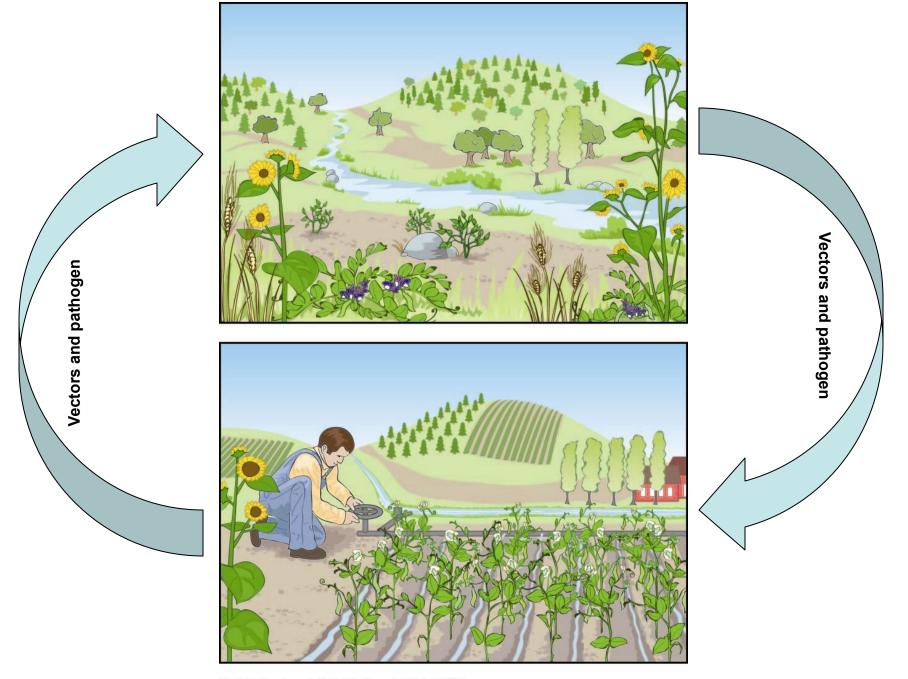


Layers of ecological complexity:

- environment (e.g. temperature)
- vector ecology
- pathogen ecology
- host plant ecology
- ✓ outcome of various interactions
- ✓ disease management

