Department of
Primary Industries

Navigating the World of *Xylella* spp.: Insights and Strategies

Welcome to Country

May I begin by acknowledging Australia’s first farmers, in particular the Kaurna peoples, on whose lands we meet on today. I pay my respects to their Elders past and present, and acknowledge their historic and continuing role in the great story of South Australian agriculture.

I also pay my respect to the cultural authority of other Aboriginal peoples visiting /attending from other areas of Australia.

What has brought us here today

Xylella spp. is Australia's number 1 plant pathogen

Project and funding source for the workshop:

- **Hort Innovation Project MT17006:** Improving preparedness of the Australian horticultural sector to the threat potentially posed by *Xylella fastidiosa* (a severe biosecurity risk)
- This workshop was funded through the National Plant Biosecurity Diagnostics Network (NPBDN) under the National Plant Biosecurity Diagnostic Professional Development and Protocols Project. This project is coordinated and delivered by Plant Health Australia and is funded by the Department of Agriculture, Fisheries and Forestry. The objectives of the Project are to enhance and strengthen Australia's diagnostic capacity and capability to identify priority plant pests that impact on plant industries, environment and the community

Hort Innovation Project MT17006: Improving preparedness of the Australian horticultural sector to the threat potentially posed by *Xylella fastidiosa* (a severe biosecurity risk)

Objectives:

- To increase Australia's capabilities in the detection and identification of *Xylella fastidiosa*
- To test existing diagnostics available, EPPO, IPPC and recent protocols
- To develop a generic assay for *Xylella* spp.
- To visit countries with *Xylella fastidiosa* to learn how to identify symptomatic hosts, isolate the bacteria and the best methods for detection, plus tips and tricks that aren't available in protocols!

Project Team

Victoria

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AGRICULTURE VICTORIA

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Agenda

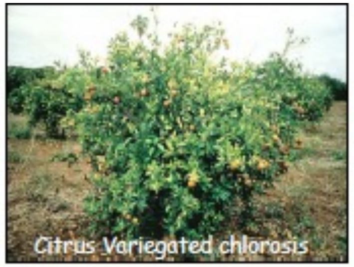
9:00	Welcome, Introduction and Background on *Xylella* spp.	Toni Chapman
9:15	Introduction and Background on *Xylella* spp. vectors	Piotr Trebicki
9:35	*Xylella fastidiosa* learnings and perspectives from the National *Xylella* coordinator	Craig Elliot
9:55	A New Zealand perspective, given the presence of a vector	Luciano Rigano
10:05	Importation of *Xylella* spp. and culture methods	Luciano Rigano
10:30	**Morning Tea**	
11:00	*Xylella* spp. a Plant Health Perspective, including the NDP verification process and validation	Rachel Mann
11:15	The new *Xylella* spp. National Diagnostic Protocol	Toni Chapman Monica Kehoe Luciano Rigano
11:45	A guide to sampling in the field	
12:45	**Lunch**	
13:30	Learnings from Overseas Study Tours Italy, Spain, France	Toni Chapman Monica Kehoe Luciano Rigano
14:00	The Americas	Pragya Kant
14:10	Contingency Planning and Gaps	Craig Elliot
15:00	**Finish**	
15:15	Bus departs to the National Wine Centre	

Introduction

Xylella spp. is not present in Australia

Xylella spp. is number one on Australia’s National Priority Plant Pest list

- Broad host range, which includes crops of horticultural importance to Australia (e.g. citrus, grape, olive, apple, pear, cherry, nuts and berries)
- Host range is expanding
- Unknown what impact *Xylella* spp. would have on native species



Olive quick decline syndro

Pierce's disease

Oak leaf scorch

https://gd.eppo.int/taxon/XYLEFA/photos

Order: Hemiptera, Suborder: Cicadomorpha

- Superfamily Membracoidea

  Family Cicadellidae
    Subfamily Cicadellinae

- Superfamily Cercopoidea

  Family Aphroporidae
  Family Cercopidae

- Superfamily Cicadoidea

  Family Cicadidae
  Familiy Tibicinae

The vector species can vary depending on the geographical region and the crop

The pathogen *Xylella* spp.

- First reported in California as a vine disease by Newton Pierce in 1892
- The first isolation of the pathogen was not until in 1978
- The formal description of *Xylella fastidiosa* didn’t occur until 1987
- *Xylella* is a gram-negative bacteria with a genome ~2.5 Mbp
- It is xylem-limited
- It invades xylem vessels, forms biofilms and secretes virulence factors

The pathogen *Xylella* spp.

