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HOW RESEARCH CAN SUPPORT SOLUTIONS
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The spread of *X. fastidiosa* subsp. *pauca* among the olive orchards of southern Italy (Apulia)

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Introduction

The Apulian monitoring programme of the Xylella epidemic amassed data on several hundreds of thousands of samples laboratory-screened for the presence of the bacterium, jointly with georeferenced sample information.

These data were useful for:

a) Studying the correlation between symptoms, infection and disease in a sample of thousands of trees (**Bucci EM. Biochem Biophys Res Commun. 2018;502(2):173-182)**

b) Assessing the epidemic spread and the monitoring efficacy **(Bucci EM. Rend Lincei Sci Fis e Nat. 2019:1-8)**

What can be done with the monitoring data?

a) Studying the correlation between symptoms, infection and disease in a sample of thousands of trees[1]

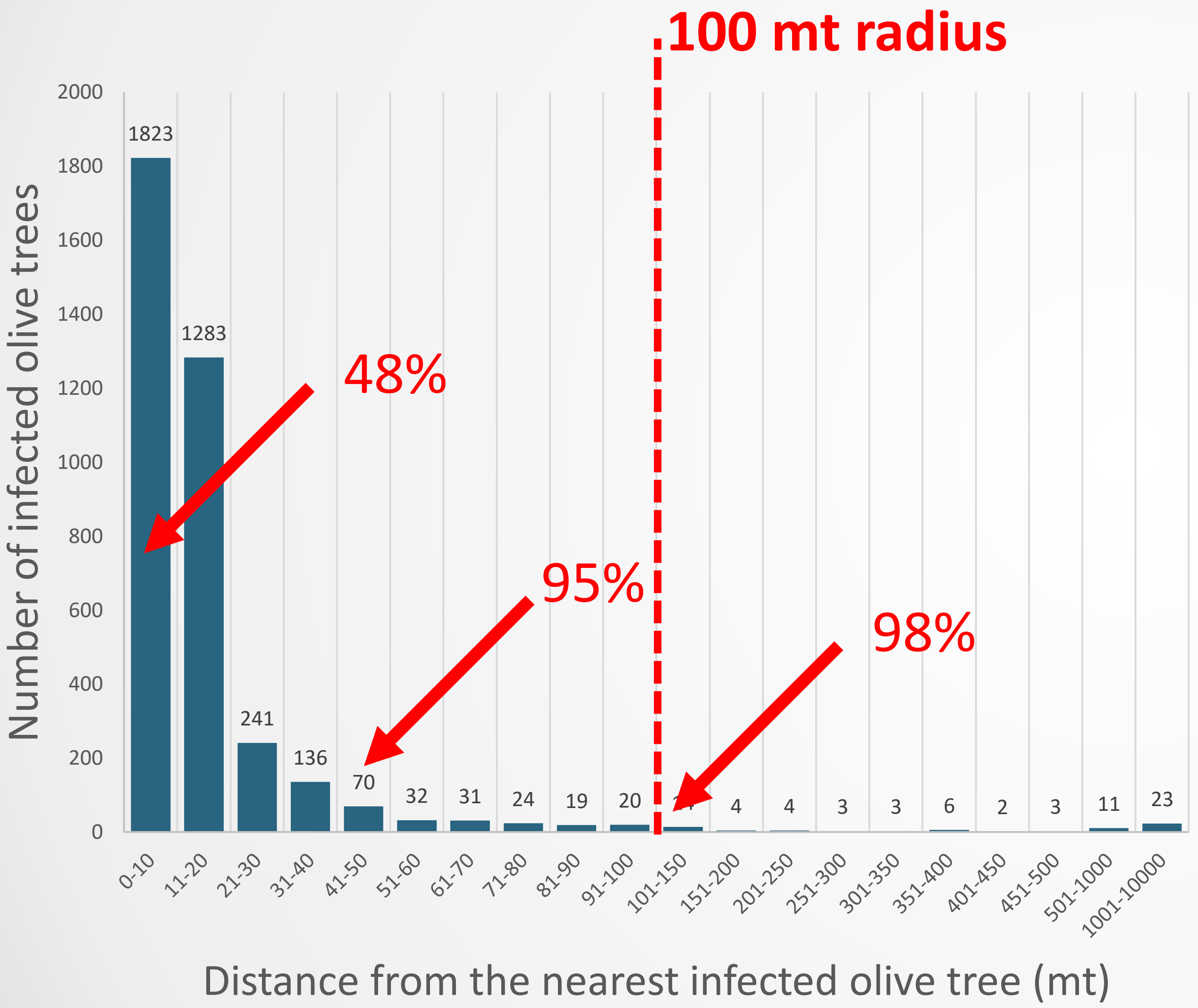
b) Assessing the epidemic spread[2]

c) Putting the uprooting policy on test[2]

d) Assessing the monitoring efficacy[2]

