DECIPHERING XYLELLA POTENTIAL PATHOSYSTEMS IN THE BELGIAN FLORA:

A study on northern European temperate regions with emphasis on riparian areas

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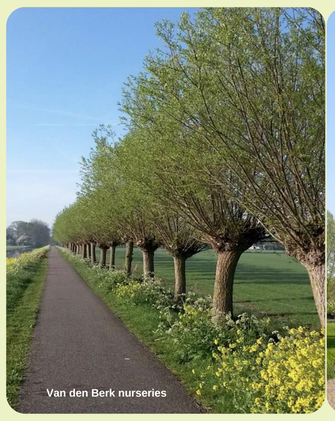
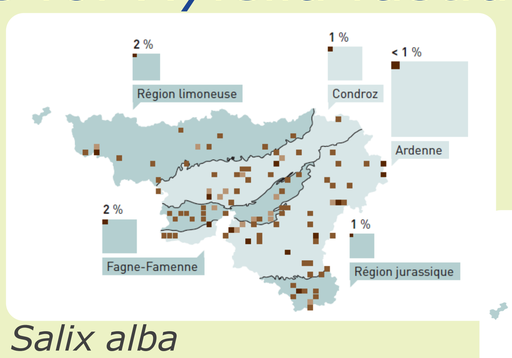
Salicaceae family are efficient host plants for *Xylella fastidiosa*



- Common in riparian tree layer
- Hosts of potential insect vectors
- Forming a closed-mesh network
- Plants can be symptomatic or asymptomatic
- Identified as potential (Purcell, 1974; Purcell & Saunders, 1999)



Salix alba

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Low presence
Average presence
Strong presence

Populus tremula

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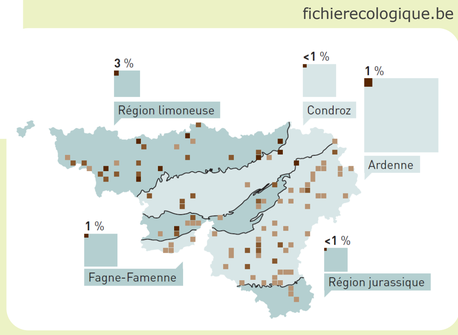
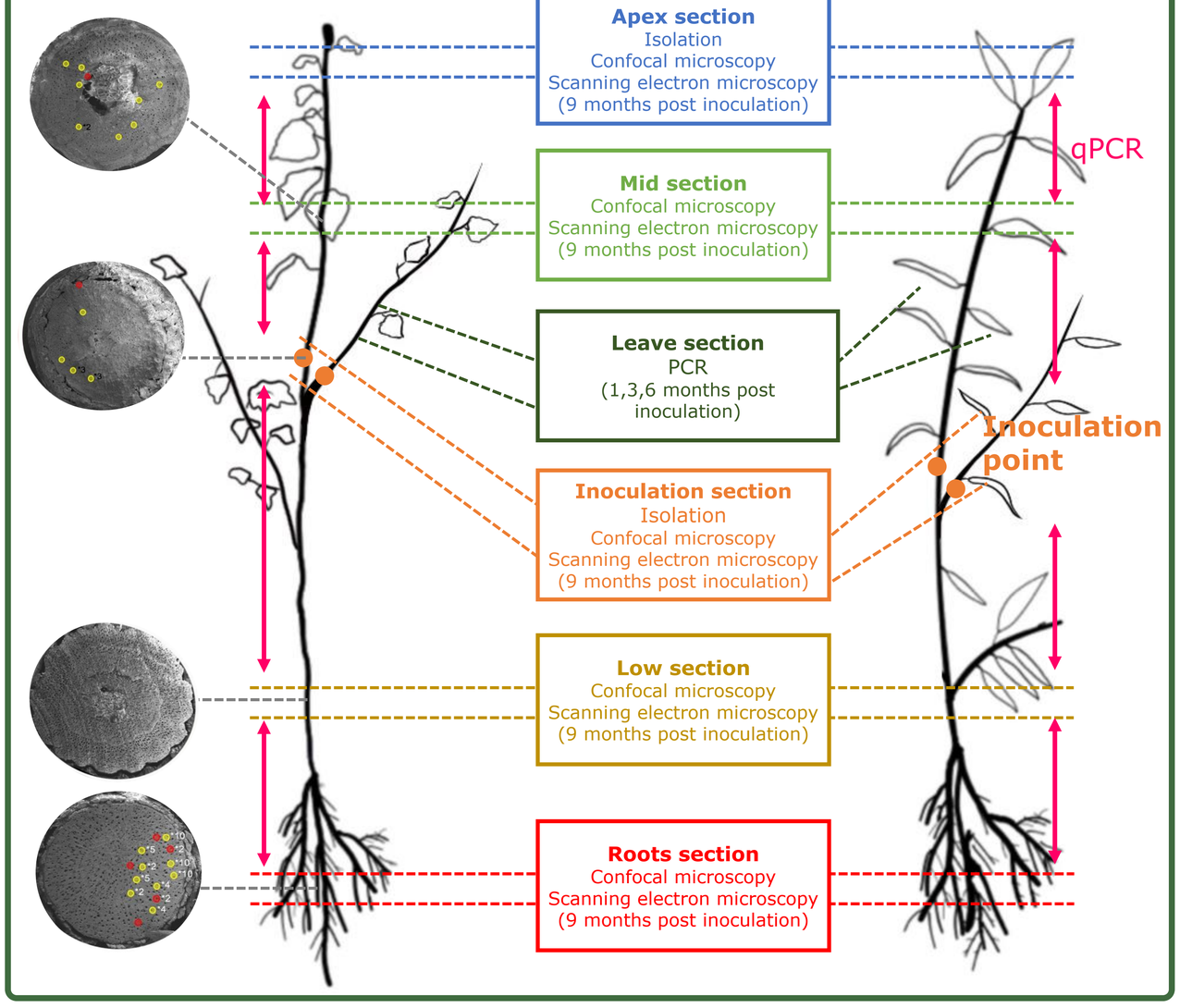


