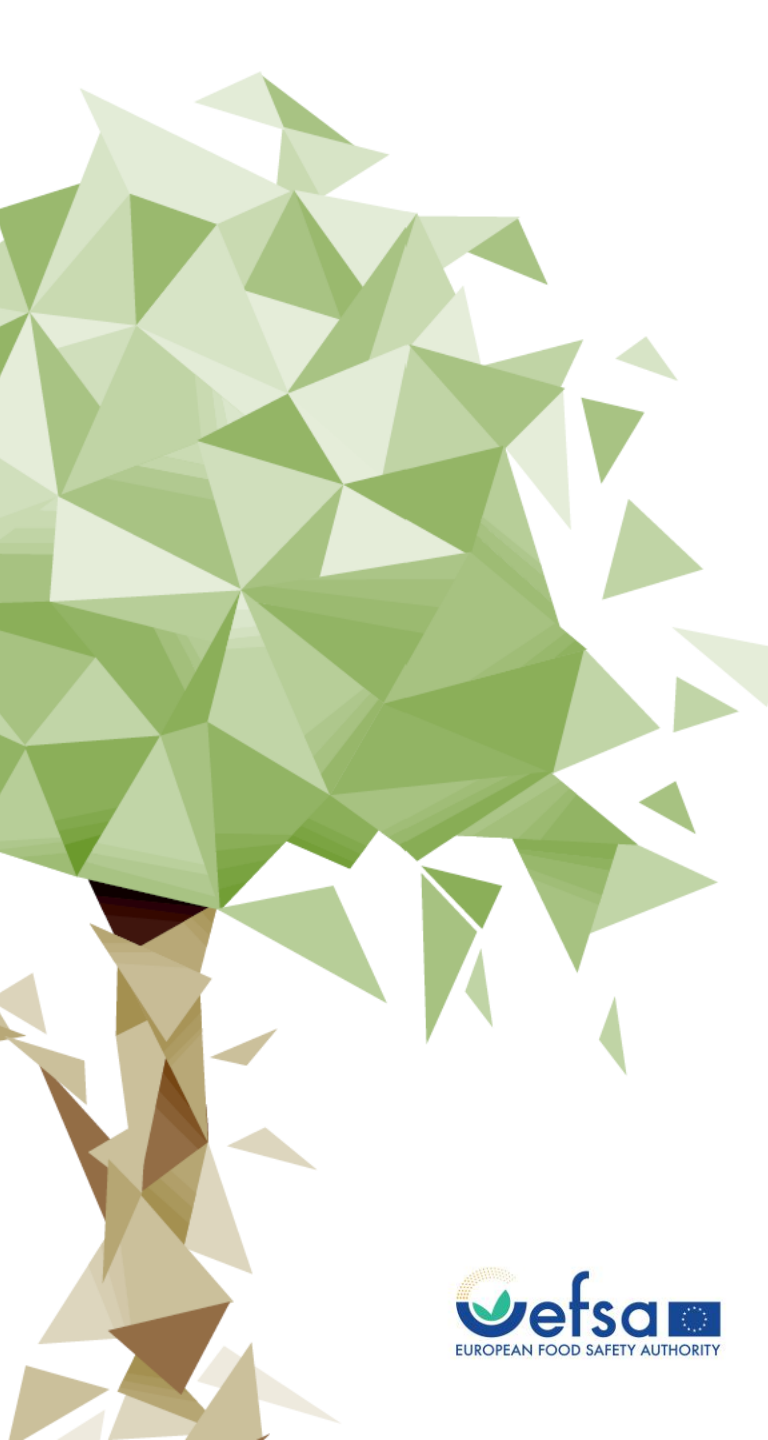




Modelling the effectiveness of *Xylella fastidiosa* monitoring and control across pathosystems and spatial scales

Rachel Russell, Martina Cendoya, Toni Vicent, Nik Cunniffe



Context

- Our Working Group is updating the 2019 scientific opinion on *Xylella fastidiosa*.
- The main driver for the update is for us to take account of potential differences between the different *Xylella* subspecies and hosts.
- The modelling work is focused on understanding which controls (if any) are most effective for controlling *Xylella* in a landscape.
- Please provide feedback!

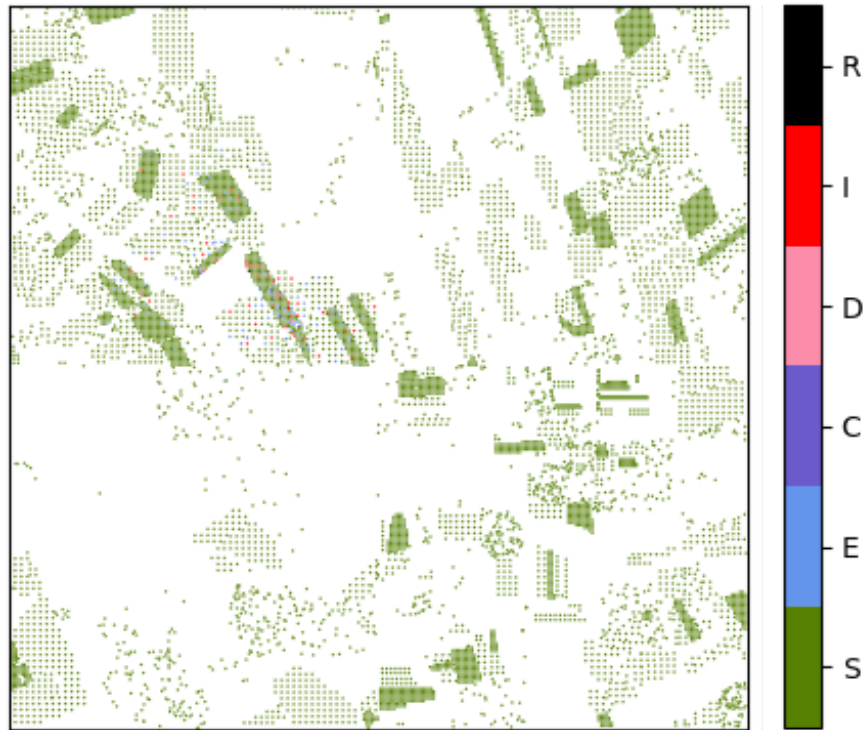




The model...

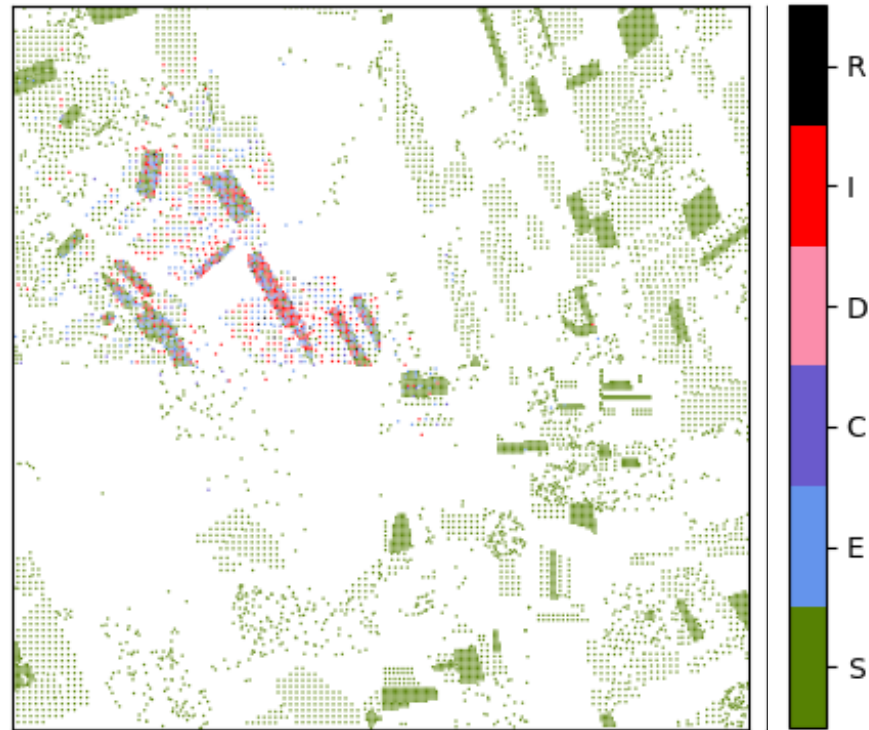
We use a stochastic individual based model

Year: 4



We use a stochastic individual based model

Year: 6

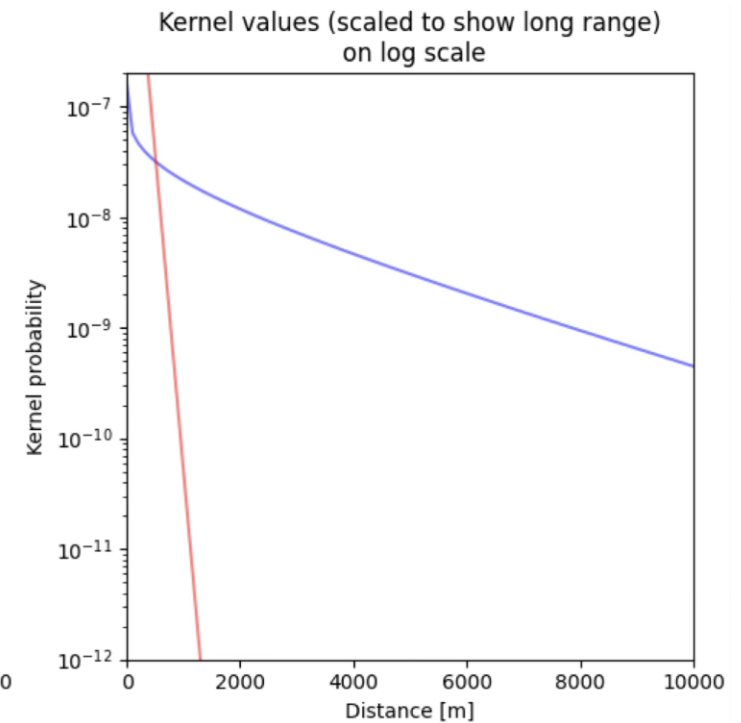
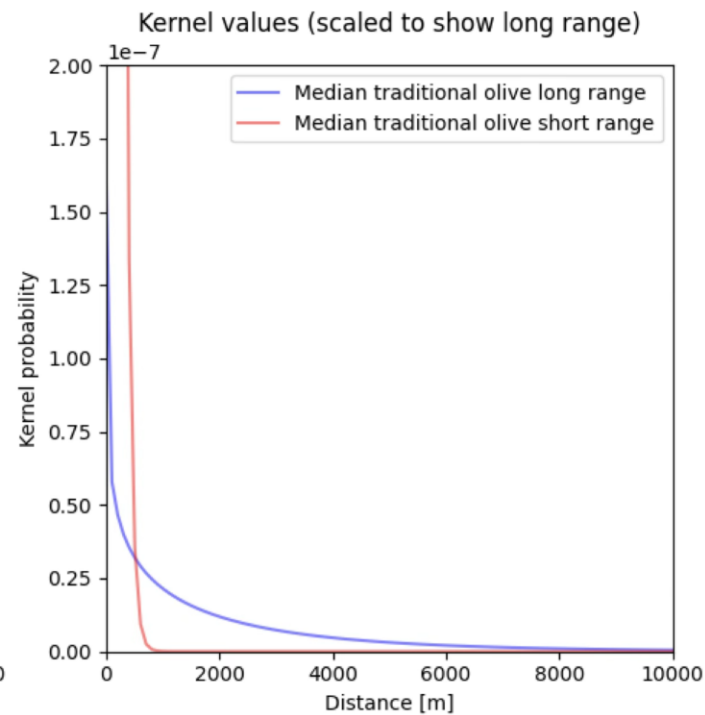
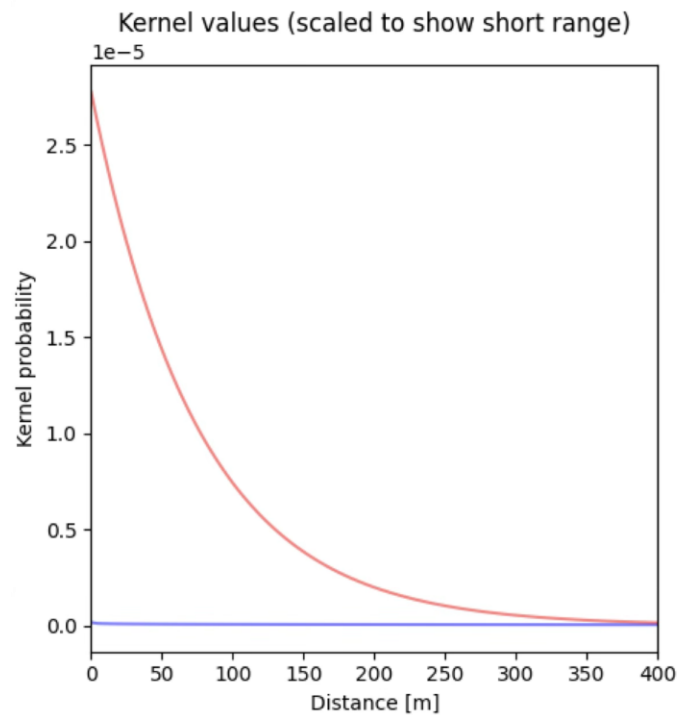