1. Bucci EM. Biochem Biophys Res Commun. 2018;502(2):173-182
2. Bucci EM. Rend Lincei Sci Fis e Nat. 2019:1-8

Xylella spreads in tightly grouped clusters of trees



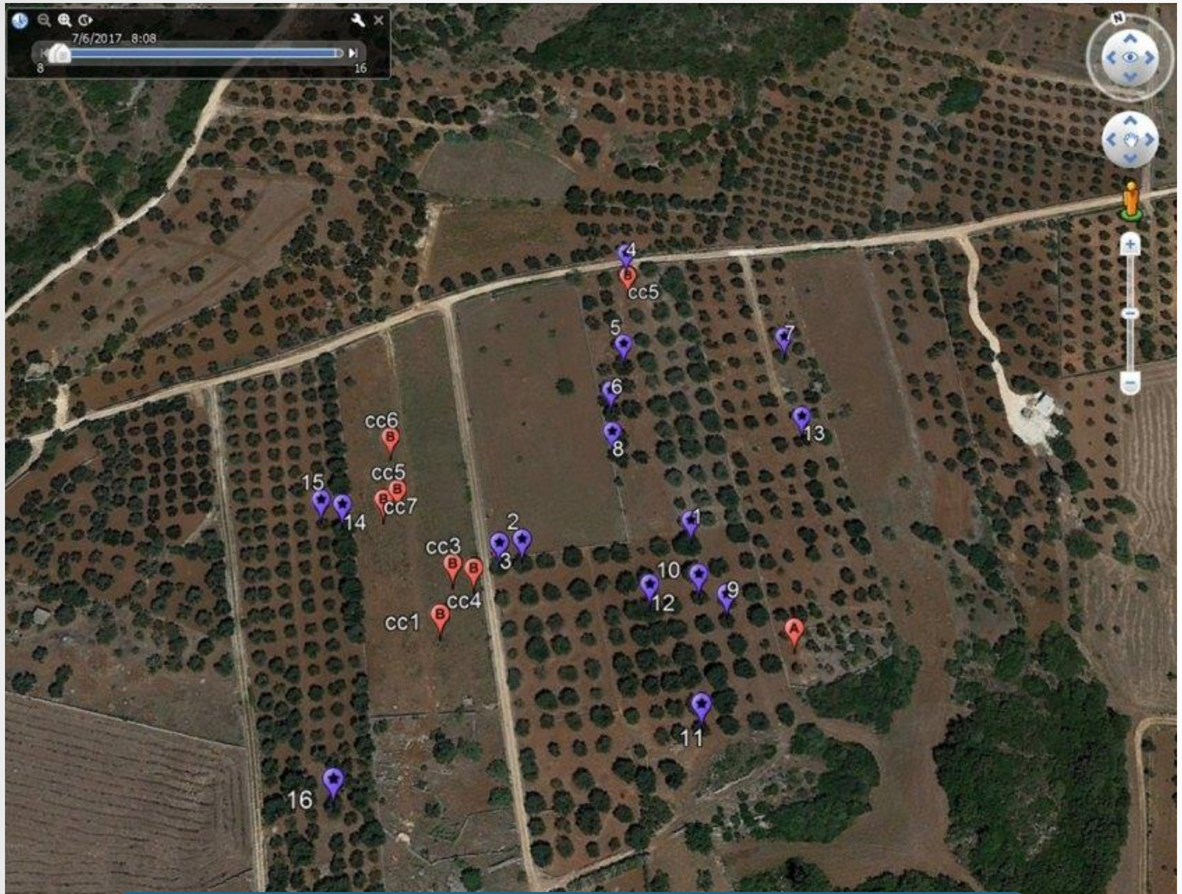
SELGE DB analysis
2017-2018

I measured the distance among 3752 infected olive trees sampled during the 2017-2018 monitoring season.