Mechanical inoculations

- *Salix alba*, *Salix caprea, Populus tremula*, *Populus canescens*
- Strain KLN59.3 Kanr GFP+ (Newman *et al*., 2003)
- **Pinprick inoculation method** (Hill & Purcell, 1995; Almeida *et al*., 2001)
- Conditions: $3x10^6$ CFU inoculated per branch, 2 branches, at 22°C and 28°C
- 10 inoculated plants + 3 mock-inoculated + 3 not inoculated.



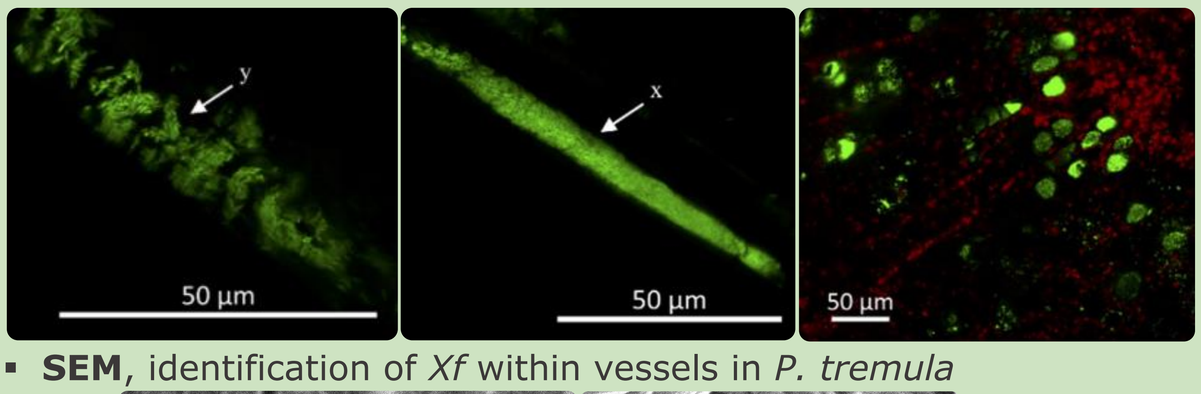
Post-inoculation

- **Symptoms monitoring**: *Xf* symptoms identified on *P.tremula* at 22°C and 28°C, 4 months post-inoc
- Monitoring colonization of *Xf* in the stem collecting leave petioles and testing them by **PCR** (Minsavage *et al*., 1994) 1-3-6 months post-inoc