- *Xylella* spp. is a fastidious bacteria
- *Xylella* spp. survives and multiples in its plant host and the insect vector
- *Xylella* spp. is transmitted via the insect vector, graft transmission and artificial inoculation
- *Xylella* spp. isolation from plant material can take 4-6 weeks to grow, experience in handling this bacteria is essential for biosecurity preparedness

Crucial life traits in *X. fastidiosa*

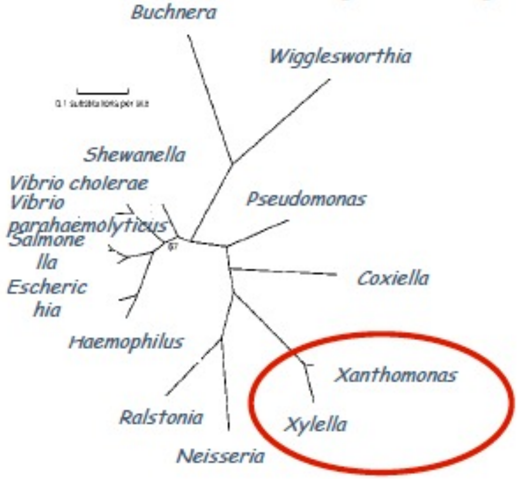
Genome reduction

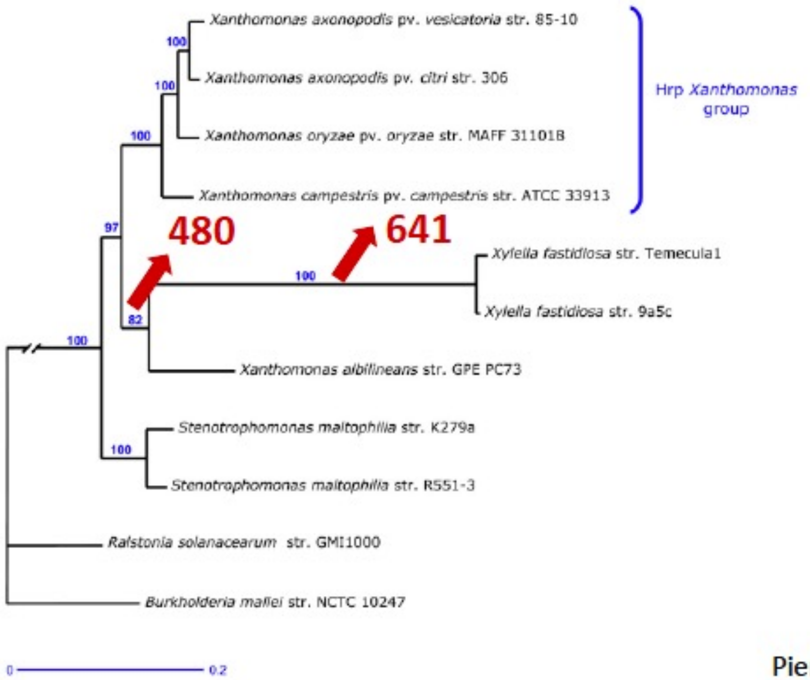
~2.5 Mb
1121 lost genes in comparison to Xcc

-Single events of deletion: flagellar gene cluster

-pseudogenization and short deletions:
2 genes of the rpf cluster (XCV1913 and XCV1914)