98% of olive trees found infected in 2017-2018 is in a 100 mt radius from another infected tree.
In the graph on the left, you may see how also the % of infected olive trees at a distance of 10 mt or 50 mt from another infected tree.

These numbers must be taken into accounts when designing the uprooting policy.

Epidemic hotspots eradication: 100 mt uprooting



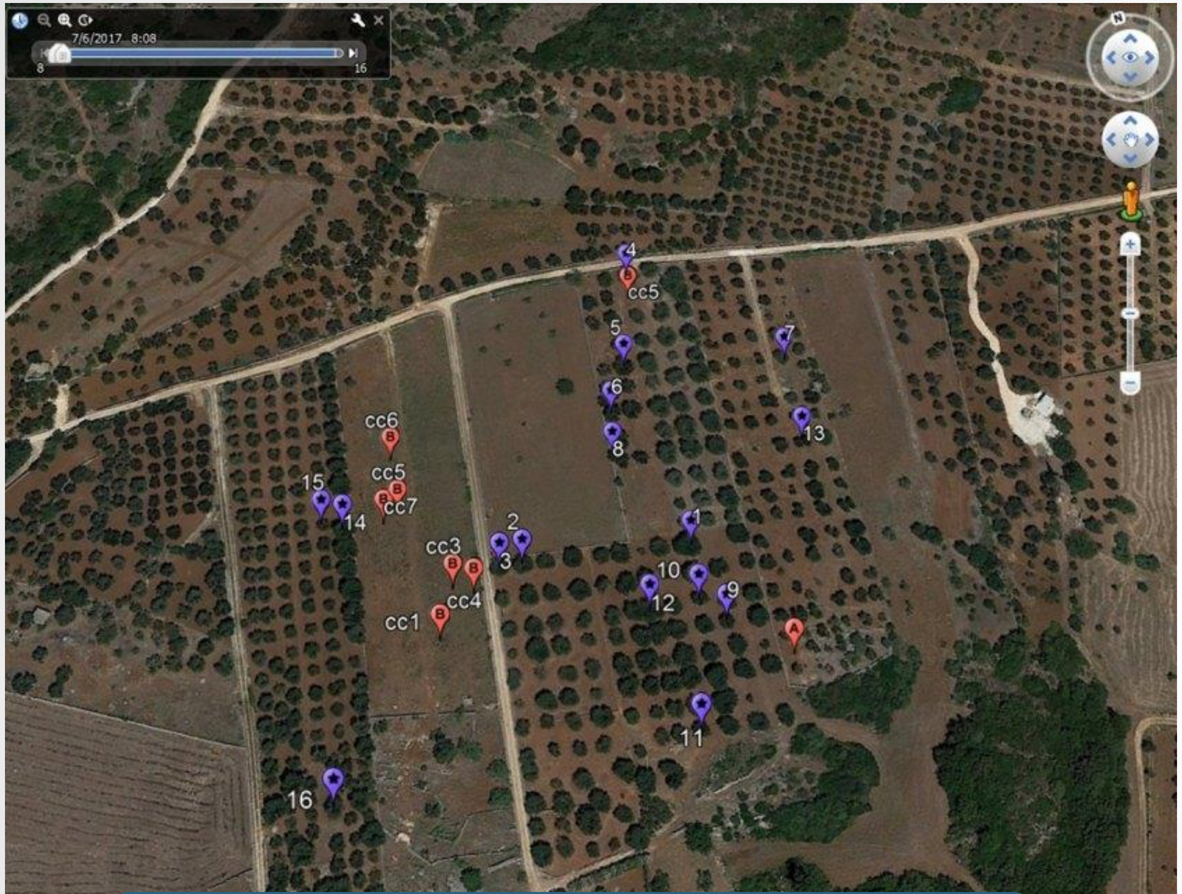
Infected trees (2017-2018)

Red, infected plants, 2017; violet, infected plants, 2018. ***Plants-free zones are due to the uprooting partial application in 2018.***

Simulated uprooting of 2017 infected trees (100 mt)

Uprooting in a radius of 100 mt from plants found infected in 2017 would have prevented new infections in 2018.

