a]

Institute for Sustainable Plant Protection, National Research Council (CNR), Bari, Italy[a]; Department of Physics, University of Bari Aldo Moro, Bari, Italy[b]; Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro, Bari, Italy[c]

A.G. and M.C. contributed equally to this work.

We determined the draft genome sequence of the *Xylella fastidiosa* CoDiRO strain, which has been isolated from olive plants in southern Italy (Apulia). It is associated with olive quick decline syndrome (OQDS) and characterized by extensive scorching and desiccation of leaves and twigs.

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Complete Genome Sequence of the Olive-Infecting Strain *Xylella fastidiosa* subsp. *pauca* De Donno

Annalisa Giampetruzzi,[a] Maria Saponari,[b] Rodrigo P. P. Almeida,[c] Salwa Essakhi,[b] Donato Boscia,[b] Giuliana Loconsole,[a] Pasquale Saldarelli,[b]

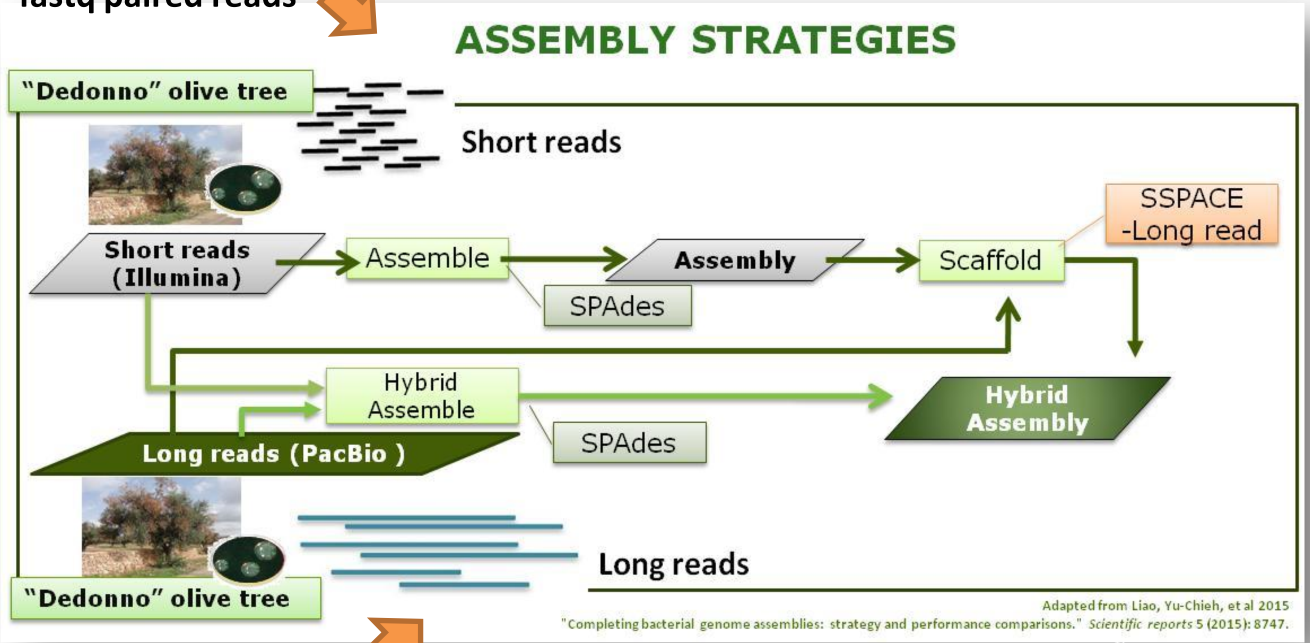
Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro, Bari, Italy[a]; Institute for Sustainable Plant Protection, National Research Council (CNR), Bari, Italy[b]; Department of Environmental Science, Policy and Management, University of California, Berkeley, Berkeley, California, USA[c]

COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

HiSeq 4000 Illumina platform

5,700,601 (2 × 150-bp) **fastq paired reads**

Vincent J. Coates Genomics Sequencing Laboratory at the University of California (UC), Berkeley



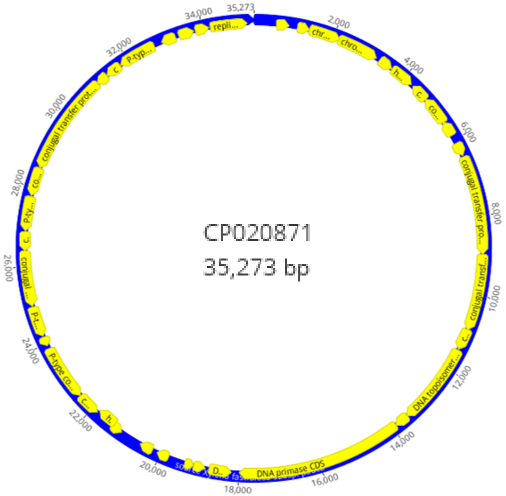
HiSeq 4000 Illumina platform and PacBio RSII platform

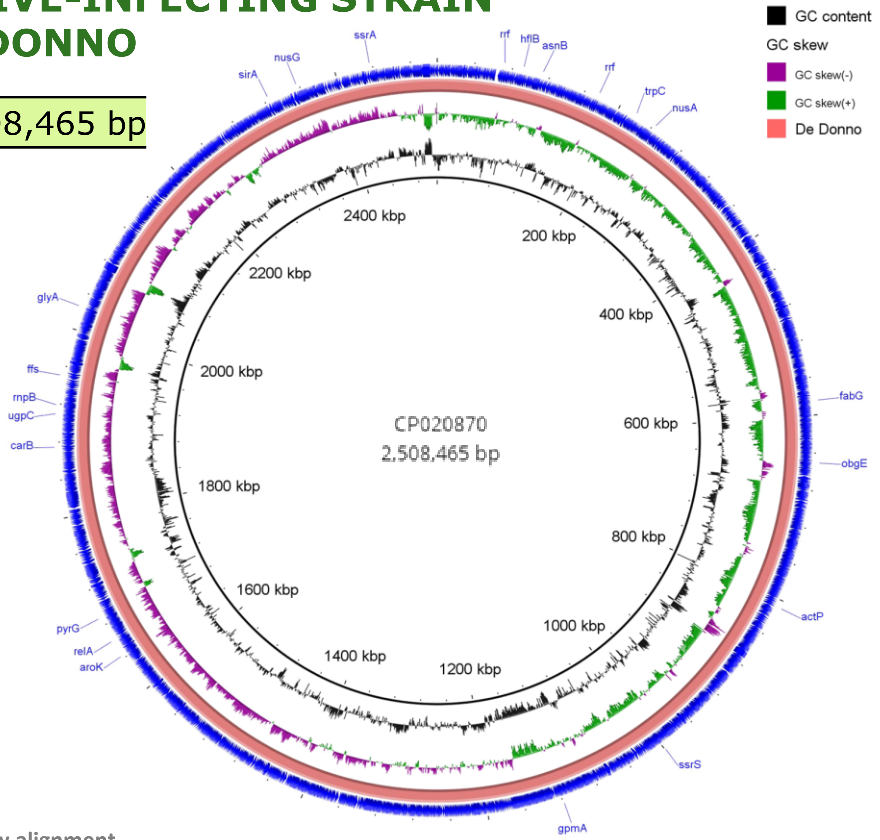
105,585 fastq reads, mean length of 8,527 bp (longest read, 56,602 bp)

COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

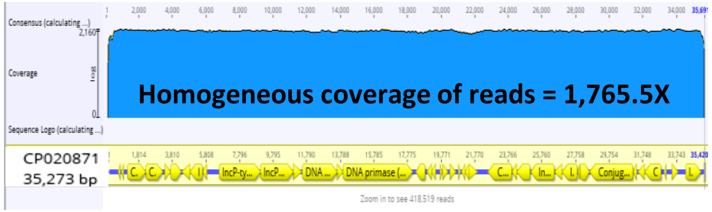
Chromosome De Donno	2,508,465 bp

Plasmid pXF-De_Donno	35,273 bp

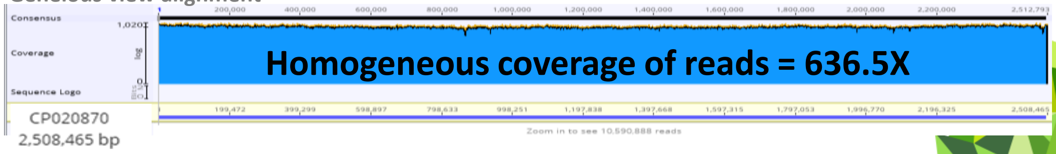




Geneious view alignment



Geneious view alignment



COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

PROKARYOTIC GENOME ANNOTATION: PGAP and RAST

NCBI Resources How To

Nucleotide Nucleotide Advanced

GenBank

Xylella fastidiosa subsp. pauca strain De Donno

GenBank: CP020870.1

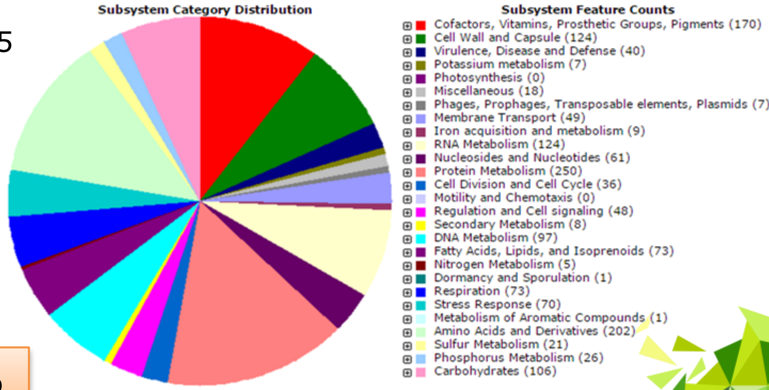
FASTA Graphics

```
Annotation Provider              :: NCBI
Annotation Date                  :: 04/19/2017 11:28:27
Annotation Pipeline              :: NCBI Prokaryotic Genome
                                    Annotation Pipeline
Annotation Method                :: Best-placed reference protein
                                    set; GeneMarkS+
Annotation Software revision     :: 4.1
Features Annotated               :: Gene; CDS; rRNA; tRNA; ncRNA;
                                    repeat_region
Genes (total)                    :: 2,420
CDS (total)                      :: 2,361
Genes (coding)                   :: 2,136
CDS (coding)                     :: 2,136
Genes (RNA)                      :: 59
rRNAs                            :: 2, 2, 2 (5S, 16S, 23S)
complete rRNAs                   :: 2, 2, 2 (5S, 16S, 23S)
tRNAs                            :: 49
ncRNAs                           :: 4
Pseudo Genes (total)             :: 225
```

RAST Rapid Annotation using Subsystem Technology version 2.0

The NMPDR, SEED-based, prokaryotic genome annotation service.
For more information about The SEED please visit theSEED.org.

Genome	**Xylella fastidiosa subsp. Pauca De Donno (Taxonomy ID: 698414)**
Size	**2,543,738**
GC Content	52.0
N50	2508465
Number of Contigs	2
Number of Subsystems	344
Number of CDSs	**2136**
Number of RNAs	55

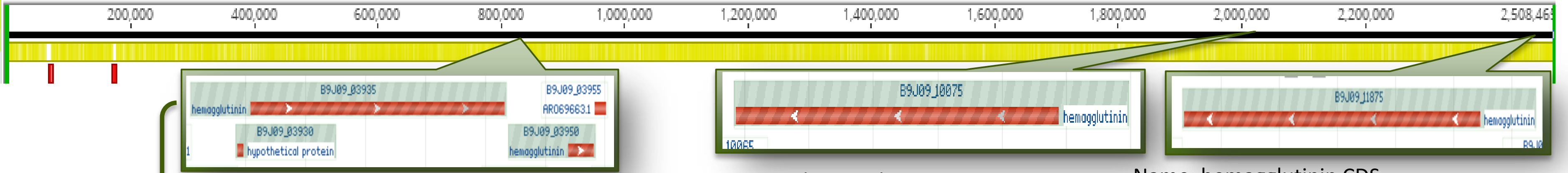


Same number of CDSs 2136

FRAMESHIFTS IN HEMAGGLUTININ CDSs

De Donno chromosome

Frameshifted hemoagglutinin-like genes



PGAP annotation description by NCBI

Name: hemagglutinin CDS
1) Length: 8,518
Interval: **864,138 -> 872,655**
locus_tag: B9J09_03935
similar to AA sequence:
RefSeq:WP_010895189.1
note: **frameshifted; internal stop; incomplete; partial on complete genome; missing stop,** pseudo:

Name: hemagglutinin CDS
2) Length: 10,024
Interval: **2,079,763 -> 2,069,740**
locus_tag: B9J09_10075
similar to AA sequence:
RefSeq:**WP_012382593.1**
note: **frameshifted;** pseudo:

Name: hemagglutinin CDS
3) Length: 10,195
Interval: **2,500,920 -> 2,490,726**
locus_tag: B9J09_11875
similar to AA sequence:
RefSeq:WP_010895189.1
note: **frameshifted**; pseudo:

*"Frameshifts in hemoagglutinin-like genes **may impair their functions** making the bactera more motile and virulent* (Pierry, PM et al 2012; MR Guilhabert and BC Kirkpatrick 2005)

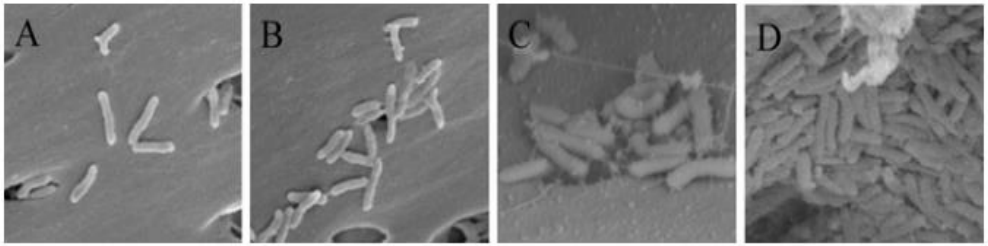


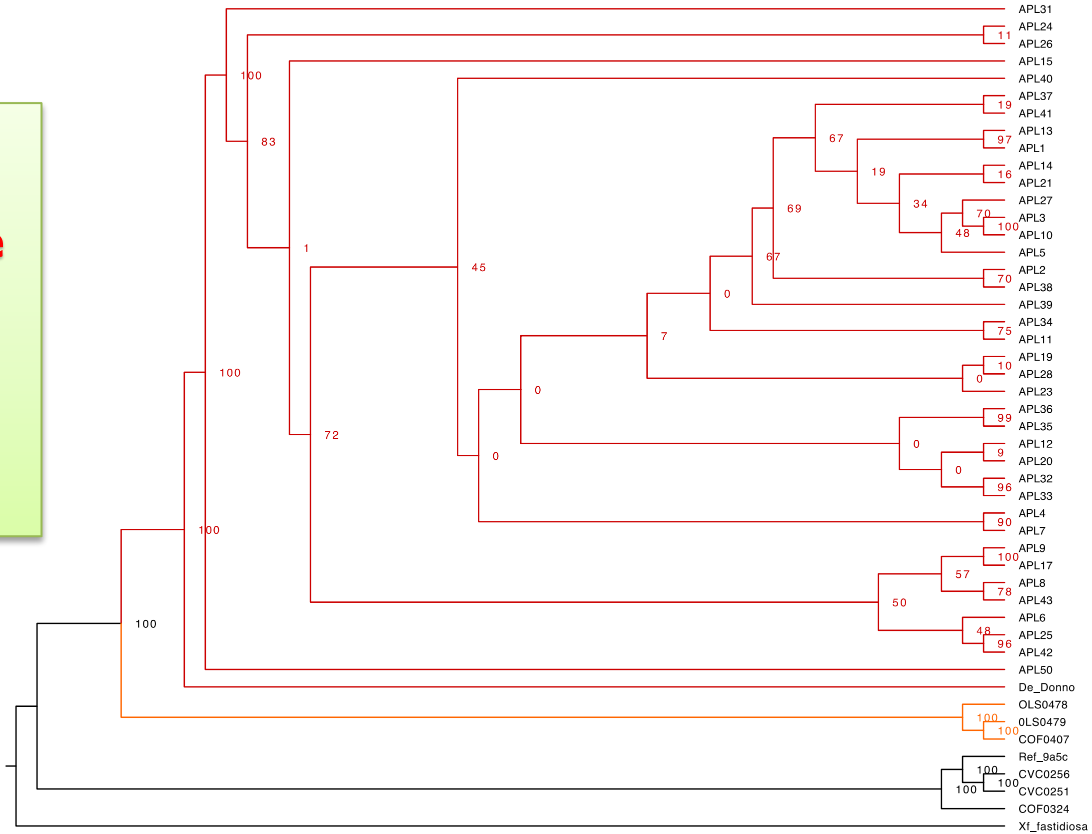
Fig. 5. Model of possible mechanisms involved in *Xylella fastidiosa* adhesion to xylem vessels of grapevines. **A,** *X. fastidiosa* bacteria attach to the surface, probably using fimbrial and nonfimbrial adhesins other than FimA, FimF, and hemagglutinins (this study, Feil et al. 2003); **B,** HxfA, HxfB, and other adhesins mediate secondary contact between *X. fastidiosa* cells, which leads to **C,** microcolony formation. Based on our results, hemagglutinins appear to be important mediators for cell-cell aggregation. **D,** Bacterial cells finally aggregate to each other via hemagglutinins HxfA and HxfB, fimbriae, and exopolysaccharides to form matured biofilms within the xylem vessels (this study, Feil et al. 2003).

from MR Guilhabert and BC Kirkpatrick 2005

CONCLUSIONS

- ✓ Complete genome of the *Xf* strain **De Donno** was been used as a **reference for the typing by WGS** (SNP based) of all **40 isolates** that were **sampled** in the **outbreak of Apulia** (NGS task Bari/Berkeley)

Genetic similarity among Apulian isolates



Number of SNPs in comparison to the Apulian strain De Donno:

Isolates	APL1	APL2	APL3	APL4	APL5	APL6	APL7	APL8	APL9	APL10	APL11	APL12	APL13	APL14	APL15	APL17	APL19	APL20	APL21	APL23	APL24
Number of SNPs	135	144	158	141	146	148	157	144	133	160	152	159	135	136	131	141	151	144	150	144	139
Isolates	APL25	APL26	APL27	APL28	APL31	APL32	APL33	APL34	APL35	APL36	APL37	APL38	APL39	APL40	APL41	APL42	APL43	APL50	COF0407	OLS0478	OLS0479
Number of SNPs	134	143	157	157	142	142	142	136	146	141	145	145	156	152	145	141	146	126	172	192	155