We use a stochastic individual based model

Year: 8

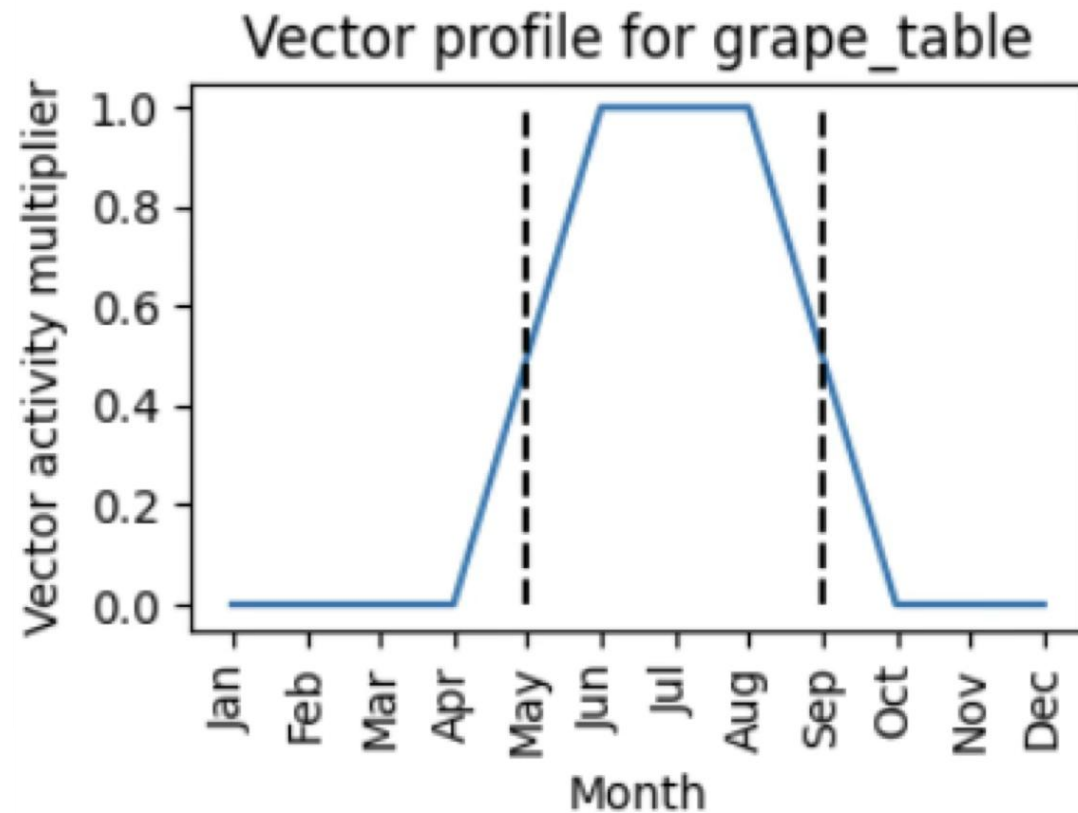


We model hosts infecting one another using transmission kernels



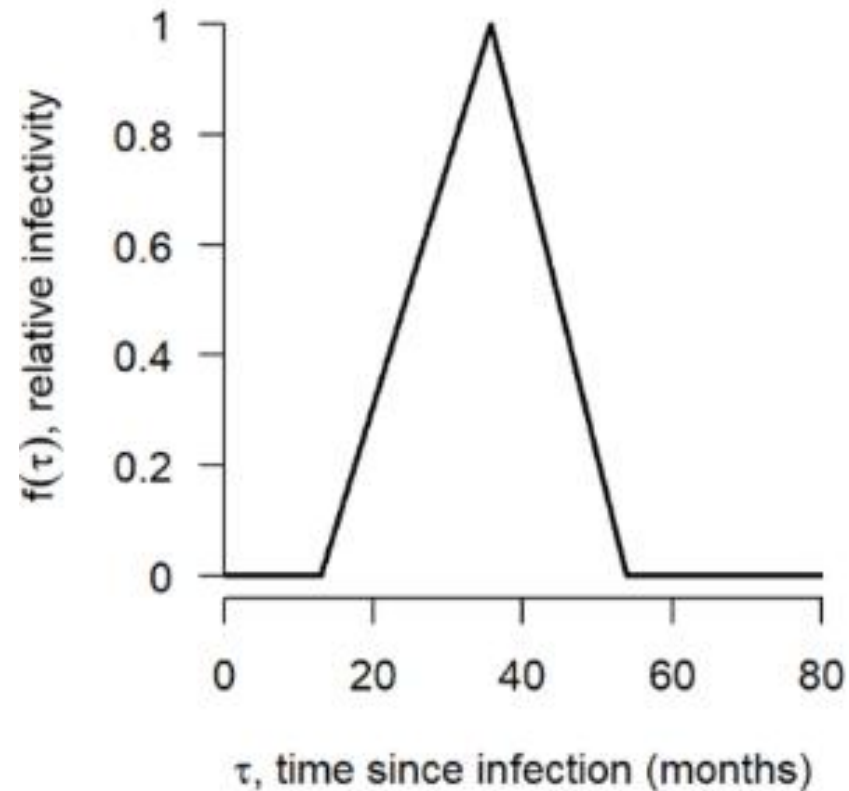


We account for simplified seasonality and host infectiousness changes



We account for simplified seasonality and host infectiousness changes

Traditional olives (EKE median)





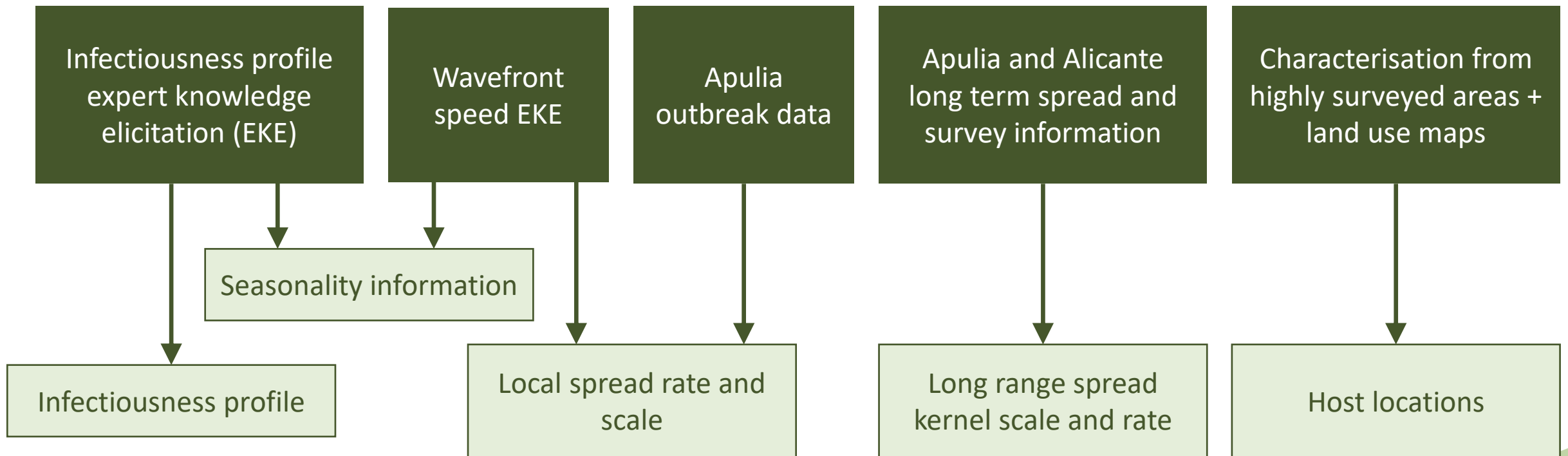
Case studies

Xf subspecies	Modelled hosts and farming system	Example	Eradication or containment
Pauca ST53	Olive (traditional)	Apulia (Italy)	Both
Multiplex ST6	Almond (rainfed)	Alicante (Spain)	Both
Fastidiosa ST1	Grape (S Europe) and almond (rainfed)	Mallorca (Spain)	Both
Fastidiosa ST1	Table grape	Rutigliano (Italy)	Eradication





Fitting and parameterization overview – where does the information come from?



Note – full version of this diagram is more complex because we take account of dependencies between parameters

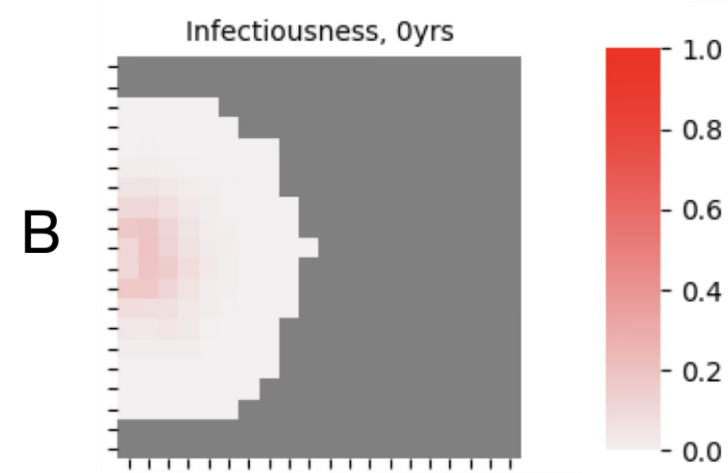
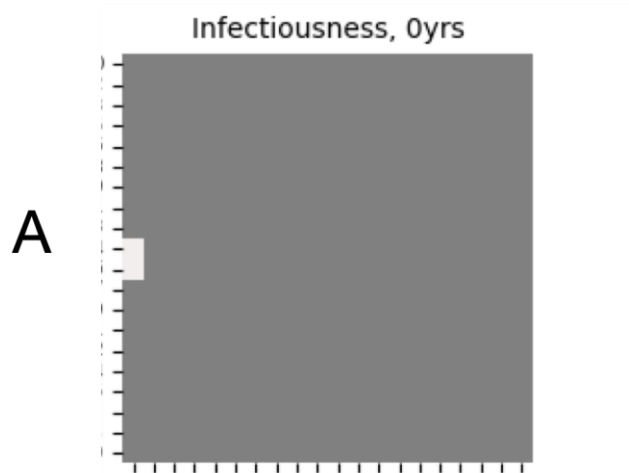




Comparing control effectiveness

Scenarios tested

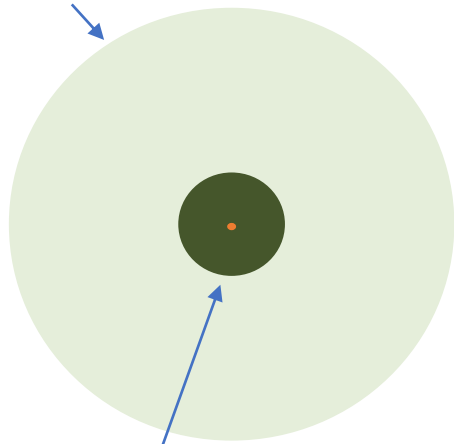
Scenario	Size of simulated landscape	Starting point
Eradication	10 x 10 km	Single host inoculated with the disease at the centre of the map.
Containment (small)	50 x 50 km	Fig A (each square is 2.5km x 2.5km)
Containment (well established)	50 x 50 km	Fig B



Overview of existing legislation

Eradication

Buffer zone (increased inspection, $r = 2.5\text{km}$)



Infected zone (host plant removal, $r = 50\text{m}$)

Containment

Direction of disease progression



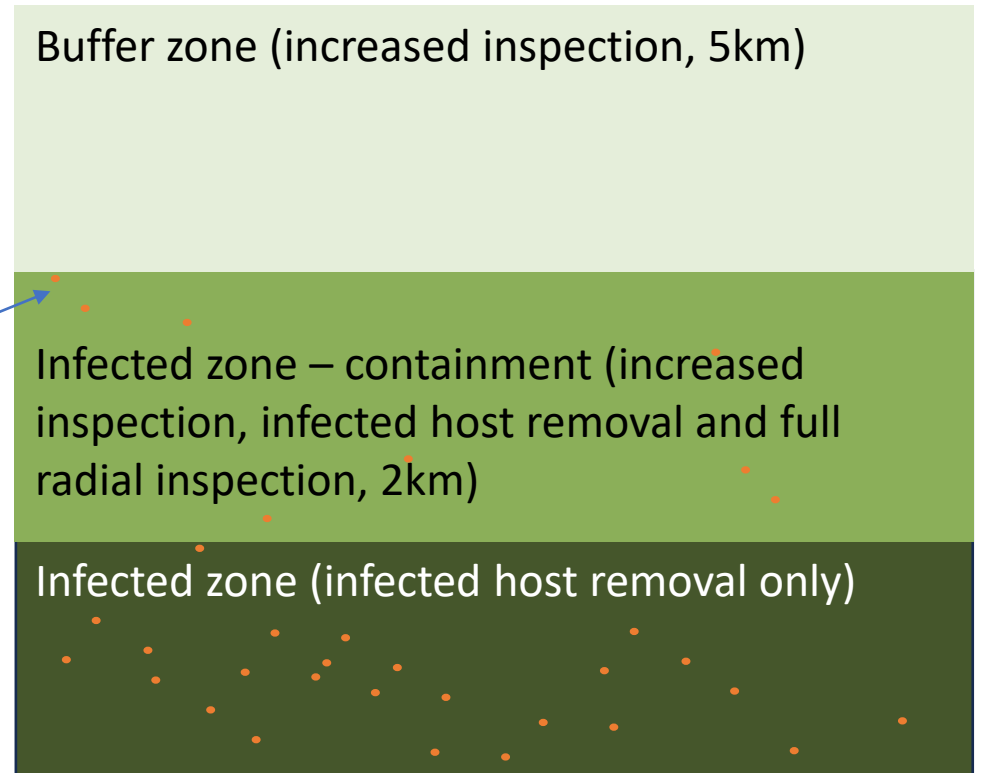
"Furthest" known infected



Buffer zone (increased inspection, 5km)

Infected zone – containment (increased inspection, infected host removal and full radial inspection, 2km)

Infected zone (infected host removal only)





Controls tested

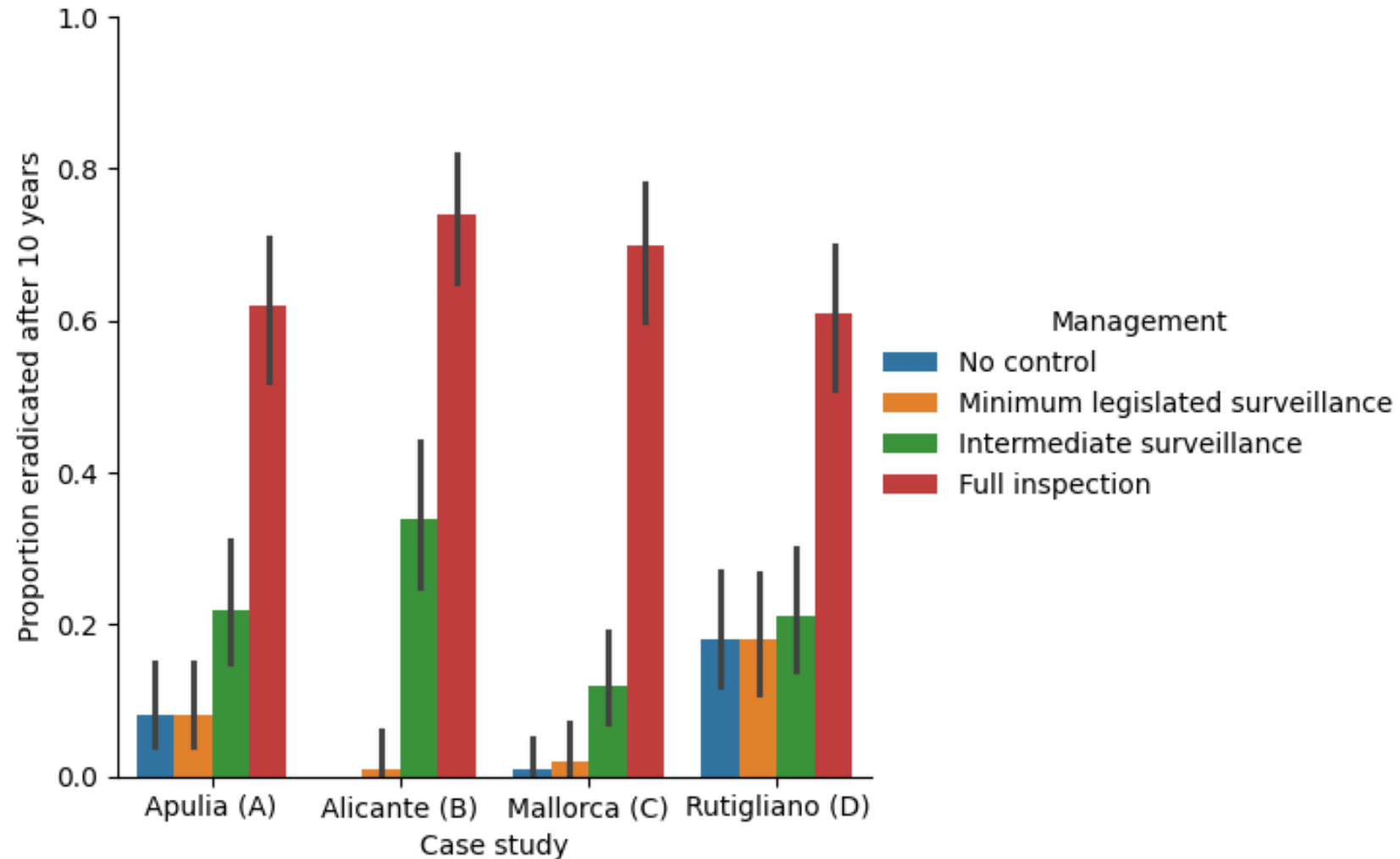
Control name	Description	Eradication or containment
No control	No surveillance or control is performed. Baseline.	Both
Minimum legislated	Surveillance and control parameterised to comply with the legislated minimum requirements.*	Both
Intermediate	“Middling” case for eradication	Eradication
Full	Every host inspected every year – bounding maximum case.	Eradication
Stringent	High levels of inspection aiming to represent an upper bound on what might be feasible.	Containment
Removal in containment	As for "stringent" but with radial removal in the containment zone instead of radial inspection	Containment

*If current legislation does not specify relevant parameters, values from previous legislation (EU, 2024) are used.