Epidemic hotspots eradication: 10 mt uprooting



Infected trees (2017-2018)

Red, infected plants, 2017; violet, infected plants, 2018. ***Plants-free zones are due to the uprooting partial application in 2018.***

Simulated uprooting of 2017 infected trees (10 mt)

Uprooting at 10 mt would not cover the plants found infected in 2018

New infected plants are far from previously identified

SELGE DB analysis 2017-2018

Red: infected trees, identified in 2016

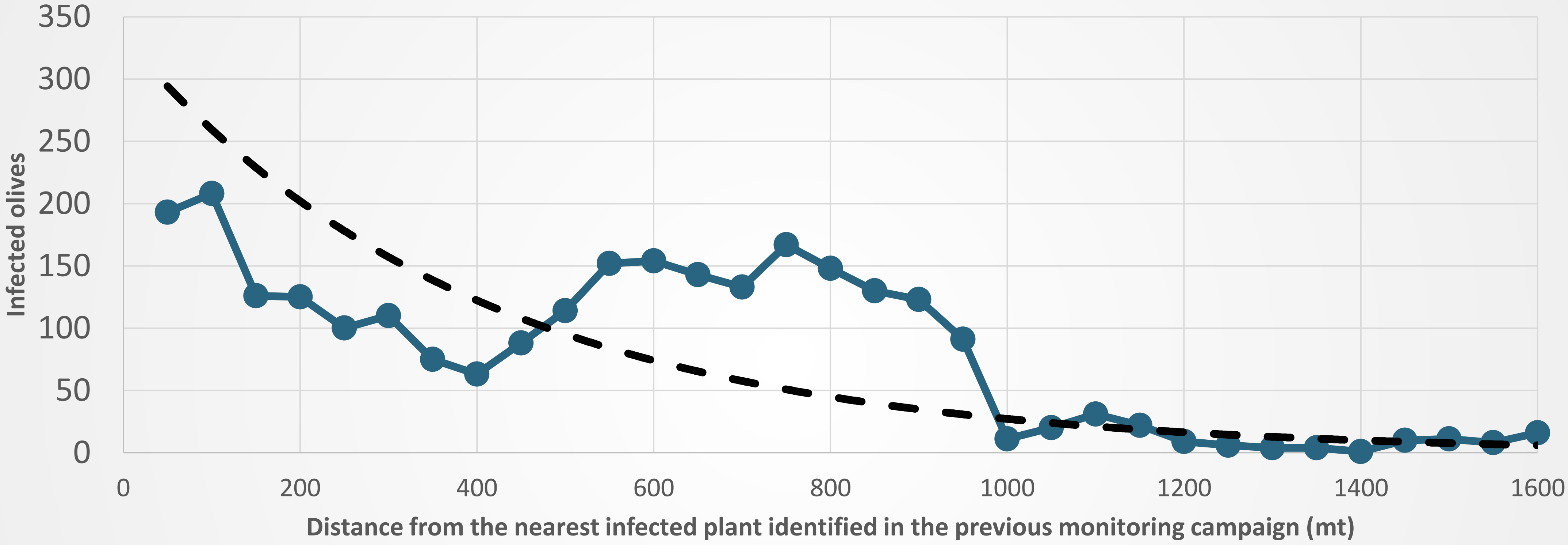
Violet: infected trees, identified in 2018, in a 100 mt radius from 2016 infected plants

Dark red: infected trees, identified in 2018, at more than 100 mt from infected plants identified in 2016

Plants found infected in 2016 generated a multitude of new infected plants in 2018.

However, there are infected trees located at more than 100mt from plants found infected in 2016.