Slide from Anne Sicard (Berkeley)

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Updating of Whole-genome phylogeny based on SNPs and of pangenome analysis of *Xf*

<u>In 2017</u>,
40 *X.fastidiosa* genomes
becomes available in the NCBI genome database

https://www.ncbi.nlm.nih.gov/genome/genomes/173

kSNP

GET_HOMOLOGUES

27 genomes
(Giampetruzzi et al 2017):

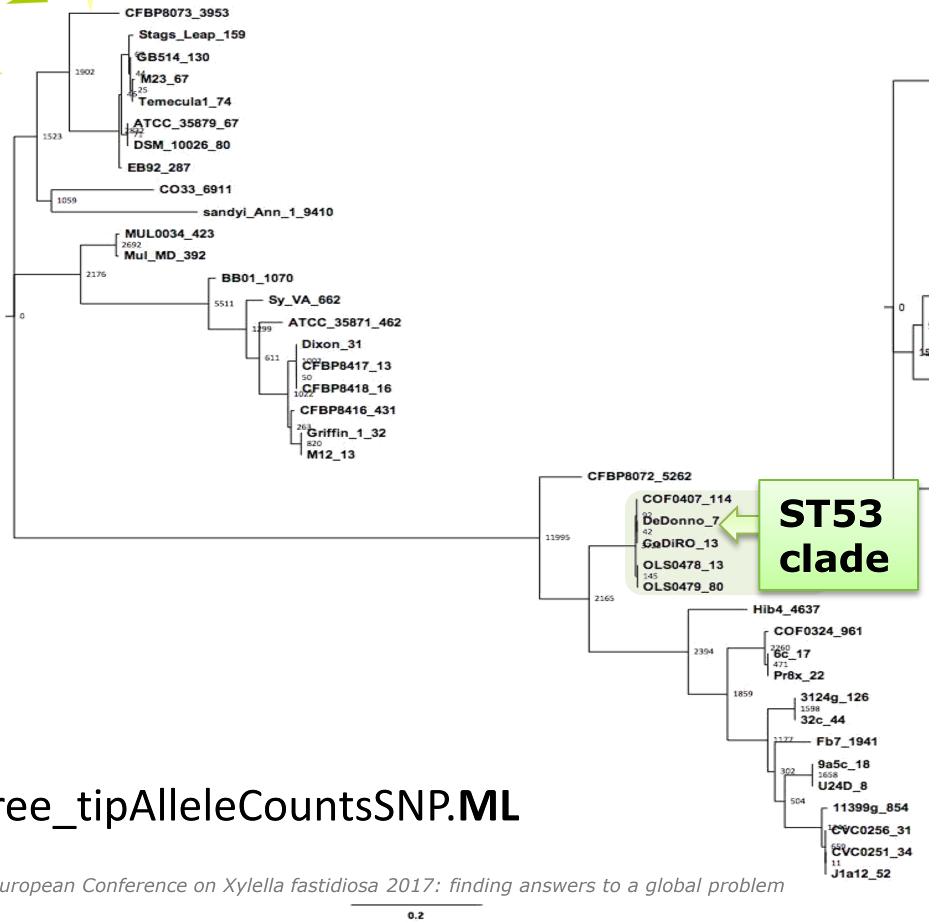
COF0324
9a5c
Temecula1
M12
M23
EB92.1
Dixon
ATCC 35871
32
Ann-1
MUL0034
Mul-MD
sycamore Sy-VA
ATCC 35879
CoDiRO
CO33
OLS0479
CVC0256
OLS0478
CVC0251
COF0407
Stag's Leap
CFBP8072
CFBP8073
6c
Griffin-1
GB514

13 Genomes available
In 2017

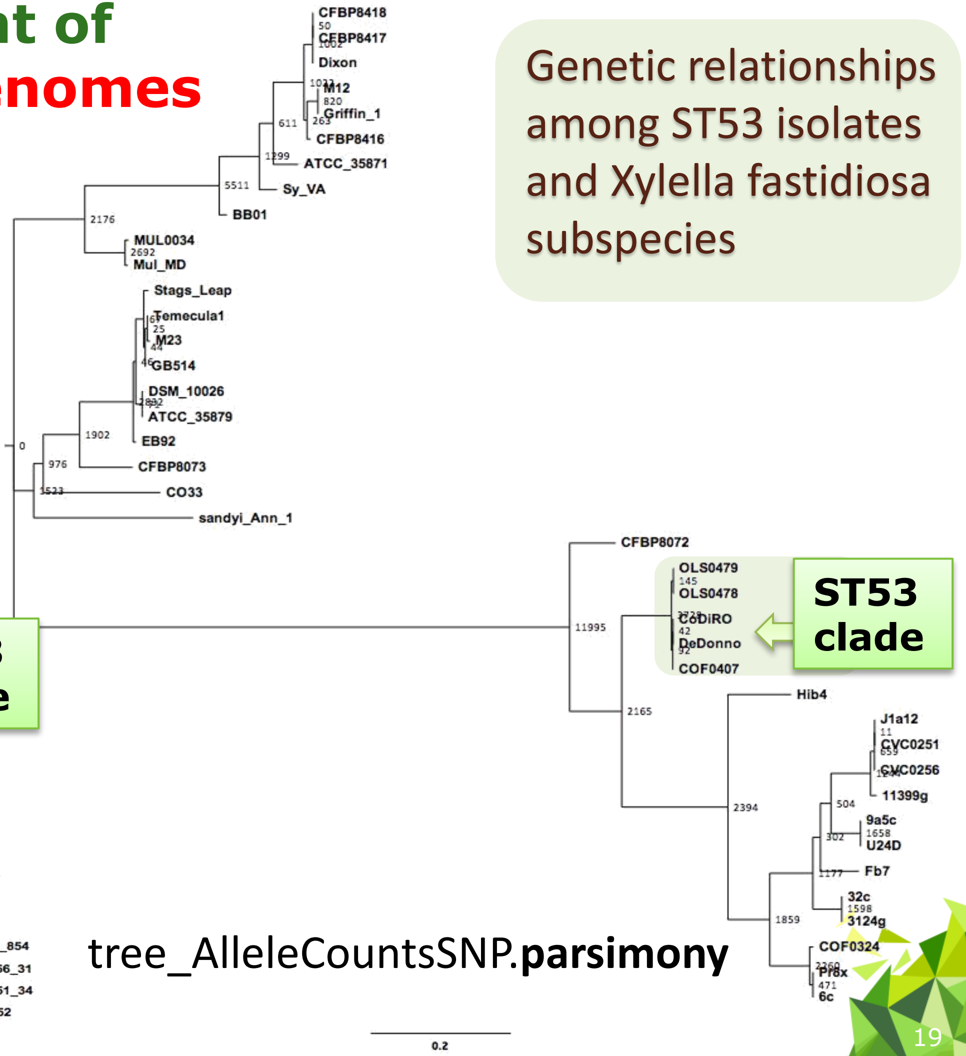
BB01
11399
DSM 10026
CFBP8418
CFBP8417
CFBP8416
Fb7
3124
J1a12
U24D
Pr8x
Hib4
<u>De Donno</u>