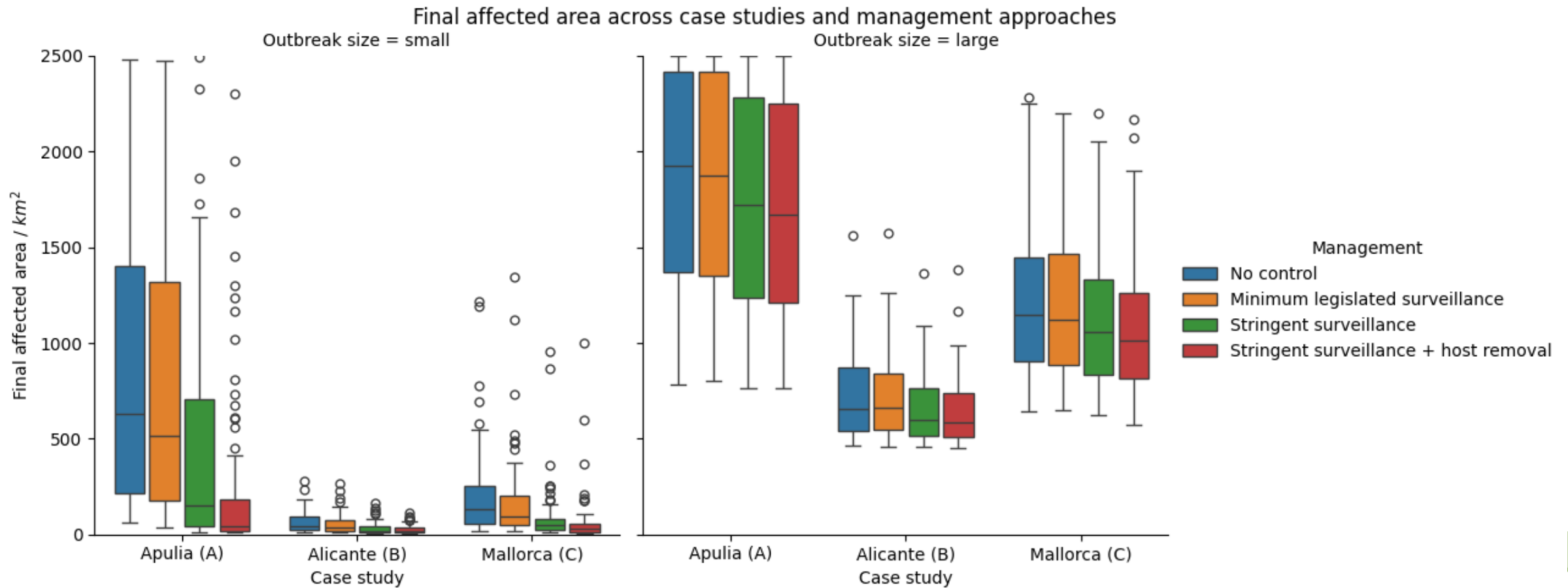


Eradication summary

Eradication success across case studies and management approaches



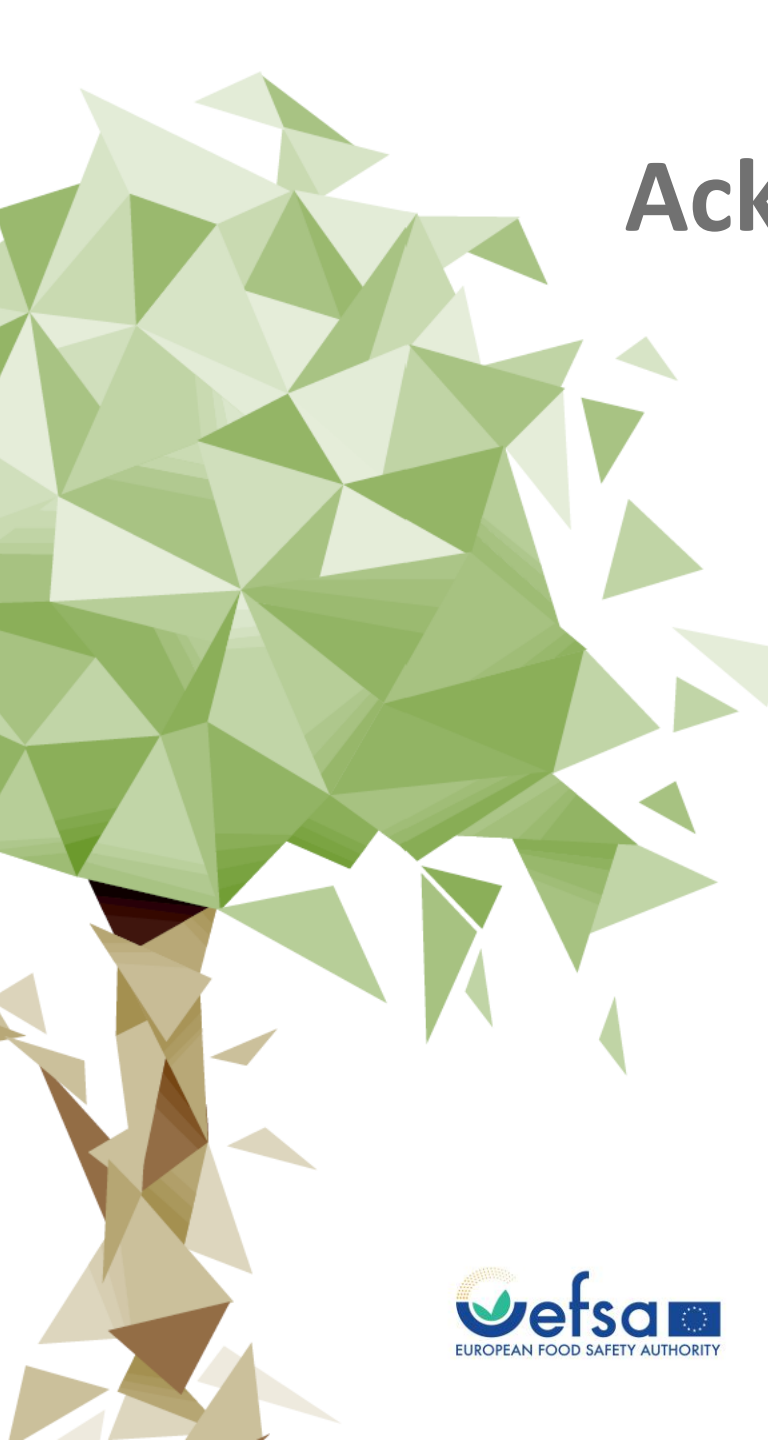
Containment results summary





Conclusions

- We've built and parameterised an individual based model which can run over landscapes up to 50 x 50km. It can account for the different pathosystem dynamics and host layouts seen over different European outbreaks of Xylella. We've run simulations for a range of eradication and containment scenarios.
 - Radial removal with a radius of 50m is not able to reliably eradicate outbreaks although it can be successful with high levels of inspection when the conditions are not favourable to disease spread.
 - Containment can slow the spread of the disease for small epidemics and if there are high levels of surveillance. Particularly if there is radial removal behind the point of furthest detection.
- 



Acknowledgements

- *Xylella fastidiosa* working group
- EFSA team and the EKE experts



Enhancing *Xylella fastidiosa* spread modelling and surveillance optimisation through remote sensing

R. Calderón^{1,2}, Y. Bourhis³, S. Parnell^{1,4,5}

¹ School of Environment and Life Sciences, University of Salford, Manchester, UK

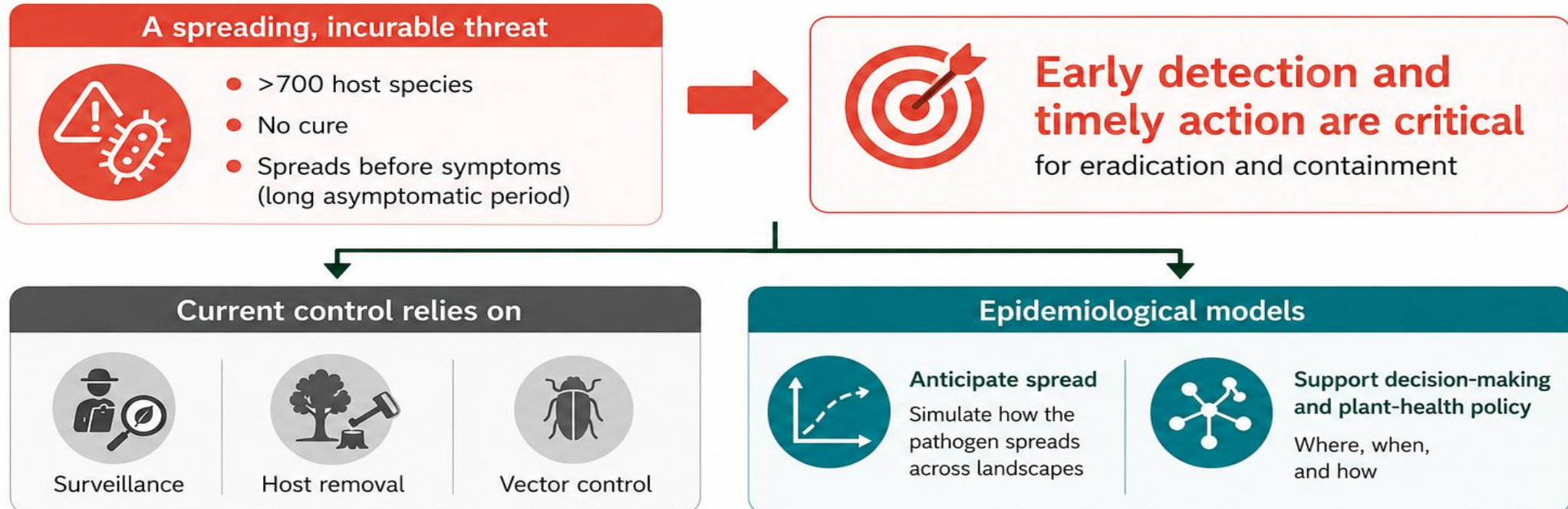
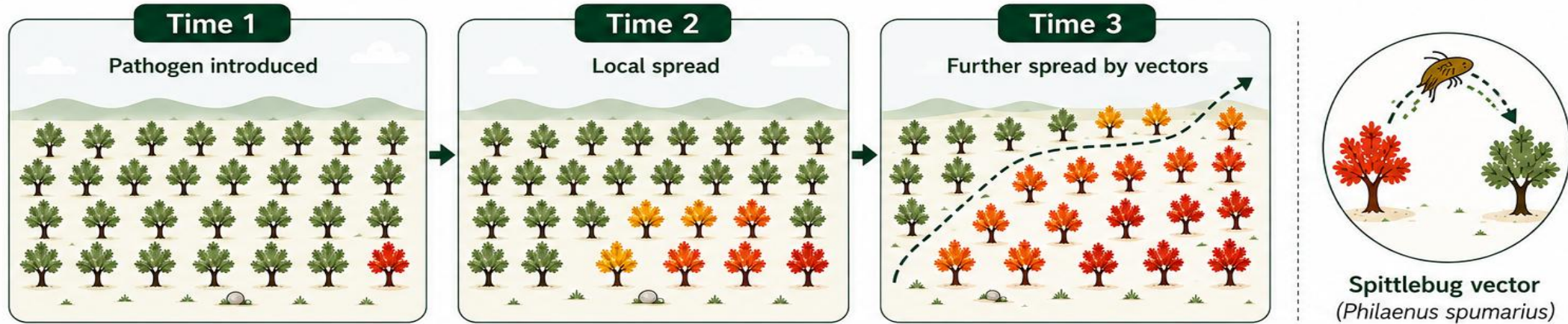
² Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Córdoba, Spain

³ Rothamsted Research, Harpenden, UK

⁴ Warwick Crop Centre, University of Warwick, Stratford-upon-Avon, UK

⁵ Zeeman Institute for Systems Biology and Infectious Disease Epidemiology Research, University of Warwick, Coventry, UK

Why do we need epidemiological models for *Xylella fastidiosa*?