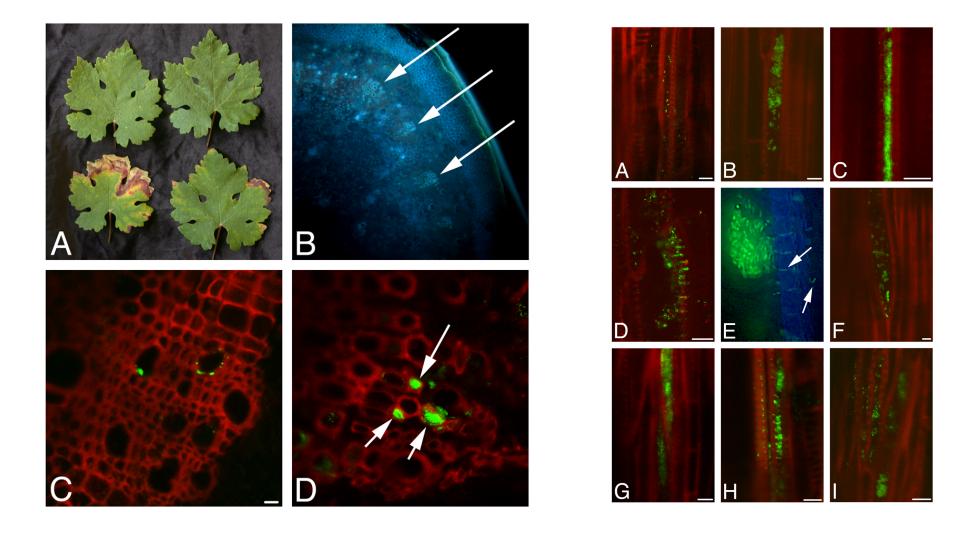


R Stukenbrock EH, McDonald BA. 2008. Annu. Rev. Phytopathol. 46:75–100

Xylella fastidiosa

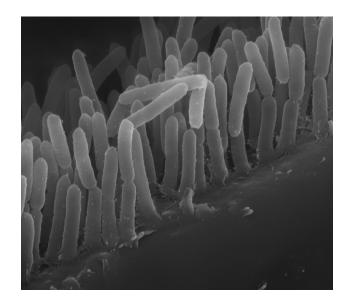
- Gammaproteobacteria, Xanthomonadaceae
- Xylem-limited bacterium
- Colonizes >350 host plant spp., usually without causing disease
- Present throughout the Americas, more recently reported in Taiwan, Italy, France, Iran, Spain...
 - Major crops affected include grape, citrus, coffee, almond, peach, plum, pecan, olive, various ornamentals and shade trees
- Xylem sap-feeding insects are only vectors
 - Cicadellinae (sharpshooter leafhoppers), Cercopoidea (spittlebugs)

Plant colonization



Vector transmission of *X*. *fastidiosa* - the basics -

- \checkmark No vector species pathogen strain specificity
- ✓ Nymphs and adults transmit *X. fastidiosa*
- \checkmark No latent period
- \checkmark No transmission after molting
- \checkmark No transovarial transmission
- ✓ Persistent



Brief introduction

Why are we here?

Drivers of disease emergence

X. fastidiosa – what does it mean?

X. fastidiosa detected in Italy in October 2013



Donato Boscia

The previous 'absence' of *Xylella fastidiosa* from Europe is not a recent interest to those working with this bacterium

Journal of Plant Pathology (1997), 79 (2), 99-105 Sedizioni ETS Pisa, 1997

99

INVITED REVIEW XYLELLA FASTIDIOSA, A REGIONAL PROBLEM OR GLOBAL THREAT? A.H. Purcell

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SUMMARY

Until now, the xylem-limited bacterium Xylella fastidiosa has been recorded only from the Americas, with the exception of a pear disease in Taiwan. Is this bacterium a potential threat to other continents and islands? Climate appears to play a major role in the geographic distribution of diseases caused by X. fastidiosa, but this differs with strain and host plant. Mild winters may be necessary for the long term persistence of X. fastidiosa within a climatic region, but the possible limiting effects of summer temperatures have not been explored. Potential vectors are widespread and often common in most parts of the world not currently affected by X. fastidiosa. An important feature to maintain endemic infections of the bacterium in temperate regions may be the occurrence of potential vectors that overwinter as adults. Previously unrecorded plant diseases in citrus and oleander, caused by X. fastidiosa, have rapidly spread, suggesting that vigilant phytosanitary measures outside the Americas should be maintained against the introduction of X. fastidiosa. Molecular detection methods such as the polymerase chain reaction for a wide spectrum of strains of X. fastidiosa are preferable to serological methods because of their sensitivity and reliability.

RIASSUNTO

XYLELLA FASTIDIOSA, UN PROBLEMA REGIONALE O UNA MINACCIA MONDIALE? Il batterio xilematico Xylella fastidiosa è stato sinora riscontrato, con l'eccezione di una malattia del pero a Taiwan, solamente nel continente americano. Il batterio costituisce una minaccia potenziale per altri paesi? Le condizioni climatiche sembrano giocare un ruolo importante nella distribuzione geografica della malattia causata da X. fastidiosa, ma vi sono anche differenze a livello di ceppo e di pianta ospite. Nell'ambito di una determinata re-

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gione climatica possono essere necessari inverni miti per assicurare la persistenza a lungo termine di X. fastidiosa, tuttavia i possibili effetti limitanti delle temperature estive non sono stati ancora analizzati. I vettori potenziali sono diffusi e frequenti in gran parte delle regioni del globo non ancora interessate da X. fastidiosa. Un elemento importante, capace di mantenere le infezioni endemiche del batterio in regioni temperate. potrebbe essere rappresentato dalla presenza di vettori potenziali svernanti come adulti. Malattie, non riscontrate in precedenza su agrumi e su oleandro e causate da X. fastidiosa, si sono diffuse rapidamente, suggerendo come, al di fuori del continente americano, debbano essere mantenute misure fitosanitarie rigide al fine di impedire l'introduzione di X. fastidiosa. Metodi di determinazione molecolare, come la PCR nei confronti di un'ampia gamma di ceppi di X. fastidiosa, sono preferibili a quelli serologici in quanto più sensibili e affidabili.