Phylogenetic placement of *Xf*-De Donno within 40 genomes

Genetic relationships among ST53 isolates and Xylella fastidiosa subspecies



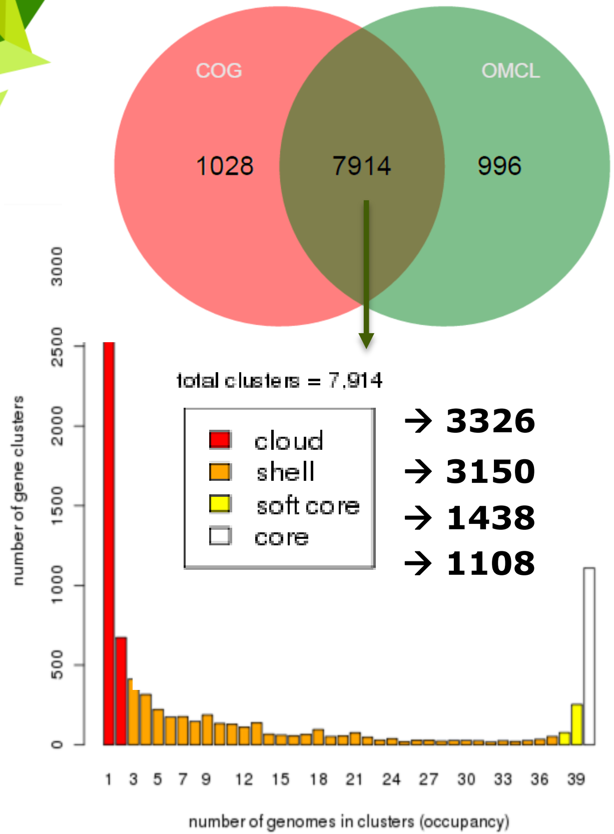
tree_tipAlleleCountsSNP.**ML**

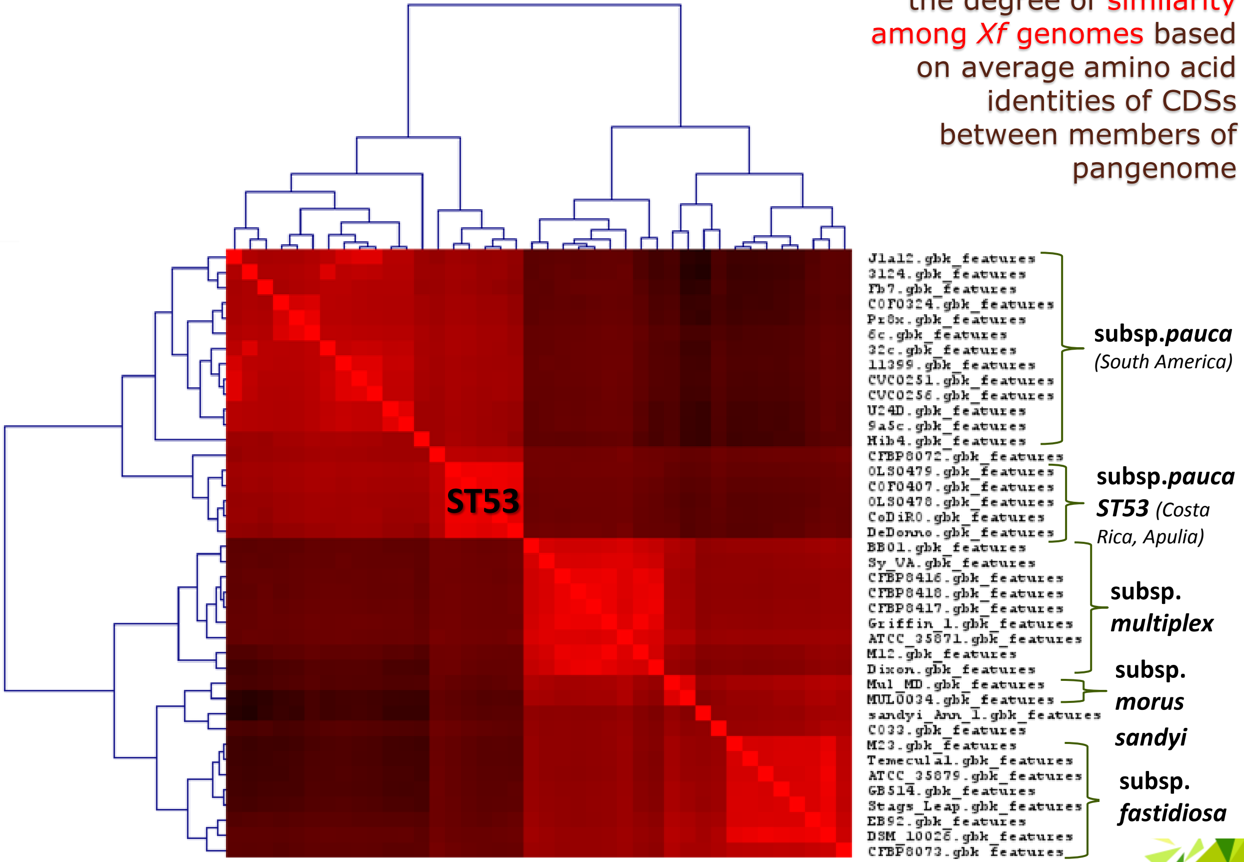


tree_AlleleCountsSNP.**parsimony**

Updating of PANGENOME ANALYSIS OF *XYLELLA FASTIDIOSA*

Heatmap representing the degree of similarity among *Xf* genomes based on average amino acid identities of CDSs between members of pangenome



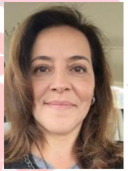


3) CONCLUSIONS

- The results of the updating of whole-genome phylogenies based on SNPs and of pangenome analysis of Xf genomes confirmed the **phylogenetic placement of "De Donno"** and the ST53 clade previously published.