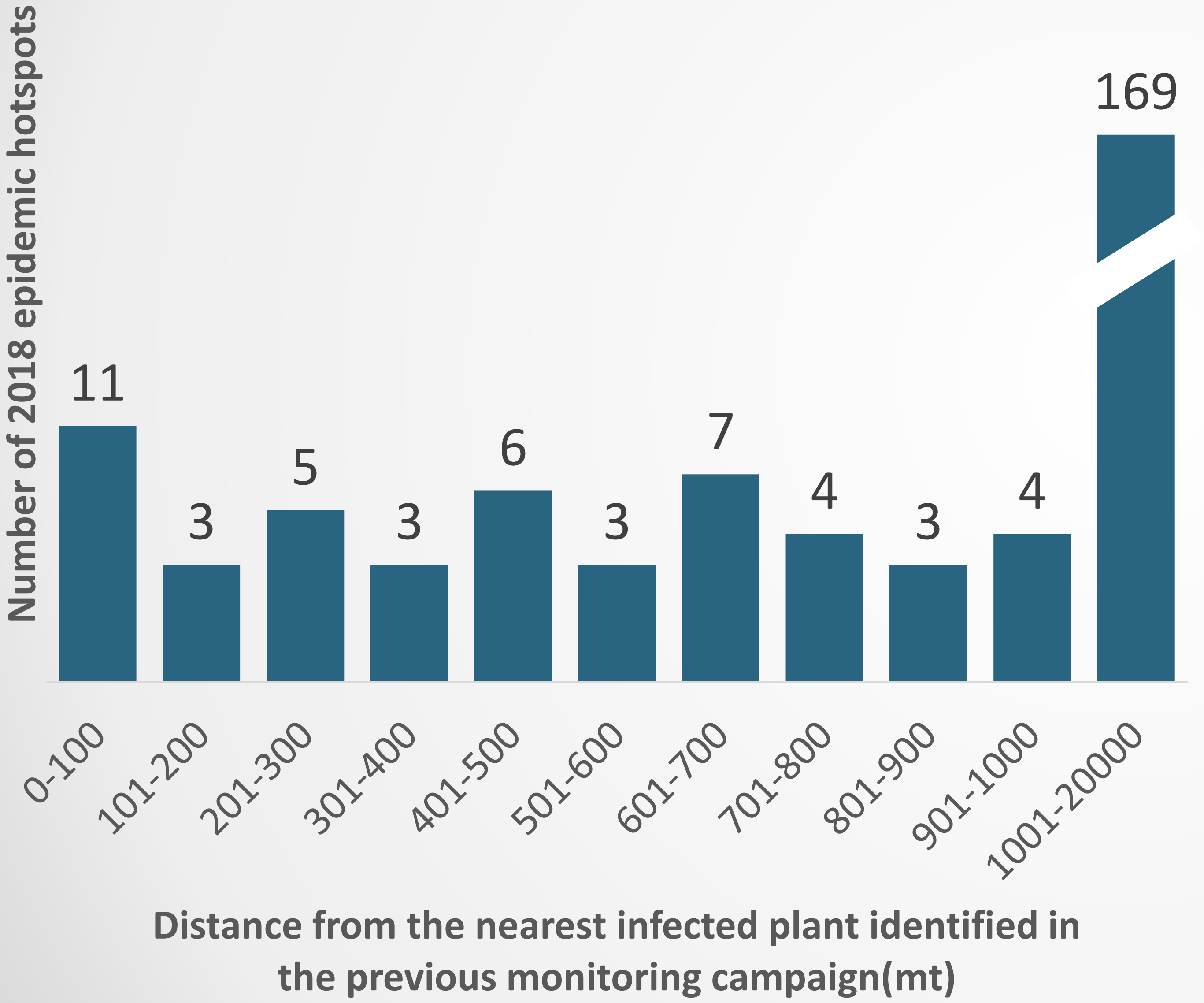
New infected plants are far from previously identified



Distance of newly infected plants from previously identified infected olive trees

The quantitative analysis of the distance of newly infected plants from previously identified epidemic hotspots shows that most newly detected infected plants are between 400 and 1000 mt from plants identified as infected in the rpeceding campaign