Key words: epidemiology, vectors, Xylella fastidiosa.

INTRODUCTION

The xylem-limited bacterium Xylella fastidiosa (Wells et al., 1987) causes diseases in many plant species in the Americas, mostly in woody perennials such as grape, peach, almond, citrus and oak (Hopkins, 1989; Purcell and Hopkins, 1996). Outside of North or South America, the bacterium has been reported to have been isolated only from Taiwan, where it causes leaf scald in pear (Leu and Su, 1993). Table 1 reviews the plant diseases proven or suspected to be caused by X. fastidiosa. Grape or alfalfa strains of the bacterium have a very wide plant host range (Freitag, 1951); essentially 3 of every 4 species were classified as symptomless hosts, based on the vector transmission of the causal agent of Pierce's disease. With such a large vector and host range, the continued restriction of these diseases to the Americas is puzzling (Purcell, 1989; Purcell and Hopkins, 1996). Does Xylella fastidiosa pose a threat to Europe, Asia, Africa, Australia, and other continents or islands where now it is unknown?

The characteristics of vector transmission of X. fastidiosa suggest that a lack of potential insect vectors should be no obstacle to sustaining introductions of the bacterium in new regions. There is broad group speci-

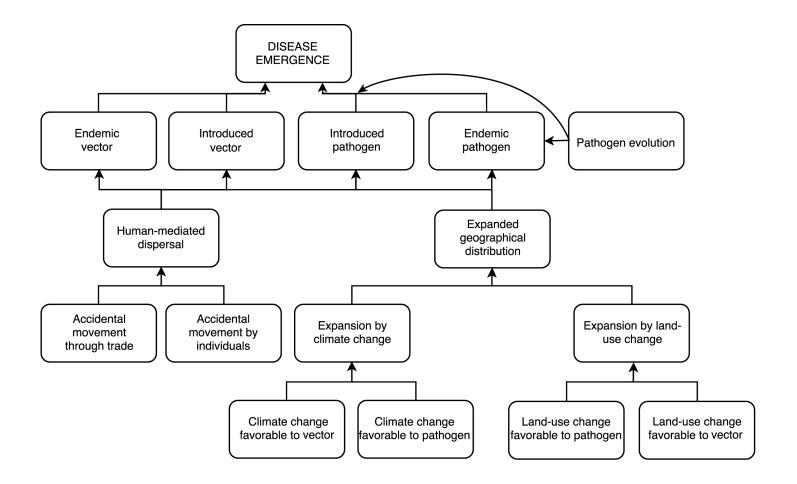
> vectors are not a limiting factor anywhere in Europe

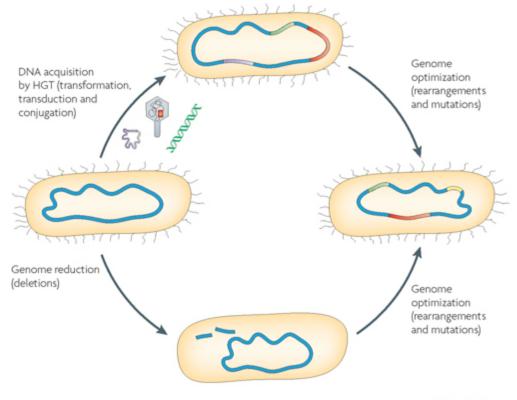
plants with lower or non-systemic populations. However the symptomless condition of most hosts is a threat because the lack of symptoms may contribute to illegal importation of seemingly healthy plants. In addition the lower populations of *X. fastidiosa* in symptomless plants may make detection of the bacterium more difficult.

the fact one cannot 'see' disease or detect the pathogen does not mean it is not present

introductions should be prevented, efforts to limit dispersal should be implemented

These indicate that the most logical emphasis of phytosanitary measures to prevent the introduction of *X*. *fastidiosa* to new regions now free of this pathogen should be to monitor the movements of live plants from regions where *X*. *fastidiosa* occurs.