- Gene encoding a putative histidine kinase-like **ATPase, identified** only in the clade of **the Italian and three Costa Rican ST53 isolates**, still remains unique to that clade.

Thanks to



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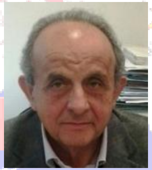

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ReCaS Selge RETI SELGE and
INFN Data Center

Add slides

Xylella fastidiosa from olive is a ST53 phylotype

MLST loci ←→ non MLST locus

ST	*leuA*	*petC*	*malF*	*cysG*	*holC*	*nuoL*	*gltT*	*pilU*
53	7-p	6-p	16-p	24-u	10-p	16-u	14-p	27-p

p: allele from *pauca*
u: allele unknown

pauca ancestry

Nunney et al. 2014. The complex biogeography of the plant pathogen *Xylella fastidiosa*: genetic evidence of introductions and subspecific introgression in Central America. PlosONE

Loconsole et al. 2016. Intercepted isolates of *Xylella fastidiosa* in Europe reveal novel genetic diversity. Eur. J. Plant Path.

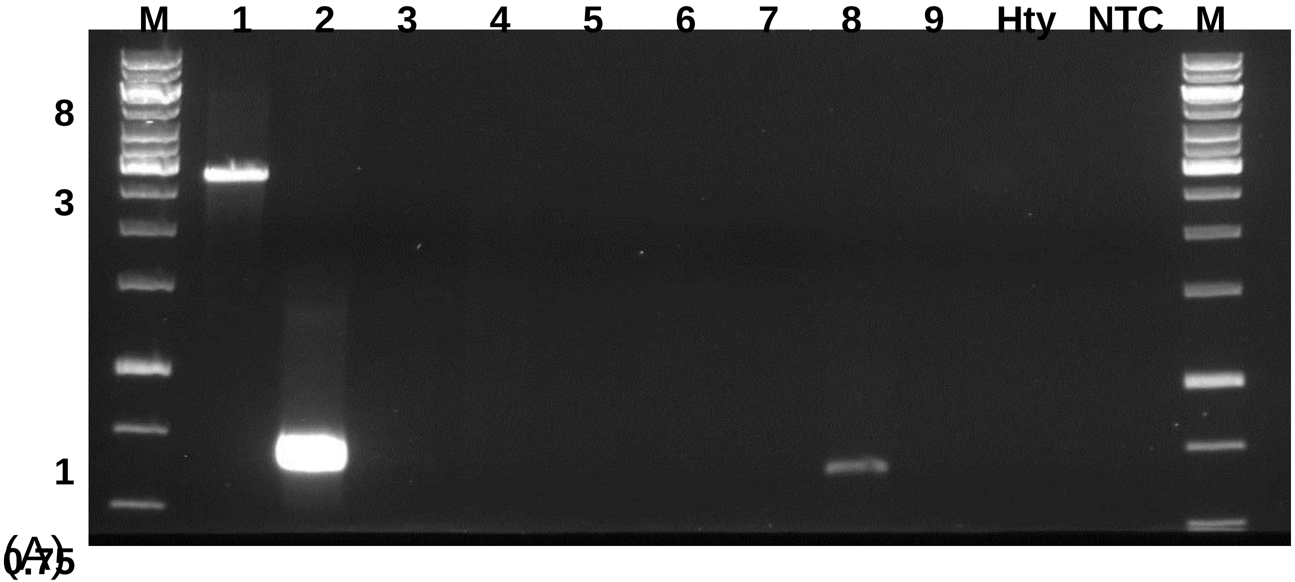

Fig. 6. Gel electrophoresis showing the products of PCR amplications of different *X. fastidiosa* subspeces with primers ATPase for1 / ATPase rev2. Amplifications were from bacterial DNA of isolates: (A) CoDiRO (lane 1), J2 (lane 2), Temecula (lane 3), Dixon (lane 4), Sandyi (lane 5), AlmaEm3 (lane 6), BB08-1 (lane 7), J4 (lane 8); CO33 (lane 9), total DNA from xylem of healthy olive tree (lane Hty) and no template control (lane NTC); Generuler 1kb DNA ladder, Thermo Scientific (lane M). (B): No3 (lane 1), Vv2 (lane 2), Ca4 (lane 3), No3 (lane 4), No1 (lane 5), No5 (lane 6), Vv1 (lane 7), Ca7 (lane 8), Ca5 (lane 9), No2 (lane 10), No4 (lane 11), No7 (lane 12) and no template control (lane NTC); O'Gene-rulerTM DNA ladder mix, Fermentas, St Leon-Rot, Germany (lane M).(C): (C): J33 (lane 1), J1 (lane 2), J41 (lane 3), J44 (lane 4), J48 (lane 5), J68 (lane 6), 6570 (lane 7), J12 (lane 8), J62 (lane 9), J55 (lane 10), J65 (lane 11), 9a5c (lane 12) and no template control (lane NTC). Relevant bands of the Generuler 1kb DNA ladder (lane M; Thermo Scientific) are reported.