The data bottleneck: a remote sensing opportunity

Challenges — ground survey



Costly & slow



Limited coverage



Biased, not representative



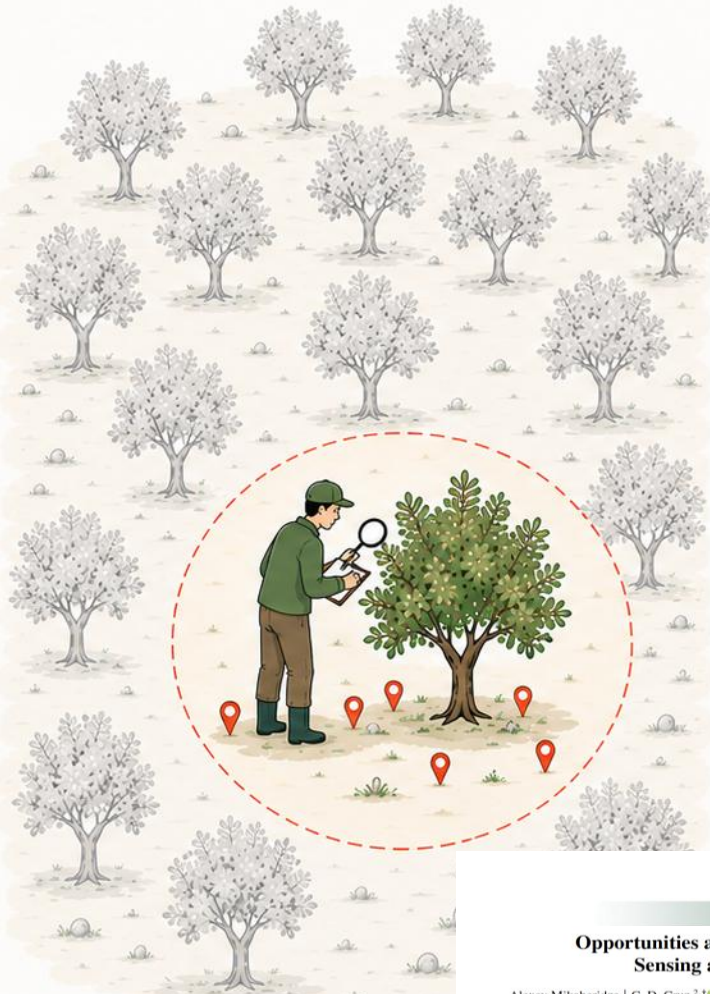
Cryptic infection missed



Delayed reporting



Observer error



Opportunities — remote sensing



Full coverage



Detects previous symptoms



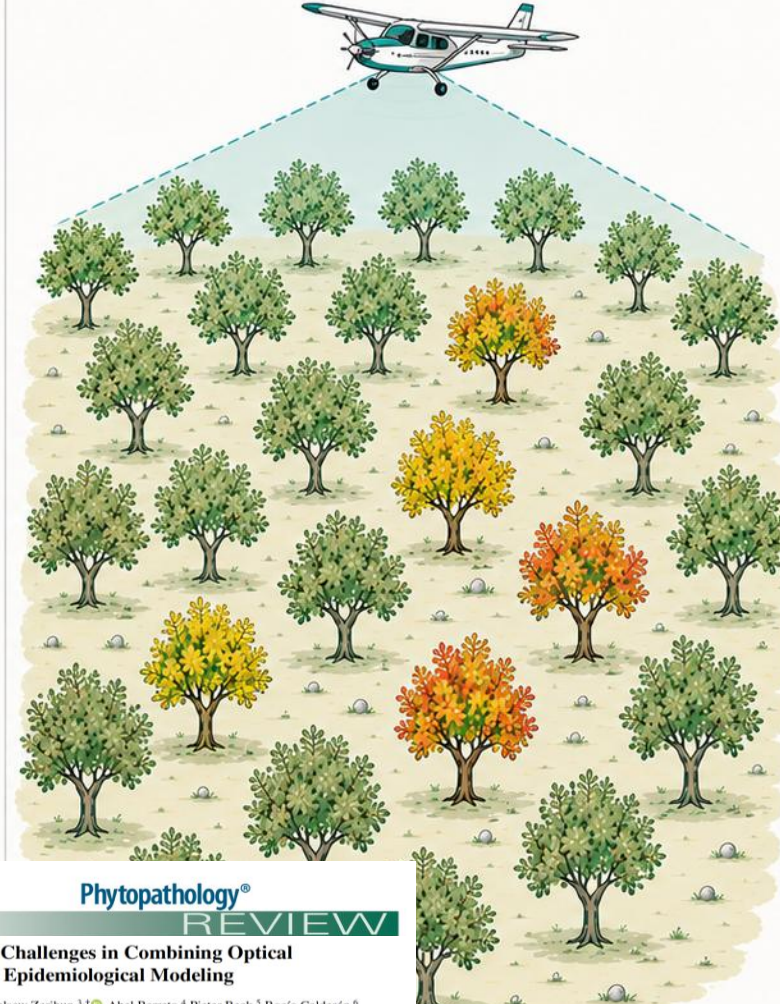
Objective, non-destructive



Repeatable & frequent



Caveat: water stress can mislead



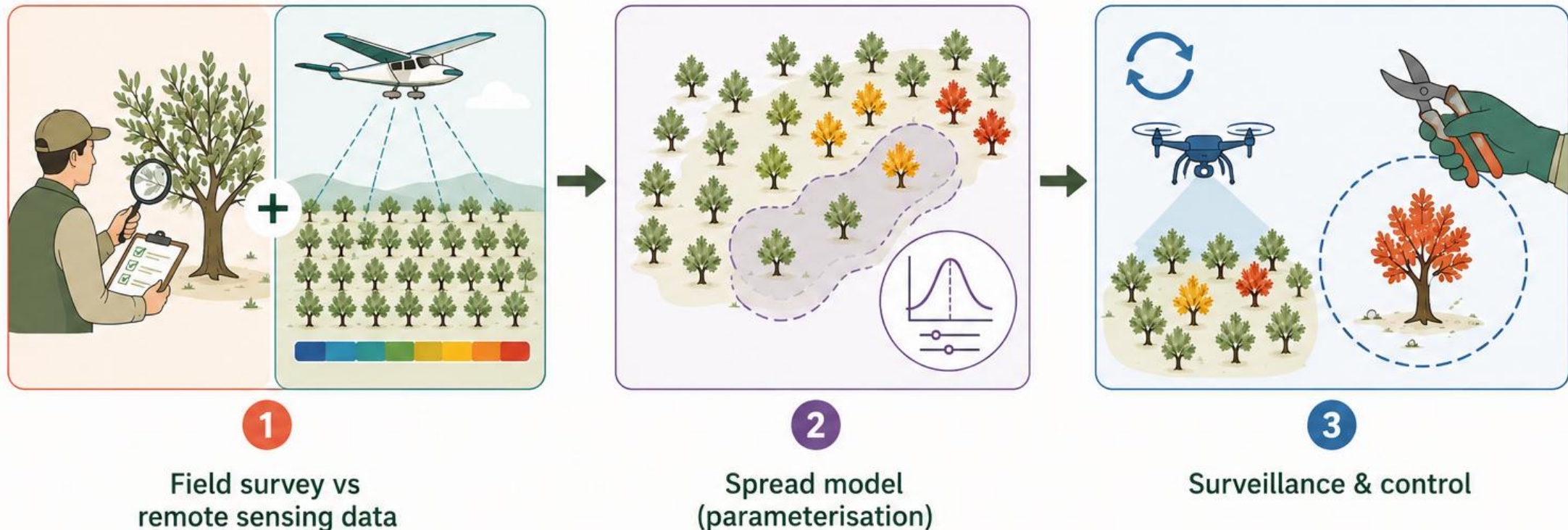
Phytopathology®
REVIEW

Opportunities and Challenges in Combining Optical Sensing and Epidemiological Modeling

Alexey Mikaberidze,¹ C. D. Cruz,^{2,1} Ayalew Zerihun,^{3,1} Abel Barreto,⁴ Pieter Beck,⁵ Rocío Calderón,⁶ Carlos Camino,⁷ Rebecca E. Campbell,⁷ Stephanie K. L. Delaune,⁸ Frédéric Fabre,^{9,10} Elin Falla,¹⁰ Stuart Fraser,¹¹ Kaitlin M. Gould,¹² Carlos Gonzaga-Carull,¹³ Frédéric Hamelin,¹³ Dalphy O. C. Harteveld,¹³ Cheng-Fang Hong,¹⁴ Melen Leclerc,¹² Da-Young Lee,¹⁵ Murillo Lobo, Jr.,¹⁶ Anne-Katrin Mahlein,¹⁴ Emily McLay,¹¹ Paul Mellor,¹⁷ Stephen Parnell,¹⁸ Uwe Rascher,¹⁹ Jack Rich,^{1,20} Irene Salotti,²¹ Samuel Soubeyrand,²² Susan Sprague,²³ Antony Surano,²⁴ Sandhya D. Takoor,²⁵ Thomas H. Taylor,²⁶ Suzanne Touzeau,²⁷ Pablo J. Zarco-Tejada,^{28,29} and Nik J. Cunniffe^{10,20,1}

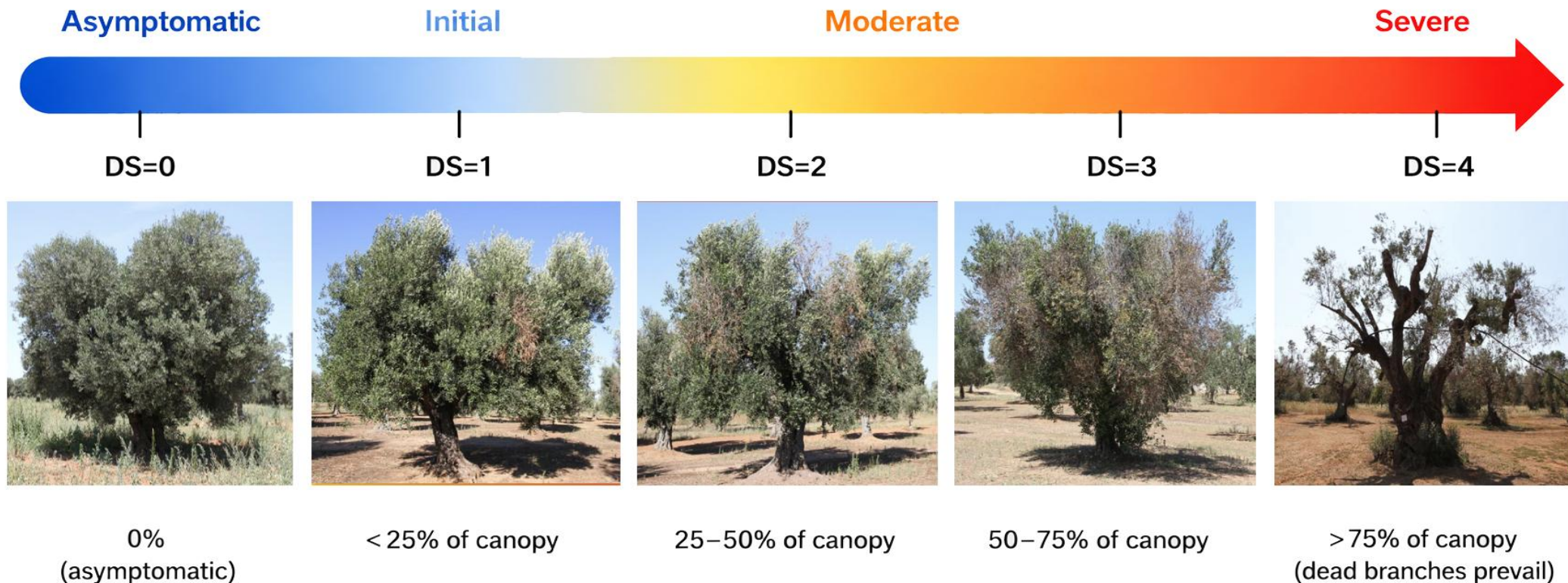
Objective

- 1 Parameterise an epidemiological model for *Xylella fastidiosa* spread using remote sensing data
- 2 Compare it against parameterisation from field survey data
- 3 Compare field survey and remote sensing as surveillance methods, evaluating containment performance across different revisit intervals and roging radii

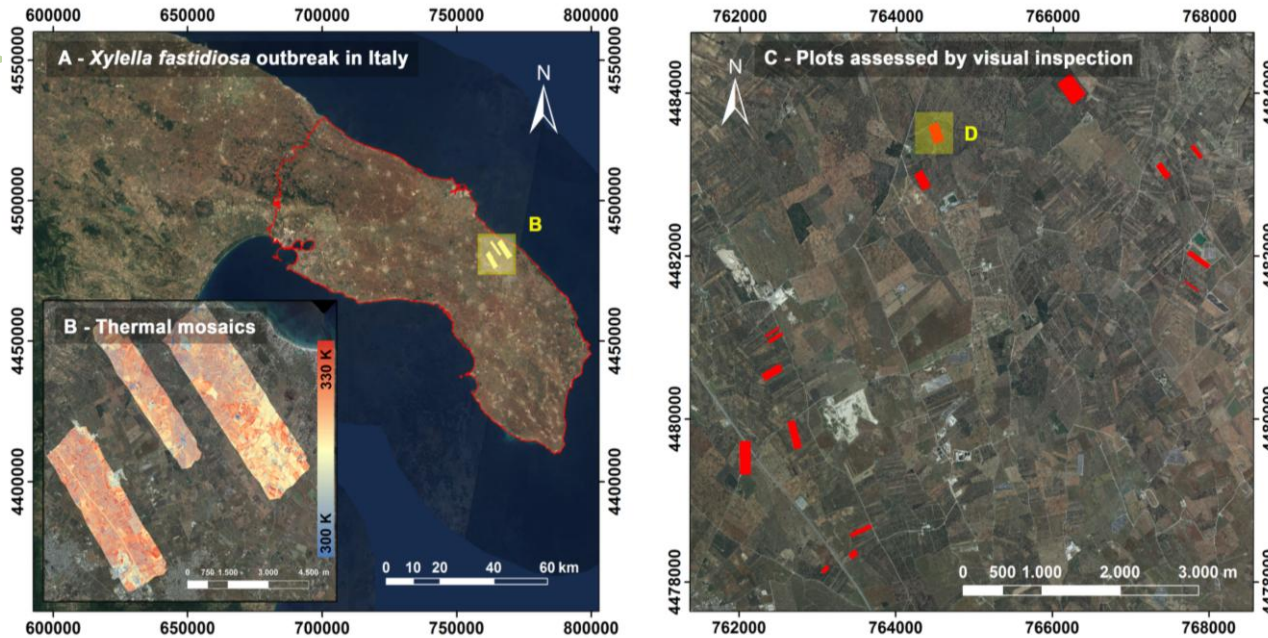


Field survey campaigns

- Two field campaigns: June 2016 and July 2017 in 15 olive orchards (Puglia, Southern Italy)
- Each tree was visually scored from 0 to 4 according to the proportion of symptomatic canopy
- 7,315 trees assessed (3,328 in 2016 / 3,987 in 2017)
- Cultivars: *Ogliarola Salentina* and *Cellina di Nardò* (susceptible), and *Leccino* (tolerant)



Remote sensing campaigns



- **Airborne campaigns** conducted on 28 June **2016** and 5 July **2017** over 1,200 ha within the *Xylella fastidiosa*-infected area of Puglia.
- **Hyperspectral** (400–885 nm, 260 bands) and **thermal imagery** acquired from a manned aircraft.
- **High-resolution** imagery (40 cm hyperspectral, 60 cm thermal) enabled individual tree crown delineation.

From remote sensing to infection probability

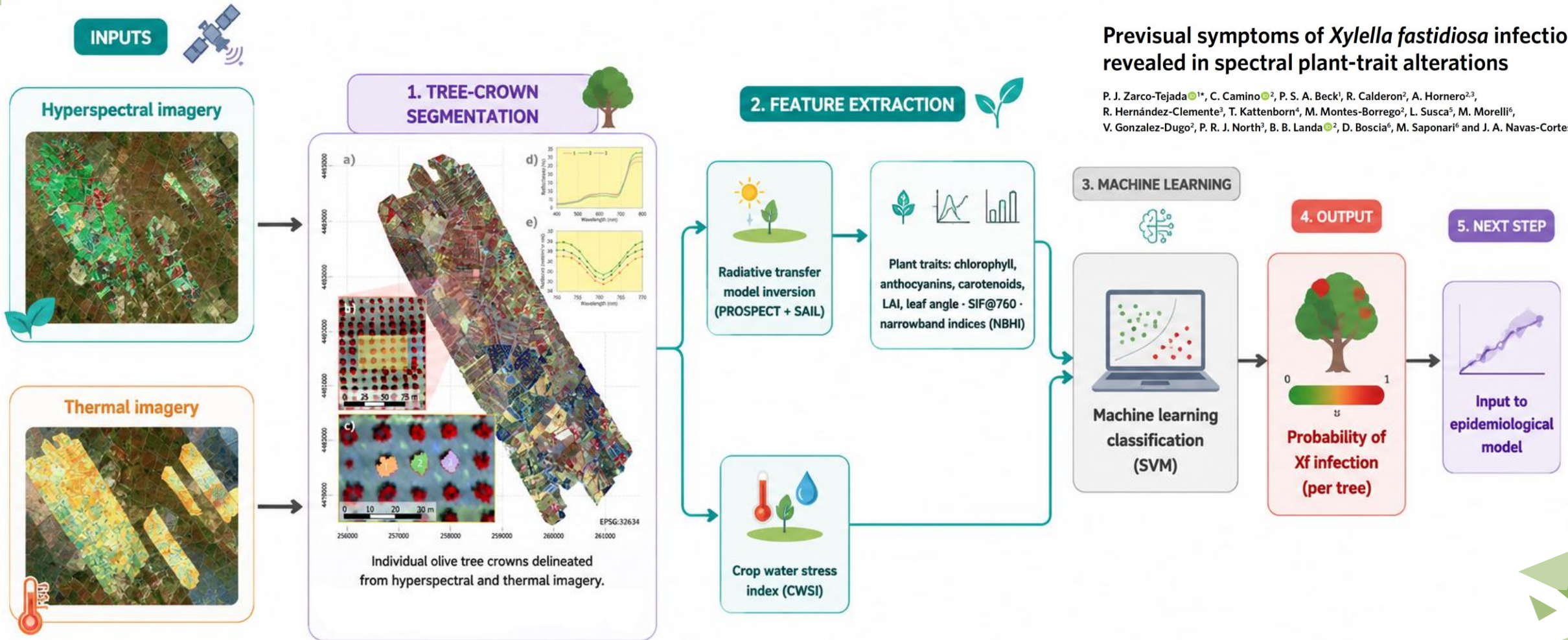
LETTERS

<https://doi.org/10.1038/s41477-018-0189-7>

nature
plants

Previsual symptoms of *Xylella fastidiosa* infection revealed in spectral plant-trait alterations