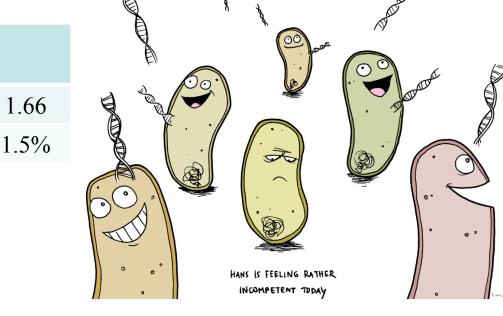
Nature Reviews | Microbiology

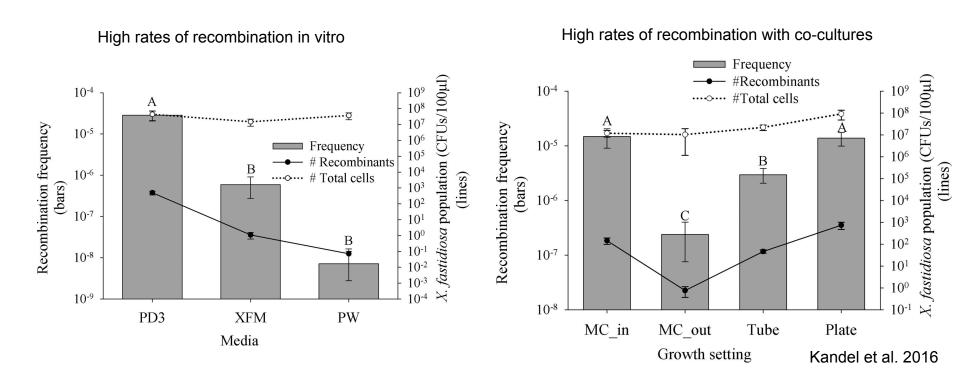
Recombination more common than mutations -using 'field' MLST data-

Relative rate of recomb	tion to mutation 1.66

Mean divergence of imported DNA

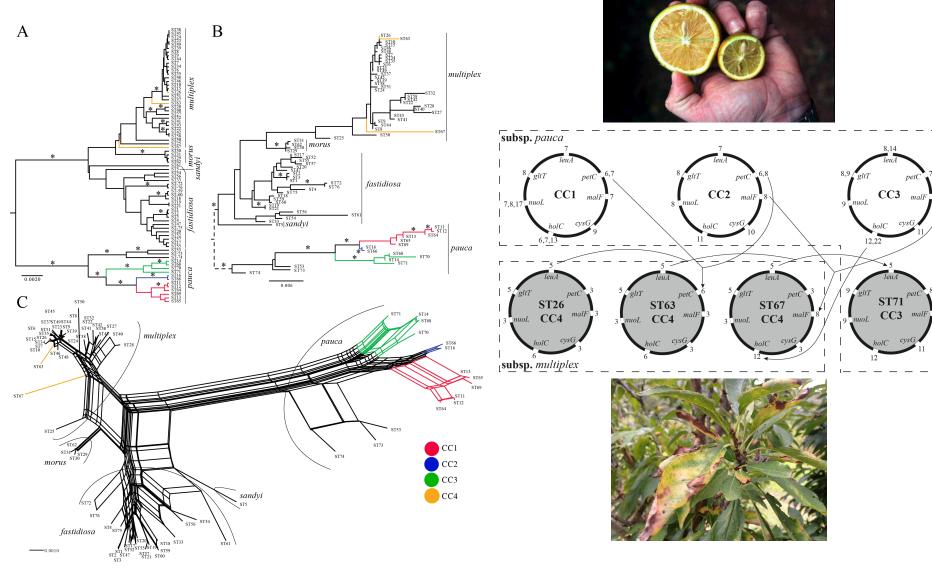
Data: all MLST data available in November 2017. Analysis done with ClonalFrameML using default settings.





Does recombination matter?