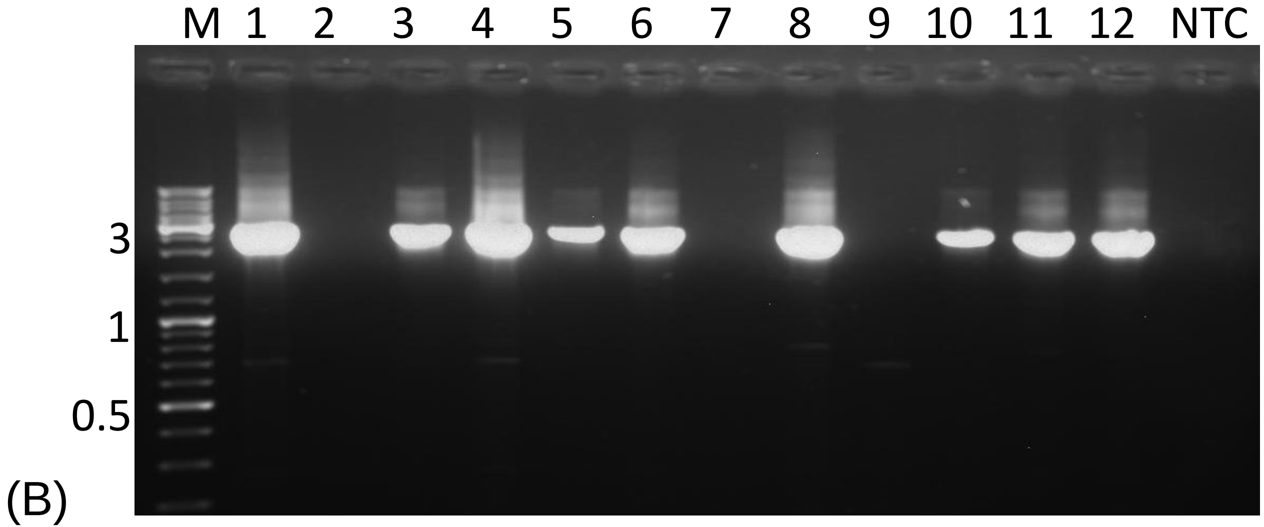

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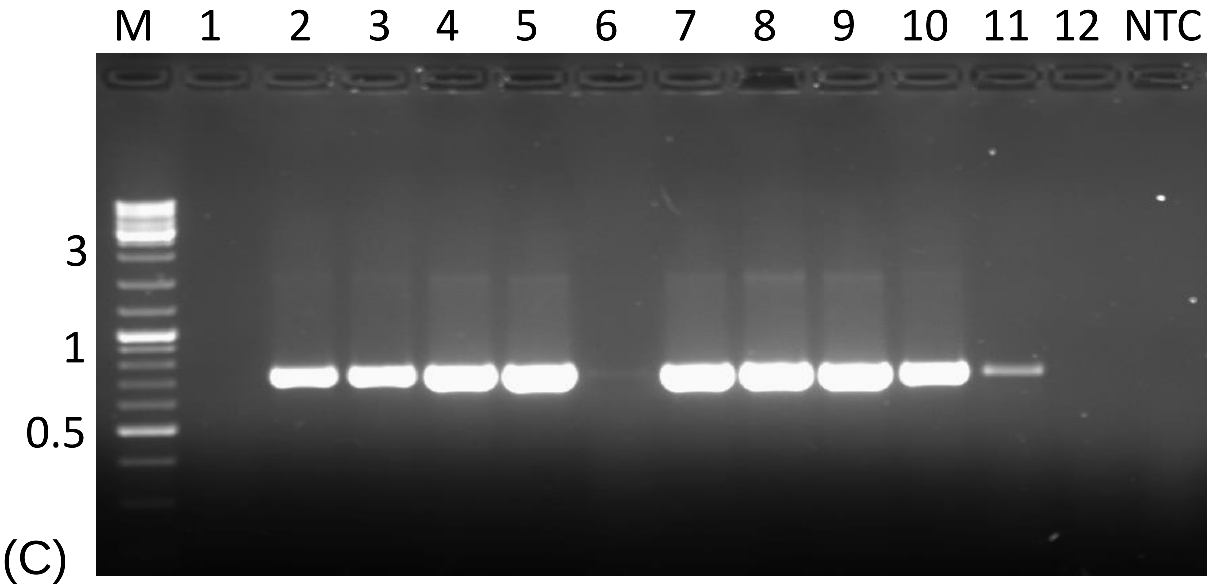
Figure 6. Giampetruzzi

Phytopathology



J33 J1 J41

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pm_pierry@msn.com**Keywords: Phytopathogen, *Xylella fastidiosa*, Leaf Scald, Pyrosequencing, Comparative genomics.**
Xylella fastidiosa is a non-flagellated Gram-negative bacterium, of the Gamma-proteobacteria subgroup, that colonizes the xylem of many cultivated and wild plants, eventually causing economically important diseases. Genomes of X. fastidiosa strains isolated from different hosts have been completely or partially sequenced and. comparative genomics studies associated with functional genomics and molecular genetics approaches have enabled detailed studies of mechanisms potentially relevant to disease development. Except for strain 9a5c, all other publicly available genome sequences are from strains isolated in North America. Here we describe the genome pyrosequencing of strains Pr8x and Hib4 isolated, respectively, from plum and hibiscus. Global nucleotide sequence comparison show extensive collinearity between both genomes, greater than with strain 9a5c. Strain Pr8x has a main chromosome of 2,666,242 bp and one plasmid, pXF39, of 39,580 bp which presents similarities with pXF51 from the reference strain 9a5c. Hib4 shows the largest chromosome (2,813,297 bp) and the largest plasmid (pXF64 with 64,251 bp) described for X. fastidiosa. pXF64 shows extensive similarity with plasmid pBVIE04 of Burkholderia vietnamensis G4 strain and is described for the first time in X. fastidiosa. This plasmid presents all repertoire for conjugal transfer, besides hypothetical proteins. Comparative analyzes of these genomes have identified several differences that may be correlated with the phenotypes displayed by these strains. Both genomes have shown some shared differences when compared to the reference genome from strain 9a5c. Two absent CDS were observed, coding for an arginine deaminase and HicB protein. The Pr8x genome showed other absent CDS: a toxin/antitoxin system (HigB/HigA) and a cluster of CDS related to conjugal transfer proteins (trb genes). Other CDS have shown deletions and polymorphisms that may impair their functions in both genomes, like "hemagglutinin-like" proteins, a surface protein and hemolysin-like proteins. For Pr8x, additional CDS, coding for PilY1 and PilQ are discrepant, as well as a fimbrial adhesin precursor and ChpA in Hib4 genome. ***Finally, we highlight that in both genomes the CDS coding for a polygalacturonase precursor was found intact, without the nucleotide insertion observed in other South-American strains, which would generate a truncated protein; thus, this important enzyme must be functional in these strains, as observed in North-American strains. Therefore, genome sequencing of these Xylella strains isolated from different plant hosts brings new information that might explain host specificity and disease development.******Financial Support: CNPq, FINEP and FAPESP***.

COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

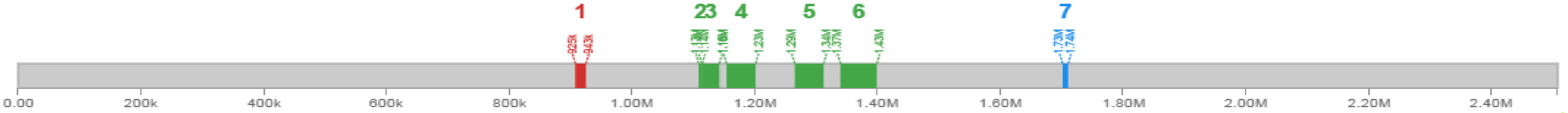
PROPHAGE REGIONS ANNOTATION

PHASTER

Total: 7 prophage regions have been identified, of which 5 regions are intact, 1 regions are incomplete, and 1 regions are questionable.

Region	Region Length	Completeness	Score	# Total Proteins	Region Position	Most Common Phage	GC %	Details
De_Donno Xylella fastidiosa subsp. pauca								
1	17.7Kb	incomplete	60	19	925482-943270	PHAGE_Cyanop_S_RIM50_NC_031242(6)	58.72%	Show
2	5.9Kb	intact	107	8	1130312-1136279	PHAGE_Stenot_phiSMA9_NC_007189(5)	44.44%	Show
3	29Kb	intact	128	38	1135598-1164639	PHAGE_Stenot_phiSMA7_NC_021569(6)	43.70%	Show
4	48.4Kb	intact	150	51	1176535-1225033	PHAGE_Xylell_Xfas53_NC_013599(32)	54.68%	Show
5	47.9Kb	intact	100	69	1289895-1337865	PHAGE_Pseudo_JBD69_NC_030908(27)	55.29%	Show
6	60.6Kb	intact	110	56	1365616-1426305	PHAGE_Pseudo_NP1_NC_031058(25)	54.19%	Show
7	9Kb	questionable	85	13	1734875-1743918	PHAGE_Stenot_phiSMA7_NC_021569(4)	43.51%	Show

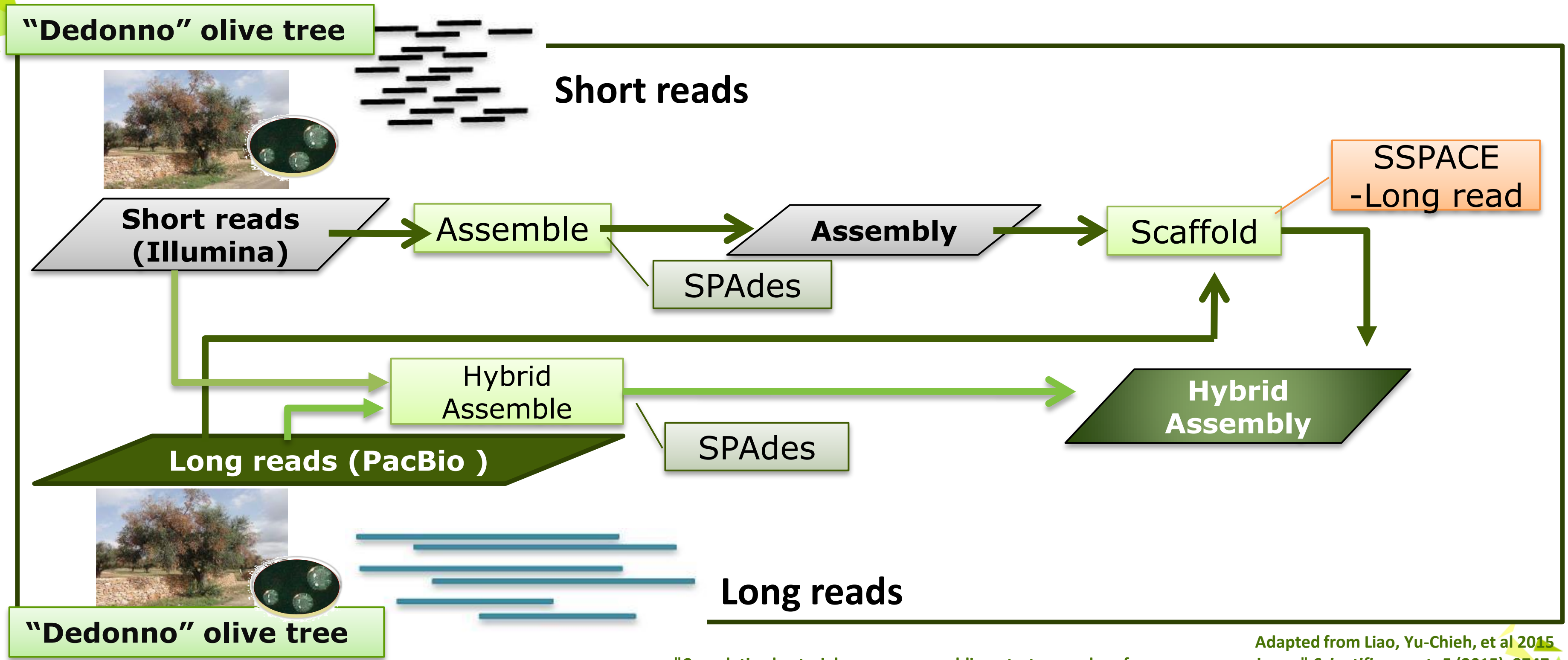
Intact (score > 90)
Questionable (score 70-90)
Incomplete (score < 70)



De_Donno Xylella fastidiosa subsp. pauca

COMPLETE GENOME SEQUENCE OF THE OLIVE-INFECTING STRAIN *XYLELLA FASTIDIOSA* SUBSP. *PAUCA* DE DONNO

ASSEMBLY STRATEGIES



Adapted from Liao, Yu-Chieh, et al 2015
"Completing bacterial genome assemblies: strategy and performance comparisons." *Scientific reports* 5 (2015): 8747.