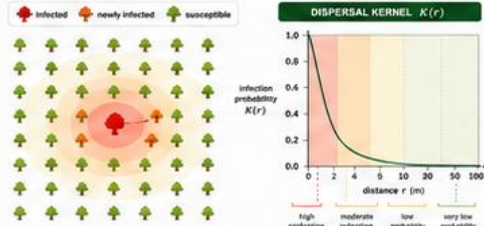
P. J. Zarco-Tejada^{1*}, C. Camino², P. S. A. Beck¹, R. Calderon², A. Hornero^{2,3}, R. Hernández-Clemente³, T. Kattenborn⁴, M. Montes-Borrego², L. Susca⁵, M. Morelli⁶, V. Gonzalez-Dugo², P. R. J. North³, B. B. Landa², D. Boscia⁶, M. Saponari⁶ and J. A. Navas-Cortes²



Modelling framework for *Xylella fastidiosa* spread and control

1 Design: spatially explicit, stochastic, discrete time spread model

a Spatial process



b Dispersal kernel

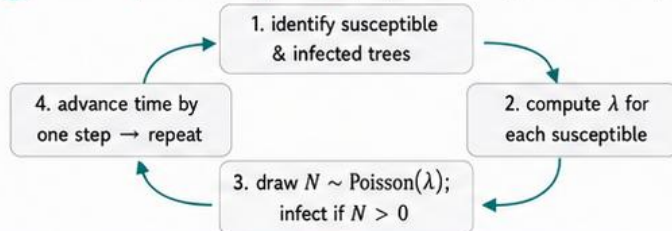
$$K(r) = \exp\left(-\left(\frac{r}{\theta}\right)^b\right)$$

heavy-tailed:
mostly local,
rare long jumps

c Response variable

new infections per susceptible tree in a step
follow a Poisson distribution:
 $N \sim \text{Poisson}(\lambda)$, $\lambda \propto \beta \sum_i e^{-(d_{ij}/\theta)^b} \delta t$

d Gillespie tau-leap loop (step = 3.65 days, until $t = 365$)



2 Fit: calibration to Apulia data

Estimate parameters
 β, θ, b
by Poisson likelihood

$$\ell(\beta, \theta, b) = \sum_p \ln \text{Poisson}(k_p | \lambda_p)$$

k_p = simulated infected trees in plot p

λ_p = observed expected infected per plot

- β - transmission rate (how readily infection spreads)
- θ - dispersal scale, in metres (typical distance of spread)
- b - kernel shape (tail heaviness; low b = rare long-distance jumps)

Field survey data
 λ_p = number of
symptomatic trees
per plot

Remote sensing data
 λ_p = sum of infection
probabilities per plot
(incl. previsual)

compare parameter posteriors
(field vs remote sensing)

3 Test: surveillance & control scenarios



Surveillance

detection method
(field survey vs remote sensing)
 x revisit interval



Control

roguing of detected trees
+ buffer radius

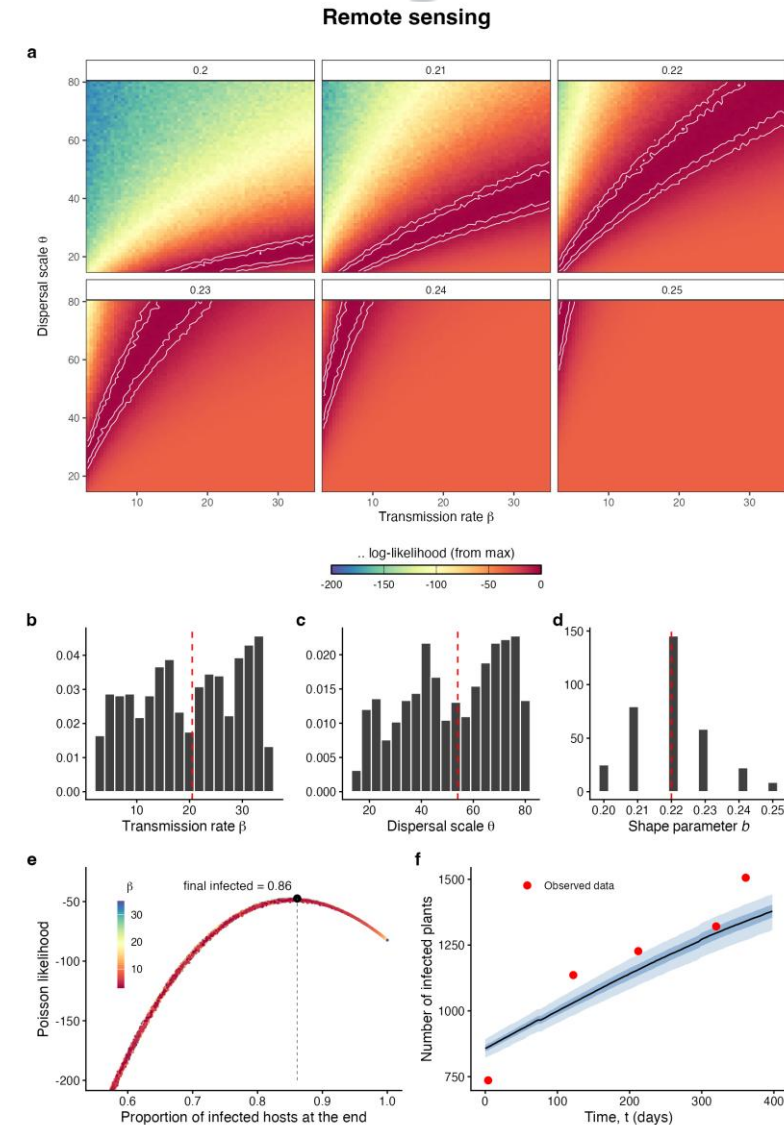
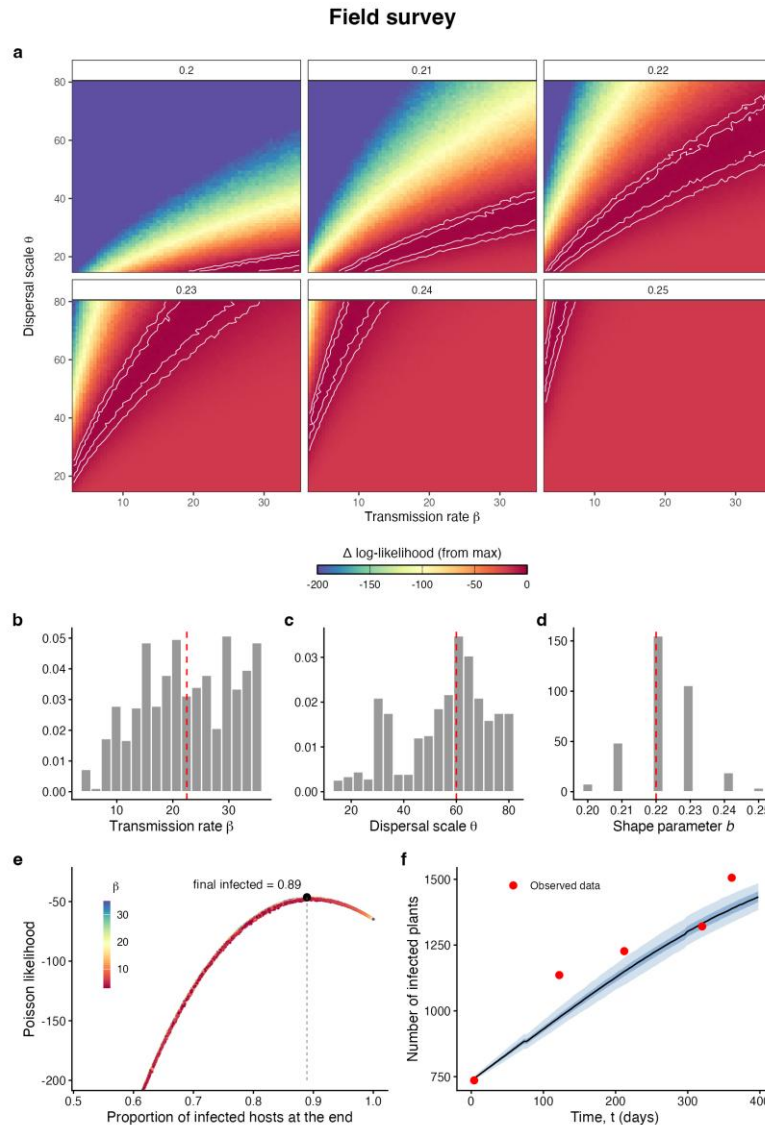


Outputs

$P(\text{containment / eradication})$
• cost (trees removed)
• spread velocity

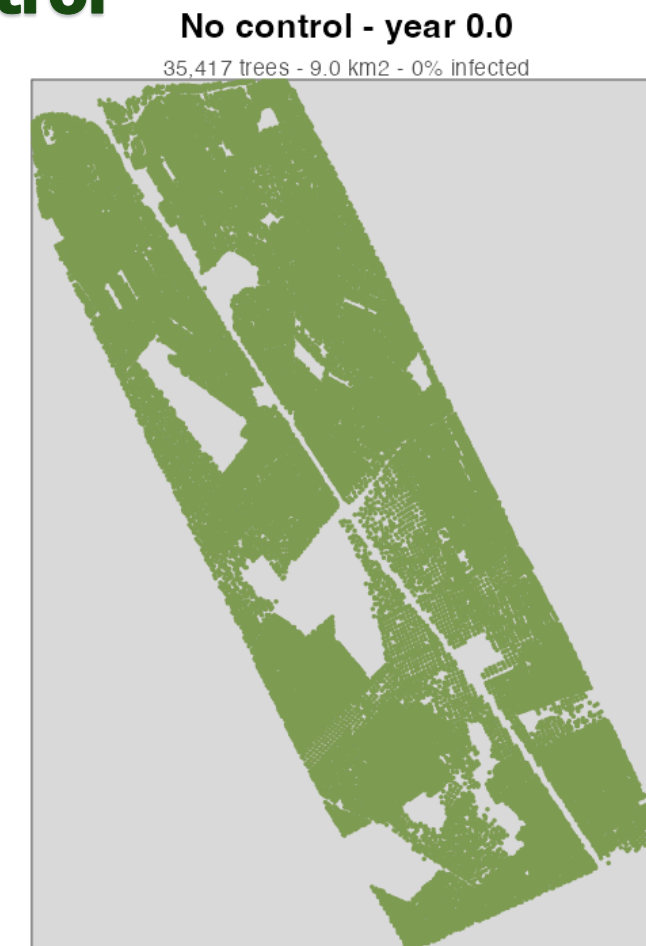
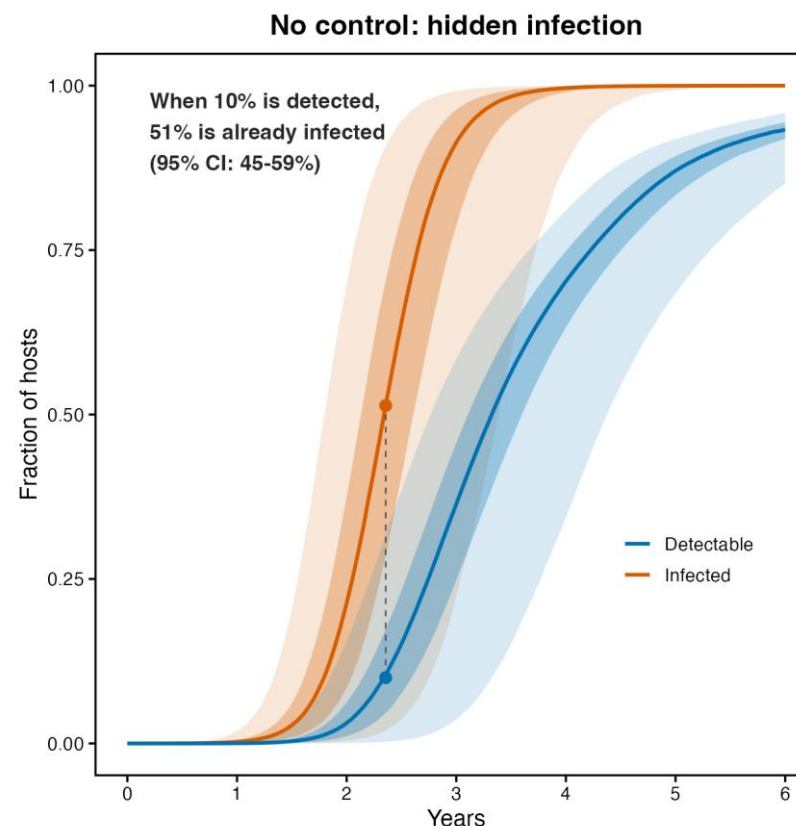
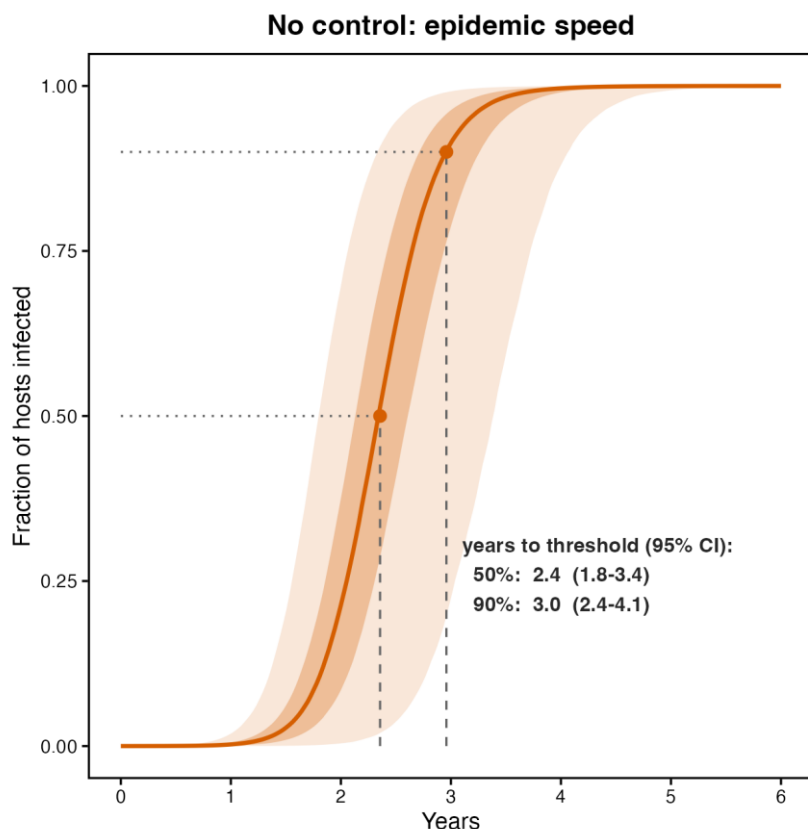
Real olive-tree landscapes in Apulia, mapped from remote-sensing flights,
are used both to calibrate the model and to run the scenarios.