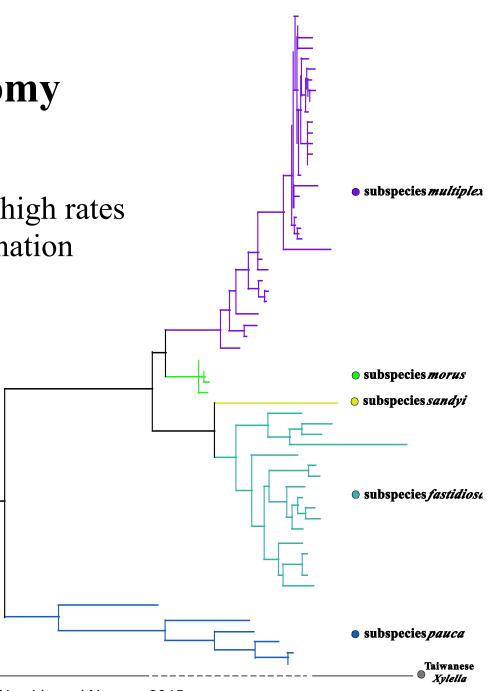
-a detection/inference example-



Coletta-Filho et al. 2017

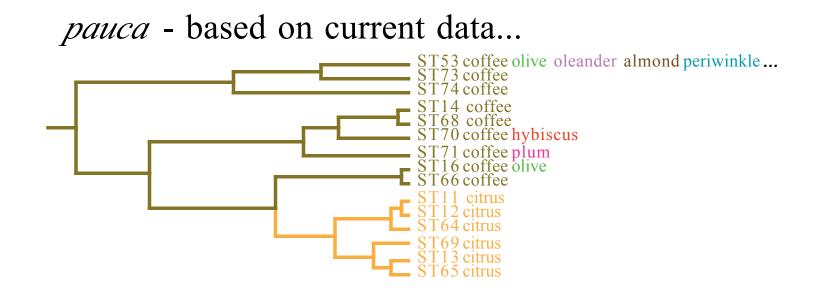
X. fastidiosa taxonomy

- based on MLST, robust
- MLST important due to high rates of homologous recombination
- but what does it tell us?

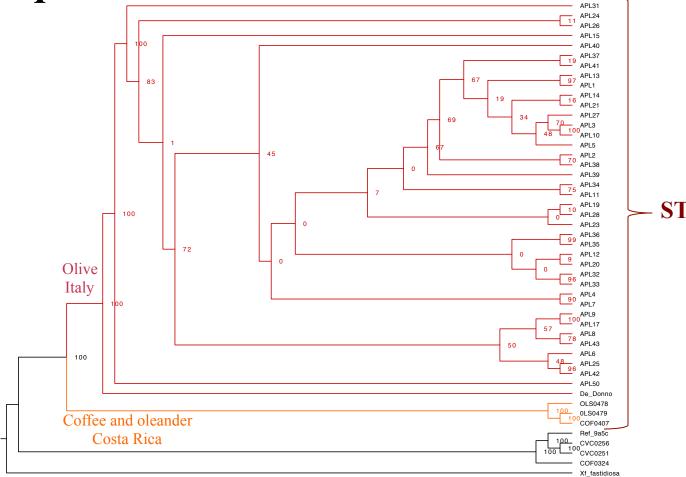


Almeida and Nunney 2015

What does subspecies mean biologically? -an example with *pauca*-



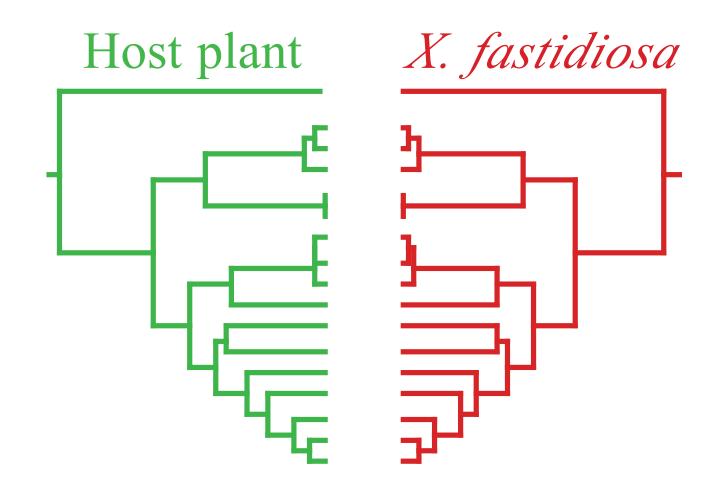
What does ST mean? -an example with subspecies pauca ST53-



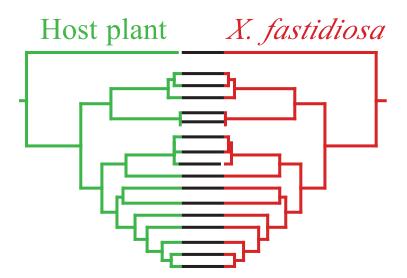
ST53

Sicard et al.