	P. tremula		*P. canescens*		*S. alba*	
	22°C	28°C	22°C	28°C	22°C	28°C
Ip observation	4/5	4/5	1/3	2/3	3/3	1/3
Apex obs.	2/5	3/5	0/3	0/3	0/3	0/3
Root obs.	1/2	3/3	0/1	0/1	0/1	1/1
Maximum spread from ip - stem	29 cm above ip	65 cm above ip	No spread	No spread	93 cm above ip	82 cm above ip
Maximum spread from ip - roots	53 cm below ip	70 cm below ip	No spread	No spread	15 cm below ip	23 cm below ip

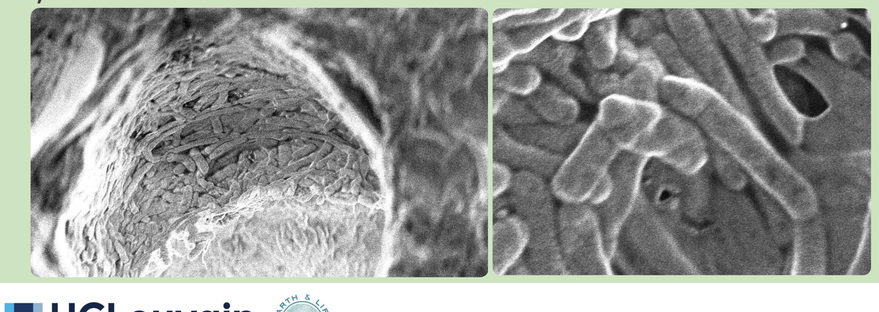
- Persistence & spread of *Xf* after 9 months in stems and roots by **confocal microscopy** and **qPCR** (Harper *et al*., 2010)

	P. tremula		*P. canescens*		*S. alba*	
	22°C	28°C	22°C	28°C	22°C	28°C
Ip CFU/g	3,11E+06	3,28E+05	5,16E+03	4,66E+04	9,61E+04	2,25E+04
Middle CFU/g	8,8E+06	4,88E+04	1,52E+03	6,18E+03	1,17E+05	2,87E+05
Apex CFU/g	3,33E+06	2E+05	5,19E+02	1,7E+03	1,82E+05	9,4E+04
Root CFU/g	5E+05	1,92E+06	3,29E+05	-	1,27E+05	5,82E+02



(Casarin et al., 2022)

- **SEM**, identification of *Xf* within vessels in *P. tremula*



Interactions between xylem endophytes and *Xylella fastidiosa* in *Salix* and *Populus*

Isolation & NGS sequencing

- 423 bacterial isolates → 340 were identified (169 from Populus and 171 from Salix)
- 4 phyla, 6 classes, 11 orders, 18 families and 39 genera

Fictibacillus, Frigoribacterium, Gottfrieda, Labedella,, Neobacillus, Paenibacillus, Priestia, Psychrobacillus, Rumeliibacillus, etc.

18 ***Populus*** 10 10 ***Salix***

Chryseobacterium, Erwinia, etc.

Bacillus, Methylobacterium, Peribacillus, Pseudomonas,Staphylococcus, Stenotrophomonas, etc.

Conclusions

- Demonstration that *Salicaceae* from European regions are hosts of *Xylella fastidiosa* and could act as efficient reservoir and stepping stones for the spread of *Xylella fastidiosa* in Northern EU
- Knowledge on *Xylella* / *Salicaceae* interactions
- Ongoing research on *Xylella* / endophytes interactions in *Salicaceae*

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