Model calibration: field survey vs remote sensing



Remote sensing-based parameterisation reproduces field-survey estimates and provides comparable model calibration performance

Predicted epidemic spread in the absence of control



Without intervention, the epidemic remains largely cryptic while spreading rapidly

Surveillance and control performance: field survey vs remote sensing

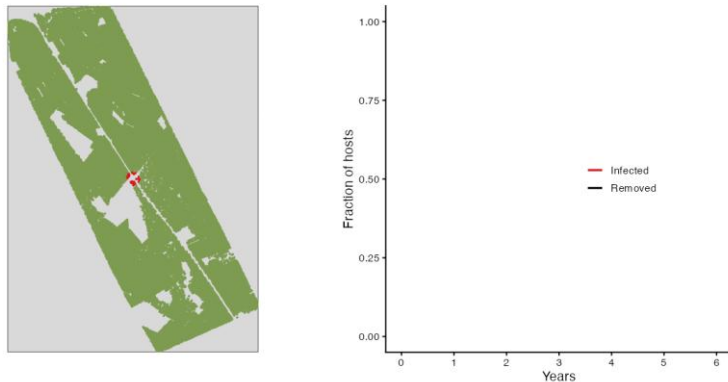
Detection probability per survey campaign

Method	Symptomatic	Asymptomatic (previsual)
Field survey	0.77	0.00
Remote sensing	0.87	0.25

Zarco-Tejada et al. (2018) (Nature Plants)

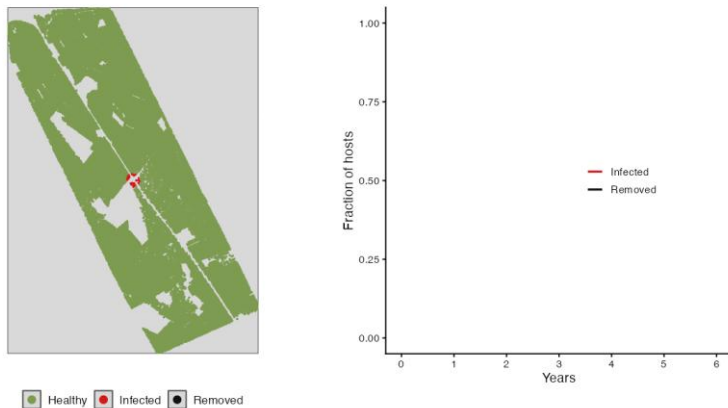
Field survey - year 0.0

revisit 30 d, radius 60 m | 0% infected, 0% removed

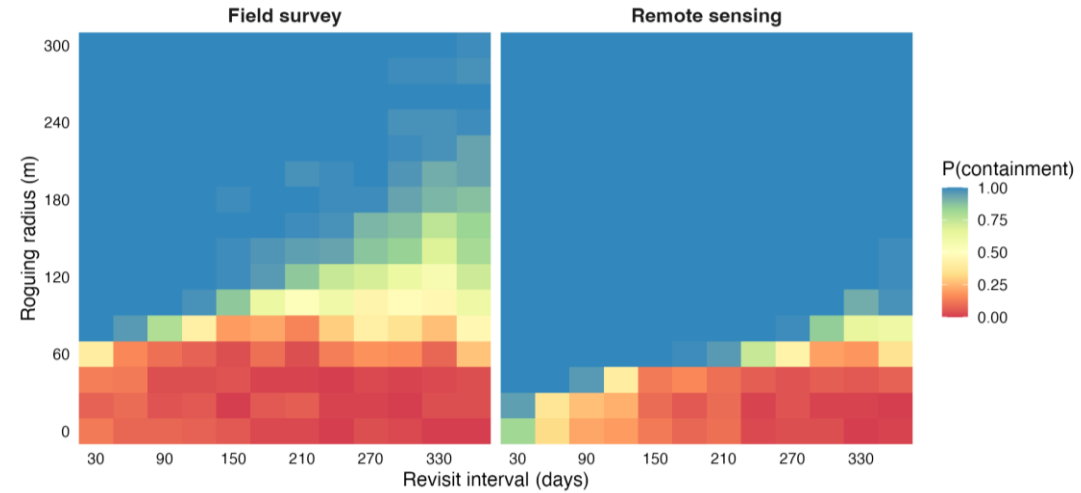


Remote sensing - year 0.0

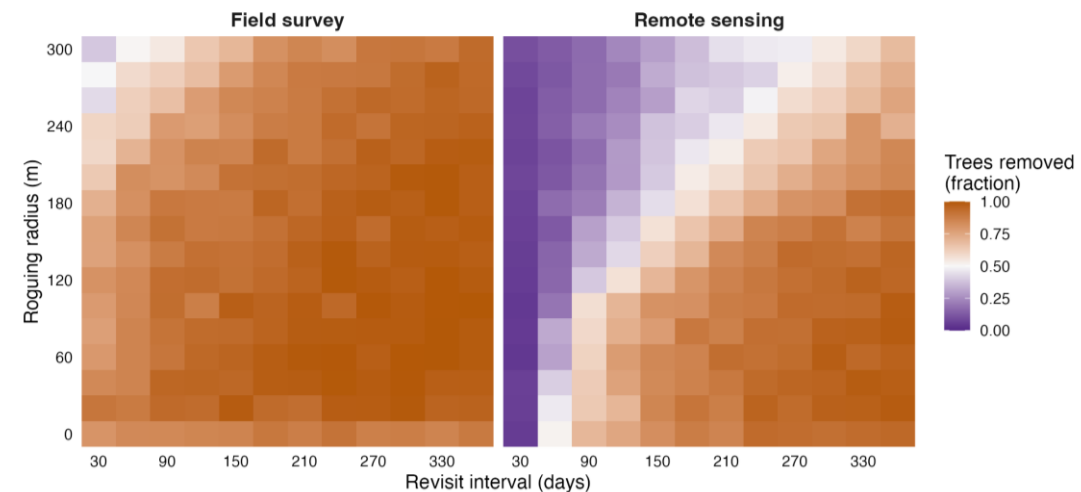
revisit 30 d, radius 60 m | 0% infected, 0% removed



Probability of containment



Cost: trees removed



Remote sensing achieves epidemic containment with longer revisit intervals, smaller roguing radii, and substantially fewer trees removed

The story thus far...



Remote-sensing disease maps robustly parameterise spatial spread models and are consistent with field-based estimates while capturing pre-symptomatic infection at landscape scale.



In the absence of control, the epidemic spreads rapidly with ~90% incidence within ~3 years and a large cryptic fraction. Symptom-based detection lags true infection, with ~50% infected when only ~10% are detected.



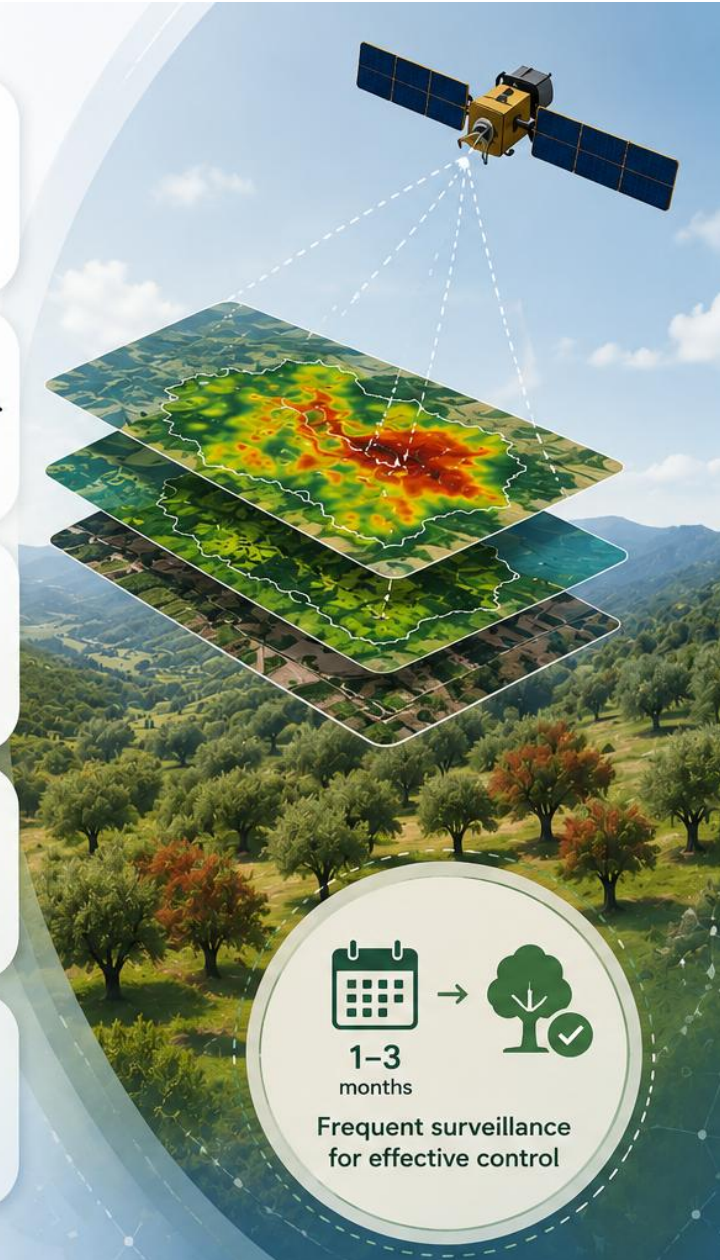
Surveillance strategy is the main determinant of control success. Remote sensing outperforms field surveys, achieving broader containment and lower removal costs under the same effort.



This advantage is driven by earlier detection of asymptomatic infections (~25% per campaign vs 0% for visual inspection), enabling earlier and more targeted roguing.



Effective containment requires frequent surveillance (~1–3-month revisit). Satellite remote sensing offers a scalable solution, although detection performance for *Xylella fastidiosa* is still being evaluated.





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Adapting Surveillance Design to Outbreak characteristics: A Dynamic Framework

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REGIONE PUGLIA



Context

Effective plant health surveillance is essential for early outbreak detection, prevalence estimation, and delimitation of pest distribution.

The EU Plant Health Law promotes risk-based surveillance and rapid response to priority quarantine pests.

EFSA guidelines support Member States in designing surveys that inform regulatory decisions, determine pest status, and provide confidence in pest absence.

A key component of these surveillance systems is the survey design, which integrates statistical and epidemiological parameters to ensure effective and reliable sampling strategies.

The survey design is the structured process of defining where, when, and how observations are made.



Surveillance Definition

Surveillance is the observation of n inspection units' infection statuses, **initially unknown**, within a total population composed of N individuals.

A subset of n individuals is sampled and observed from the full population of size N .

The collected observations are used to:

- Infer properties of the total population;
- Delimitate infected regions;
- Support decision-making processes.

How to design the sample size n ?



Standard Sample Size Calculation

Following EFSA guidelines (EFSA, 2025), the sample size is based on the hypergeometric distribution:

$$n = (1 - (1 - CL)^{1/(N \cdot DP)}) \cdot (N - 1) \cdot (N \cdot DP \cdot MS - 1) / MS,$$

where the sample size (**n**) depends on the population size (**N**),
the confidence level (**CL**), i.e., the level of accuracy achieved by the survey;

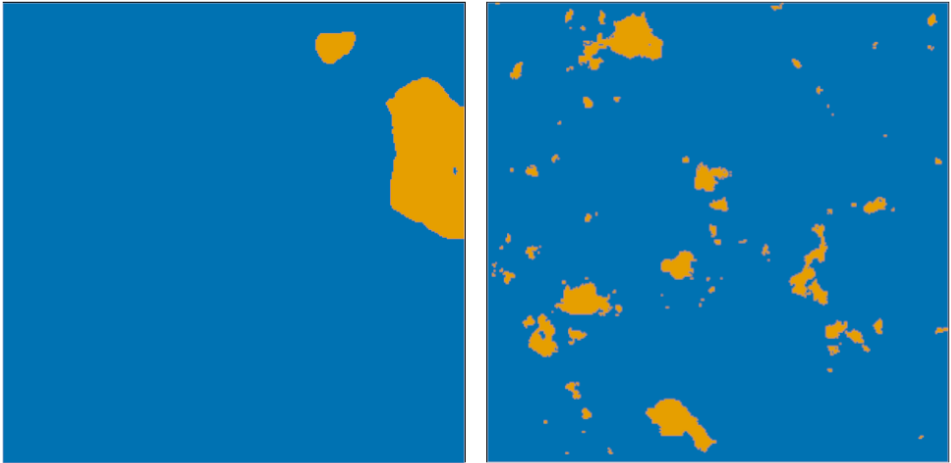
the design prevalence (**DP**), i.e., **the prevalence the survey aims to detect** if the pest or pathogen is present with probability greater than **CL**;

and the method sensitivity (**MS**), i.e., the probability that a positive individual will be identified accordingly.

Decreasing design prevalence (**DP**) increases the sample size (**n**).

Goal : Adapt the design prevalence DP to the spatial structure.

Dynamic Design Prevalence Adaptation



Within a spatially aggregated outbreak :

- a sample is **more informative**.
- the outbreak is **more easily controlled**.

A fixed sample size for all spatial structures treats all outbreaks as if they had the same controllability.

This is not the case.

Sample size must account for this spatial dependence.

The design prevalence must be **lower** for **less aggregated outbreaks**.

We propose to adapt the design prevalence dynamically from outbreak characteristics :

$$\text{DP} = \text{DP}(\text{spatial structure})$$

Modeling the Propagation Function

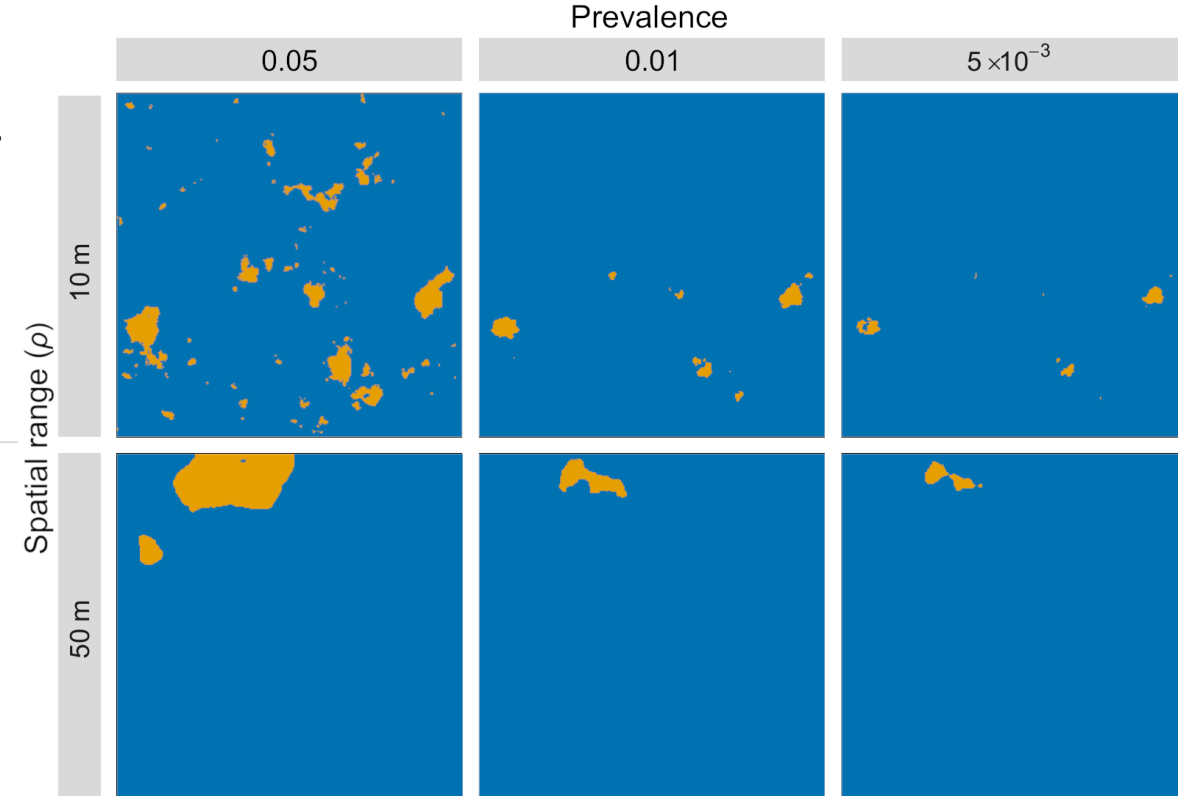
The propagation function $\mathbf{f}$ is given by a gaussian process. It gives to each plant its **order of infection**.