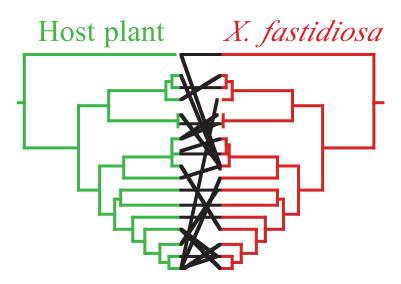
Host jump predictions



tree congruence, host jump prediction feasible

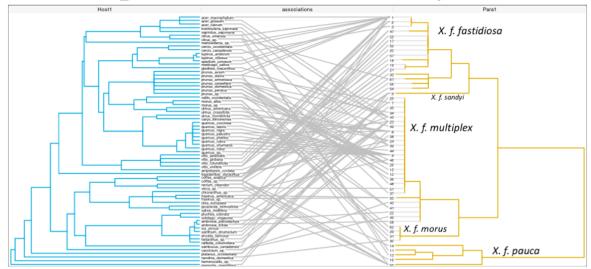


no tree congruence, host jump prediction not feasible

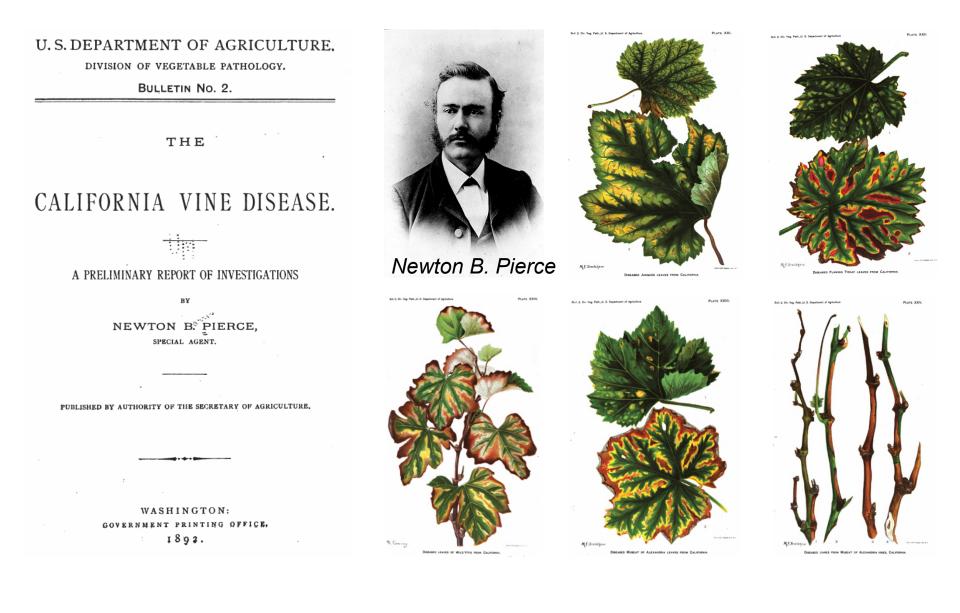


Host plant

X. fastidiosa



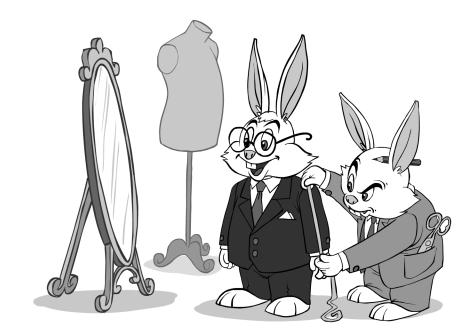
Test is statistically significant -i.e. no congruence of treesA historical perspective as Europe embarks on X. fastidiosa research



X. fastidiosa diseases are complex, multi-factorial, and management requires holistic approaches.

There is no 'one-size fits all' solution for *X. fastidiosa* diseases, or any solution available that does not require vector control and inoculum removal.





ONE SİZE FİTS ALL

MADE TO MEASURE

unknown source 'the internet'