New epidemic hotspots are far from older hotspots



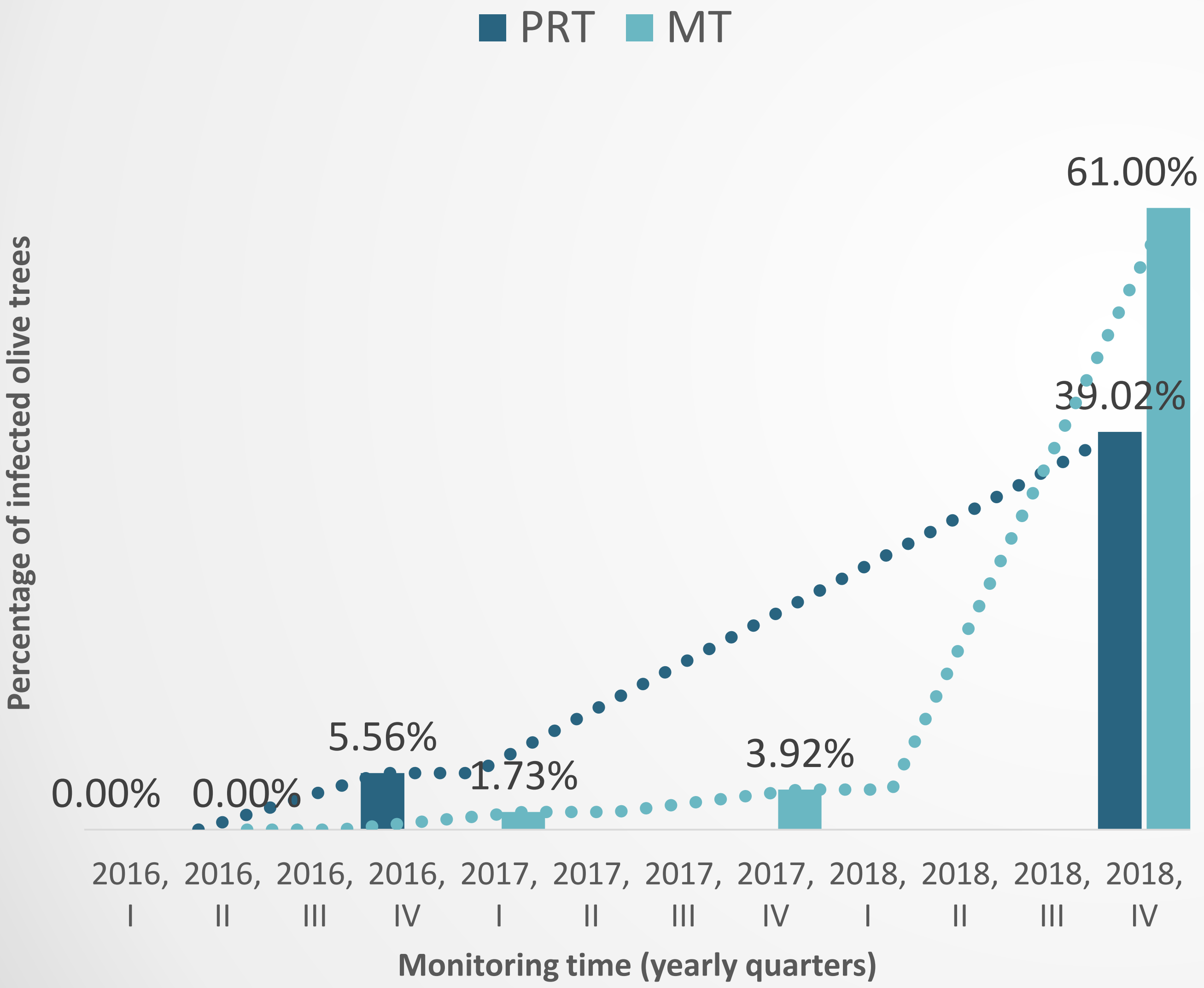
SELGE DB analysis 2017-2018

Grouping all olives which are at a distance below 100 mt, one has a quantitative definition of «epidemic hotspots»

77% of the epidemic hotspots identified in 2018 are mostly at more than 1 km from infected plants identified in the preceding monitoring campaign.

Since, however, newly infected plants are tightly grouped (as we saw in the preceding slides), **this fact points to a detection problem**, more than to far-distance spreading of the bacterium.