The range $\mathbf{R}$ of $\mathbf{f}$ specifies the distance beyond which spatial dependence becomes negligible.

Less aggregation increases the outbreak perimeter.

The outbreak perimeter depends on:

- the range $\mathbf{R}$ (the larger $\mathbf{R}$, the more aggregation),
- the prevalence.



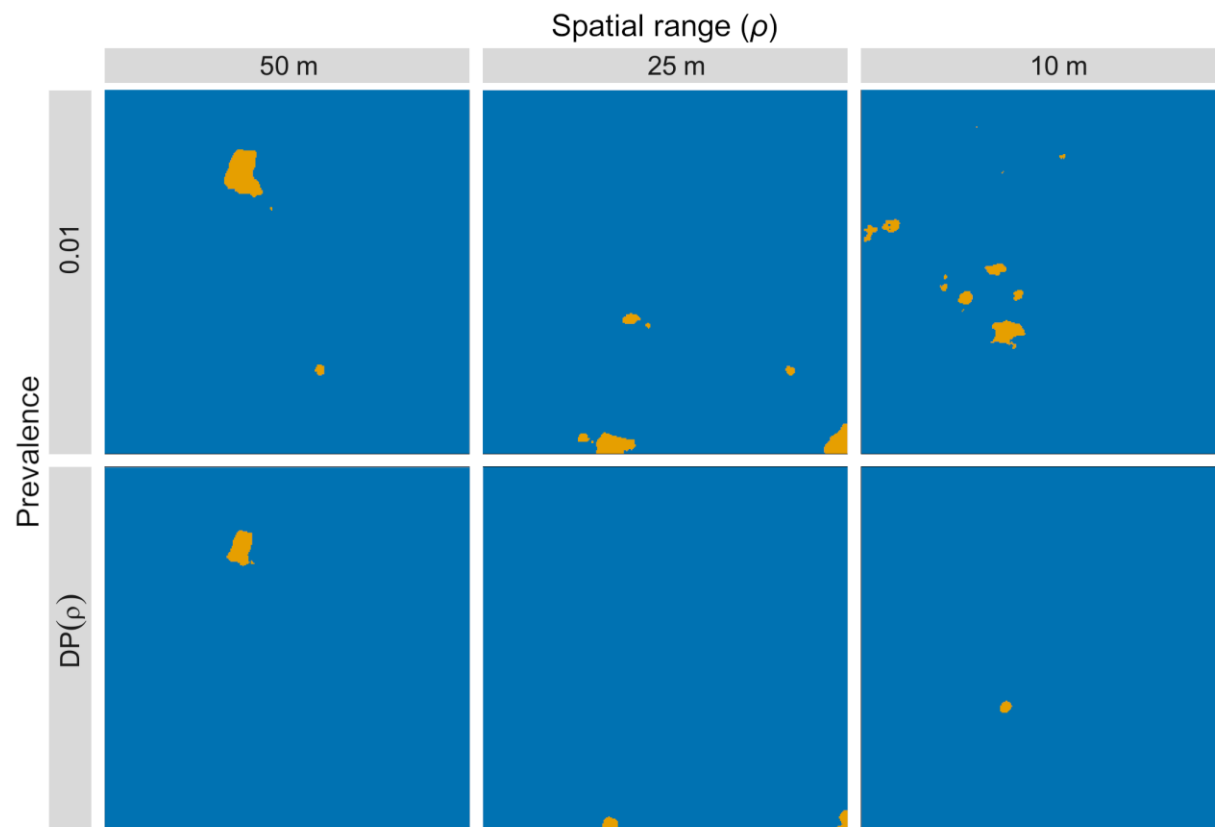
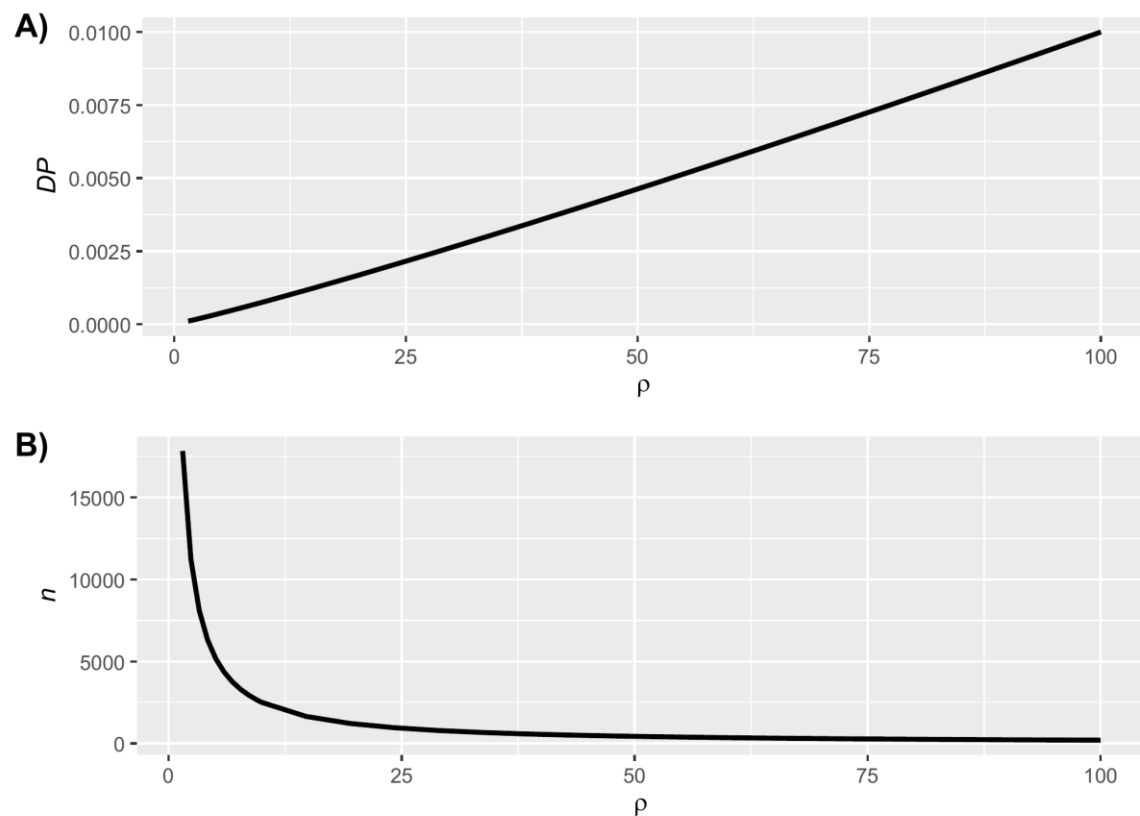
Proposed Method

We adapt the design prevalence $\mathbf{DP}$ to the aggregation level $\mathbf{R}$ so that:

$$\text{Perimeter}(\mathbf{R}, \mathbf{DP}) = \text{Perimeter}(\mathbf{R}_2, \mathbf{DP}_2)$$

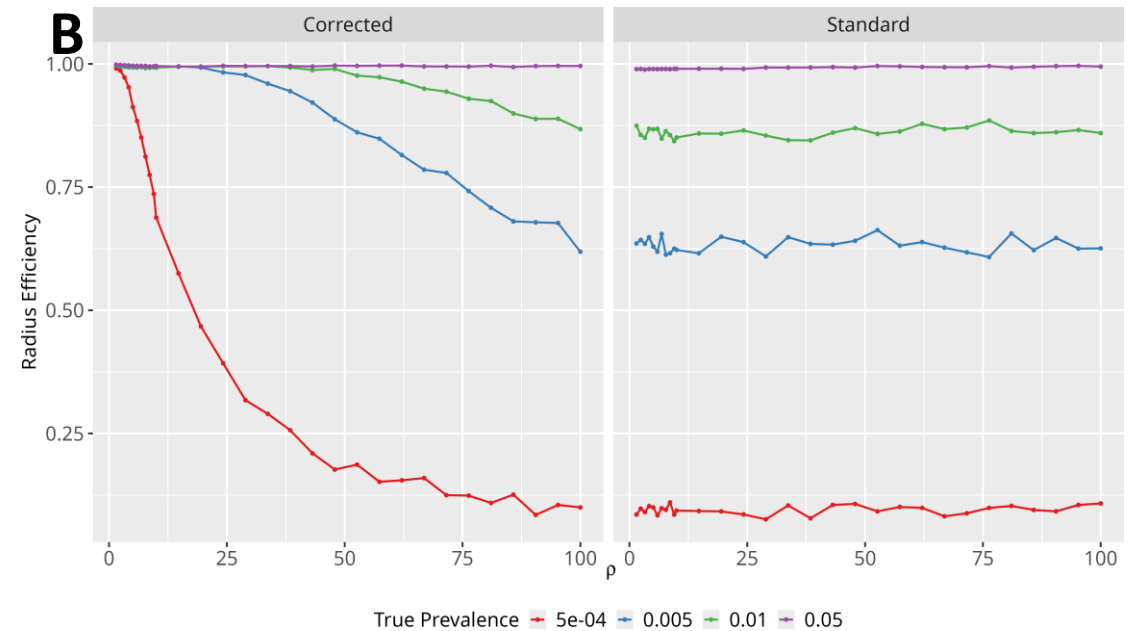
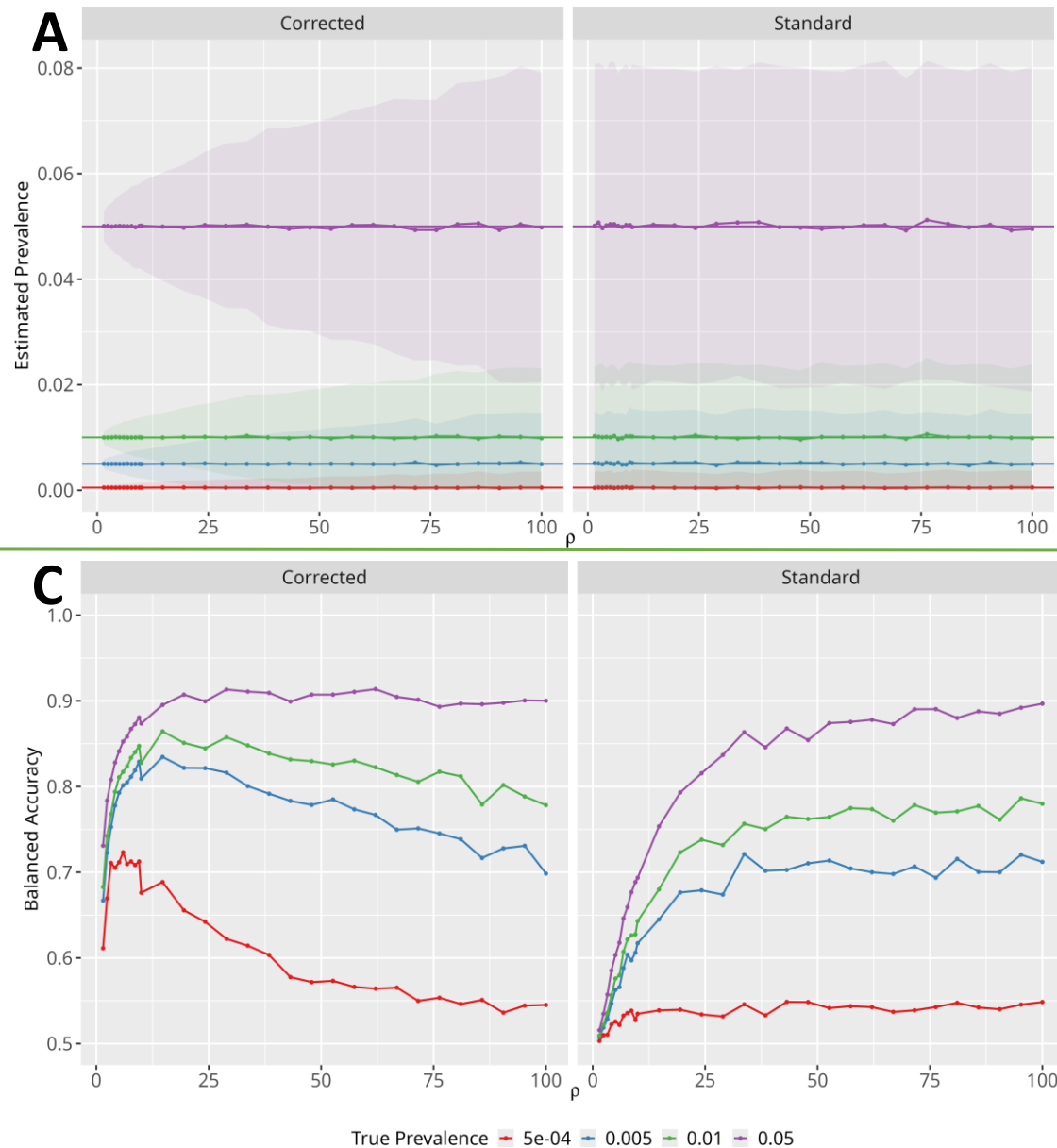
Thus, the outbreak perimeter is invariant across aggregation levels.

Adapted **DP** and sample size **n**



- Specify the **design prevalence** and the **range** in the **aggregated case**.
- For the **true range** corresponding to the true aggregation level, **lower the design prevalence** to make the **true outbreak perimeter equal** to the **aggregated outbreak perimeter**.

Comparison with Standard Method (DP = 1%)



A : Accuracy of the total prevalence prediction

B : Coverage of the infected individuals

C : Accuracy of the status prediction of unsampled individuals



Summary

- The design prevalence (DP), and consequently the sample size (n), are adjusted to ensure that the outbreak perimeter remains constant across aggregation levels.
- As a result, different aggregation scenarios achieve the same level of efficiencies.
- This adaptive approach outperforms the use of a fixed design prevalence according to three efficiency criteria.
- When the true parameter values are unknown:
 - Estimates can be derived from historical outbreaks or values reported in the literature;
 - Alternatively, parameters can be estimated through a sequential monitoring approach.