Berg and Goldberg, 2005





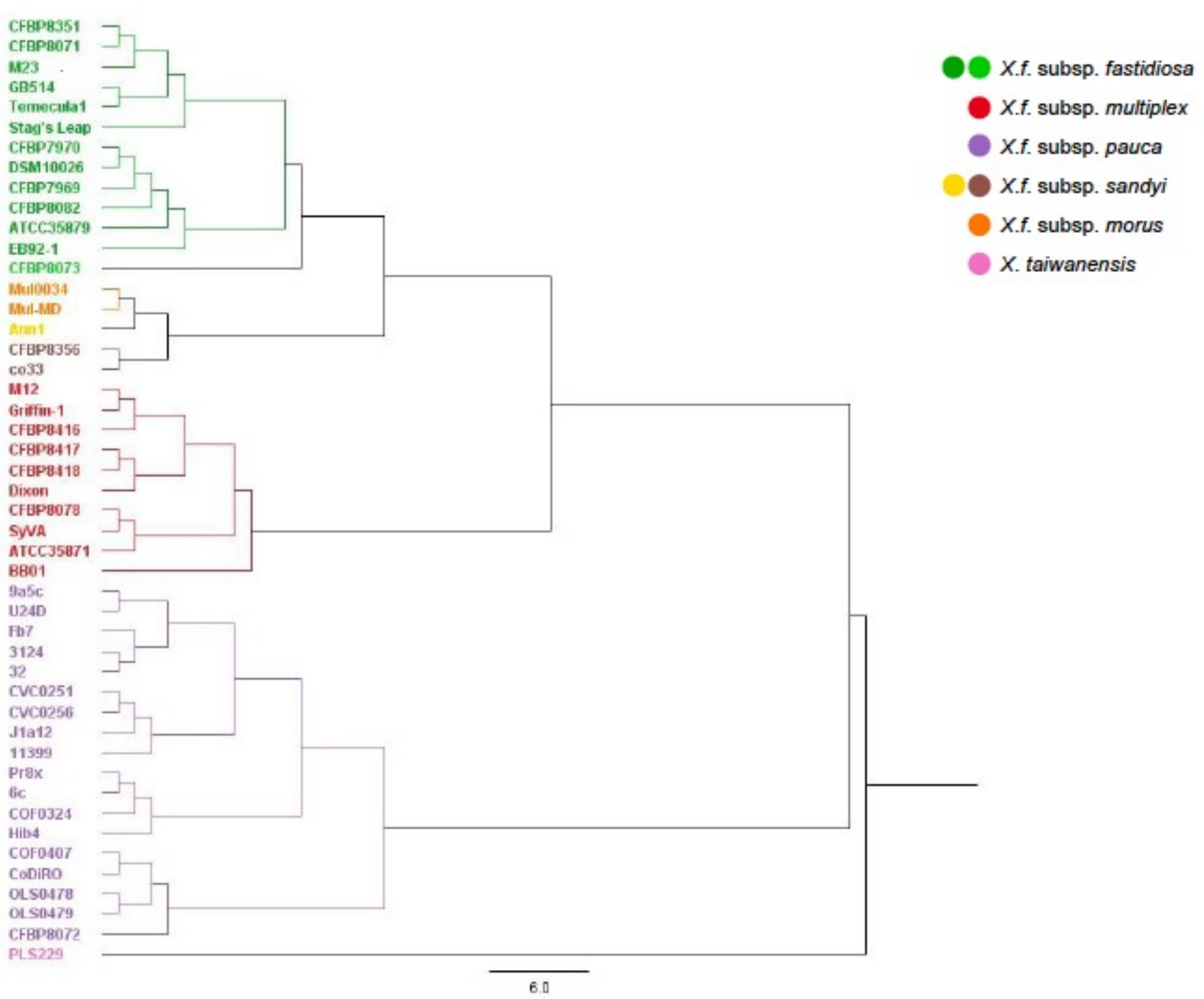
Total of 1121 lost genes

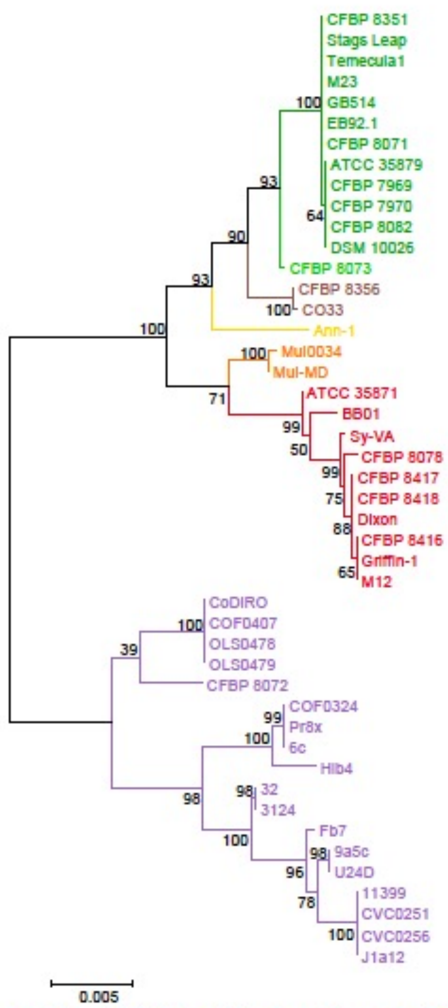
Pieretti *et al.*, 2009

The pathogen *Xylella* spp.

1 genus: *Xylella*
2 species: *X. taiwanensis*
X. fastidiosa
6 subspecies: subsp. *fastidiosa*
subsp. *multiplex*
subsp. *pauca*
subsp. *sandyi* *
subsp. *morus* *
subsp. *tashke* *
* Genomic data doesn’t support these subspecies.
* No original strains available for confirmation

The pathogen *Xylella* spp.


a. Whole genome-based dendrogram based on ANIb


b. MLSA-based ML tree

cysG, gltT, holC, leuA, malF, nuoL, petC
4161 bp

Denancé *et al.*, under revision; Marcelletti *et al.*, 2016

Mean genome length: 2.5 Mbp

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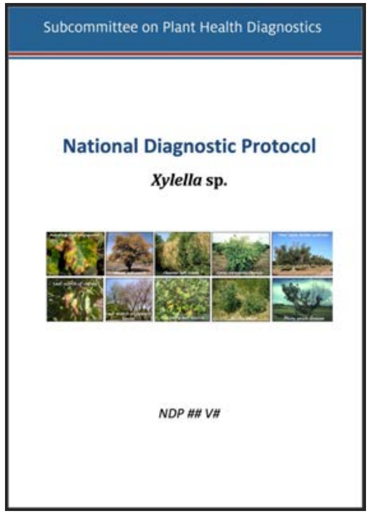
Improved diagnostics for *X. fastidiosa* to subspecies level



Subcommittee on Plant Health Diagnostics

National Diagnostic Protocol

Xylella sp.

NDP ## V#

Processing of samples & isolation of bacterial cultures

Section 9 – surveillance samples

Molecular assays

Generic *Xylella* QPCR assay

MinION genome sequencing

Differentiation between *X. fastidiosa* and *X. taiwanensis*

Subspecies identification multiplex QPCR

Multi-locus Sequence Typing (MLST)