Epidemic progression at local level



Epidemic progress over 3 years in two selected TAP plots

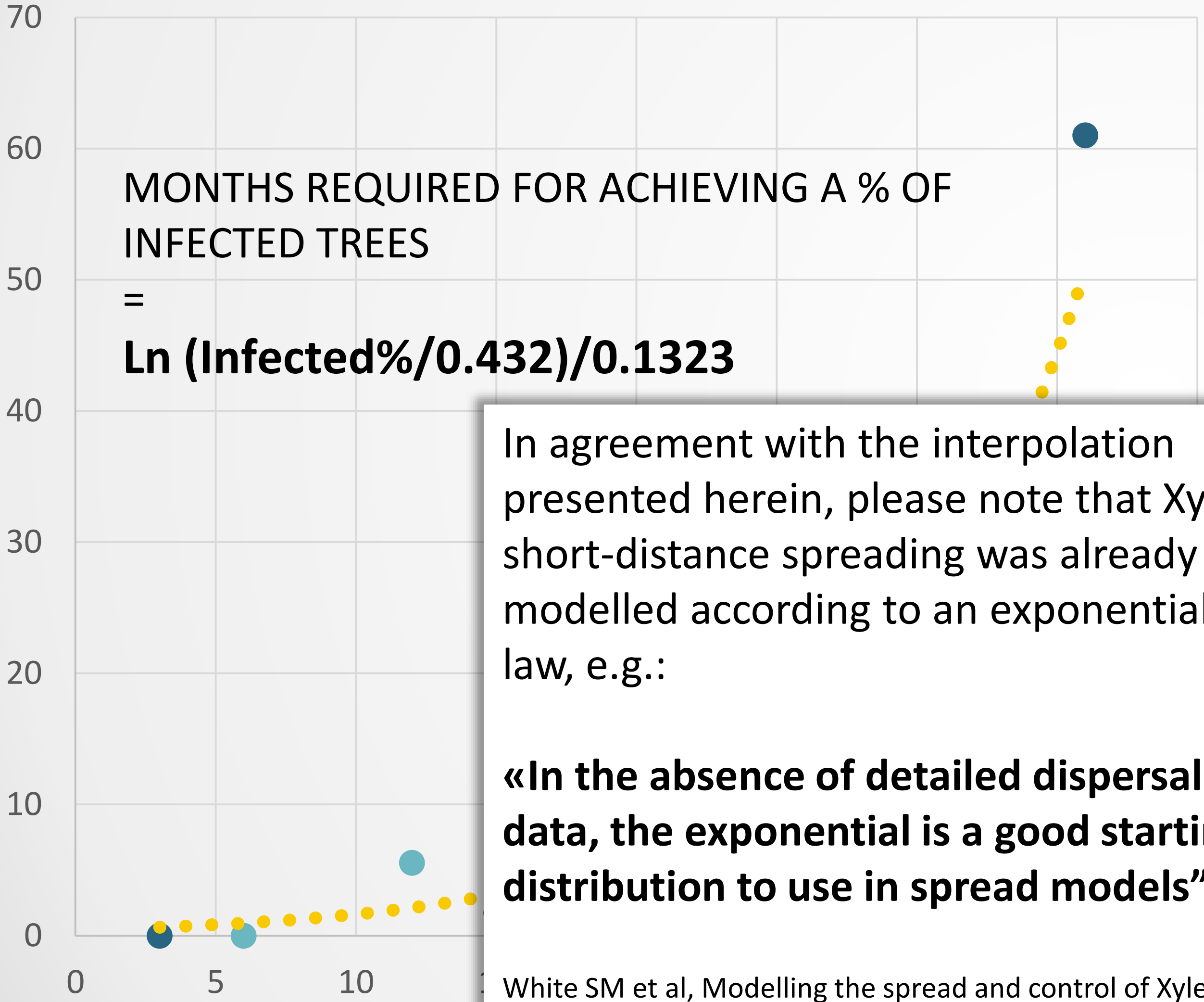
Starting from 2016, the orchards where the new TAP gas infrastructure had to pass, were monitored independently of the Regional governement.

In 2016, those orchards were already in the infected zone.

In all cases, the number of infected trees exploded after 2 years from the first detection of Xylella.

PRT pipeline receiving terminal
MT Microtunnel

Epidemic progression at local level



MONTHS REQUIRED FOR ACHIEVING A % OF INFECTED TREES

=

Ln (Infected%/0.432)/0.1323

In agreement with the interpolation presented herein, please note that Xylella short-distance spreading was already modelled according to an exponential law, e.g.:

«In the absence of detailed dispersal data, the exponential is a good starting distribution to use in spread models"

White SM et al, Modelling the spread and control of Xylella fastidiosa in the early stages of invasion in Apulia, Italy. *Biol Invasions*. 2017;19(6):1825-1837.

Epidemic local progression: forecast

Interpolating the TAP data, the following predictions may be made for the % of infected olives in an orchards, after the bacterium gained a foothold.

% of Infected Trees	Months from first infection
5%	19
10%	24
20%	29
30%	32
40%	34
50%	36
100%	41

Conclusions

1. At the forefront of the epidemic, the bacterium proceeds by establishing tight groups of newly infected plants, grouped in a 100 mt radius

2. **Under the current monitoring strategy**, point 1 implies that the uprroting radius around an infected plant should not be less than 100 mt

3. **Under the current monitoring strategy**, most newly infected plants are found between 400 mt and 1 km from the plants find infected in the preceding monitoring campaign

4. **Under the current monitoring strategy ,** 77% of new infection hotspots are found at more than 1 km from old infection hotspots

5. At the local level, the number of infected olive trees grows exponentially over time; for as many as 2 years, infected orchards may present few infected plants, but after an average of 3,5 years all plants are infected.

Thank you for your attention!