Find the paper online





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Twelve years of models of *Xylella fastidiosa* in Europe: Lesson learnt

Image: Stefano Petroni

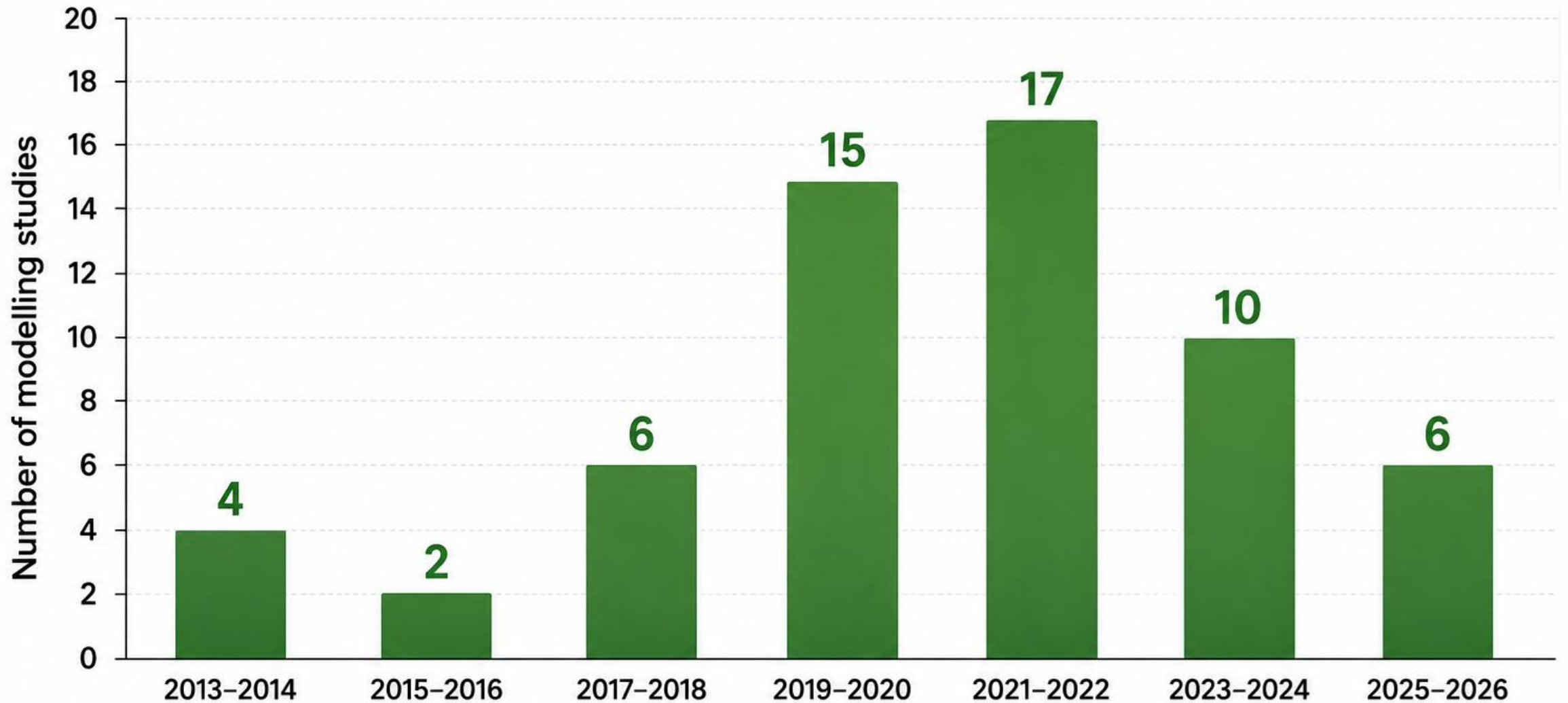
Simonetto A.⁽¹⁾, Weber I.D.⁽¹⁾, Gilioli G.⁽¹⁾, Bertoldi E.⁽¹⁾, Gervasio P.⁽¹⁾, Saponari M.⁽²⁾, Dongiovanni C.⁽³⁾, Boscia D.⁽²⁾

⁽¹⁾ Università di Brescia, DICATAM, Via Branze 43, 25123, Brescia, Italy

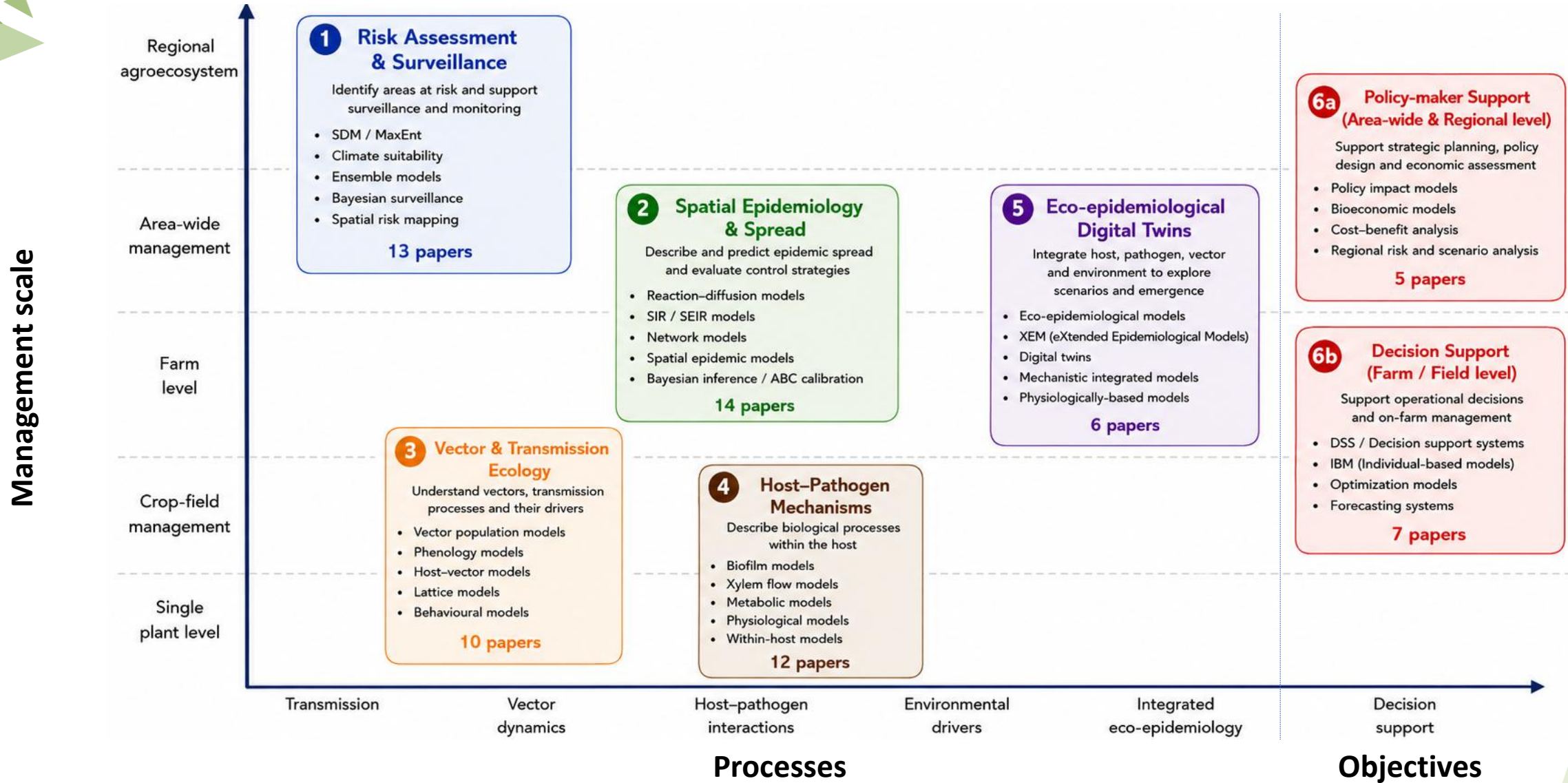
⁽²⁾ Institute for Sustainable Plant Protection (IPSP), National Research Council, Bari, Italy

⁽³⁾ Centro di Ricerca, Formazione e Sperimentazione in Agricoltura "Basile Caramia" (CRSFA), Locorotondo, Italy

Trend in modelling on *Xylella fastidiosa* and vector dynamics



Classification of modelling approaches for *Xylella fastidiosa*



What have modelling taught us about *Xylella fastidiosa*?

• Risk Assessment & Surveillance

- Where can *Xylella fastidiosa* establish?
- How will risk change under future climate scenarios?



- Climatic suitability maps
- Establishment risk assessment
- Climate change risk projections

• Spatial Epidemiology & Spread

- How rapidly the epidemic expand?
- How transmission processes influence spread?
- What is the effect of containment measures?



- Quantification of epidemic spread rates
- Understanding of transmission and invasion dynamics
- Evaluation of containment and buffer-zone strategies

• Host–Pathogen–Vector Processes?

- How does the bacterium grow and colonize the host?
- How does biofilm formation develop within the xylem?
- How do host and pathogen interact?



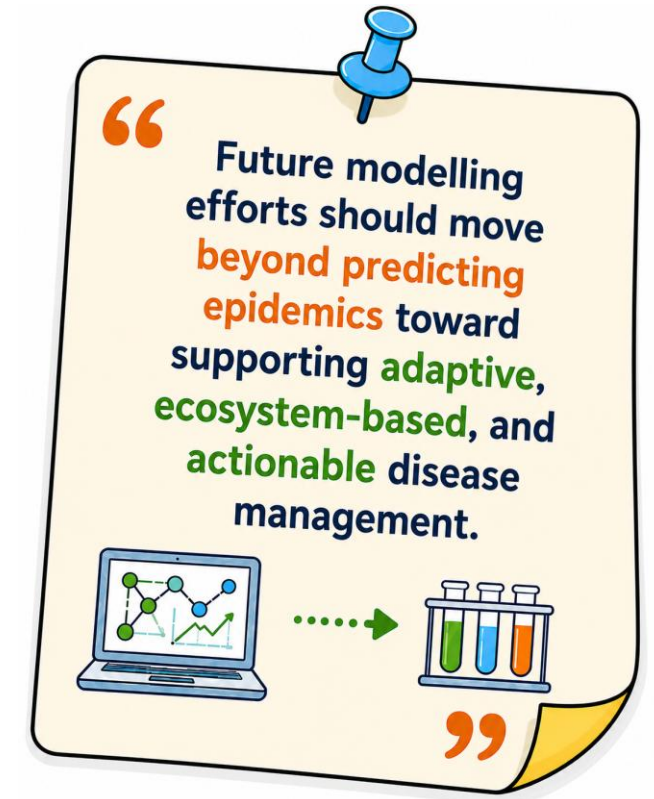
- Characterization of biofilm development and xylem colonization
- Identification of key host physiological mechanisms
- Improved understanding of vector-mediated transmission

Knowledge gaps

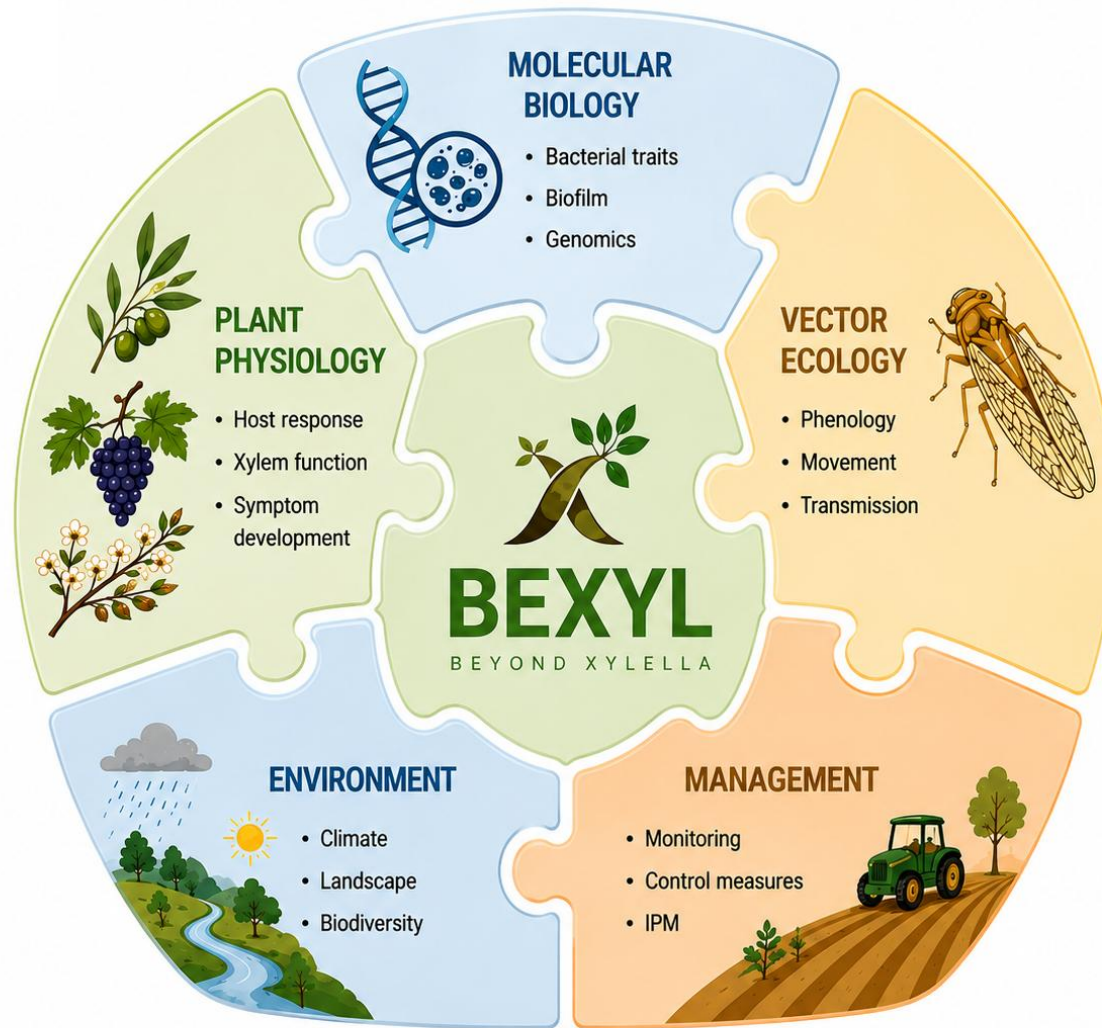
- **How do environmental factors influence epidemics?**
 - Effects of temperature and water stress on bacterial growth, transmission processes, vector competence
 - ⚠ These processes are still represented in a highly simplified way
- **How transferable are models across pathosystems?**
 - Most models focus on 🟢 Olive Quick Decline Syndrome (OQDS)
 - Far fewer address:
 - 🍇 Pierce's disease,
 - 🌰 Almond leaf scorch
 - ☕ Coffee diseases
 - 🌳 Forest hosts impact
 - ❓ Which mechanisms are universal, and which are pathosystem-specific?
- **What is the role of plant community biodiversity?**
 - Reservoir and sink species, cover crops and spontaneous vegetation
 - Landscape composition and structure
 - ⚠ These components are rarely represented in an integrated way

Future challenges for modelling and DSS

- **How do epidemics emerge from the interaction among:**
 - Host
 - Bacterium
 - Vector
 - Environment
 - Management
- **How can IPM be optimized over the long term?**
 - Current models rarely address:
 - ? Multi-year management strategies
 - ? Adaptive interventions
 - ? Combined control measures
 - ? Economic–ecological trade-offs
- **When should interventions be applied?**
 - Not only: *"What should I do?"*
 - but also: **"When should I do it? "** or **«How to combine options? "**



From domain-related knowledge to its integration



Digital lab

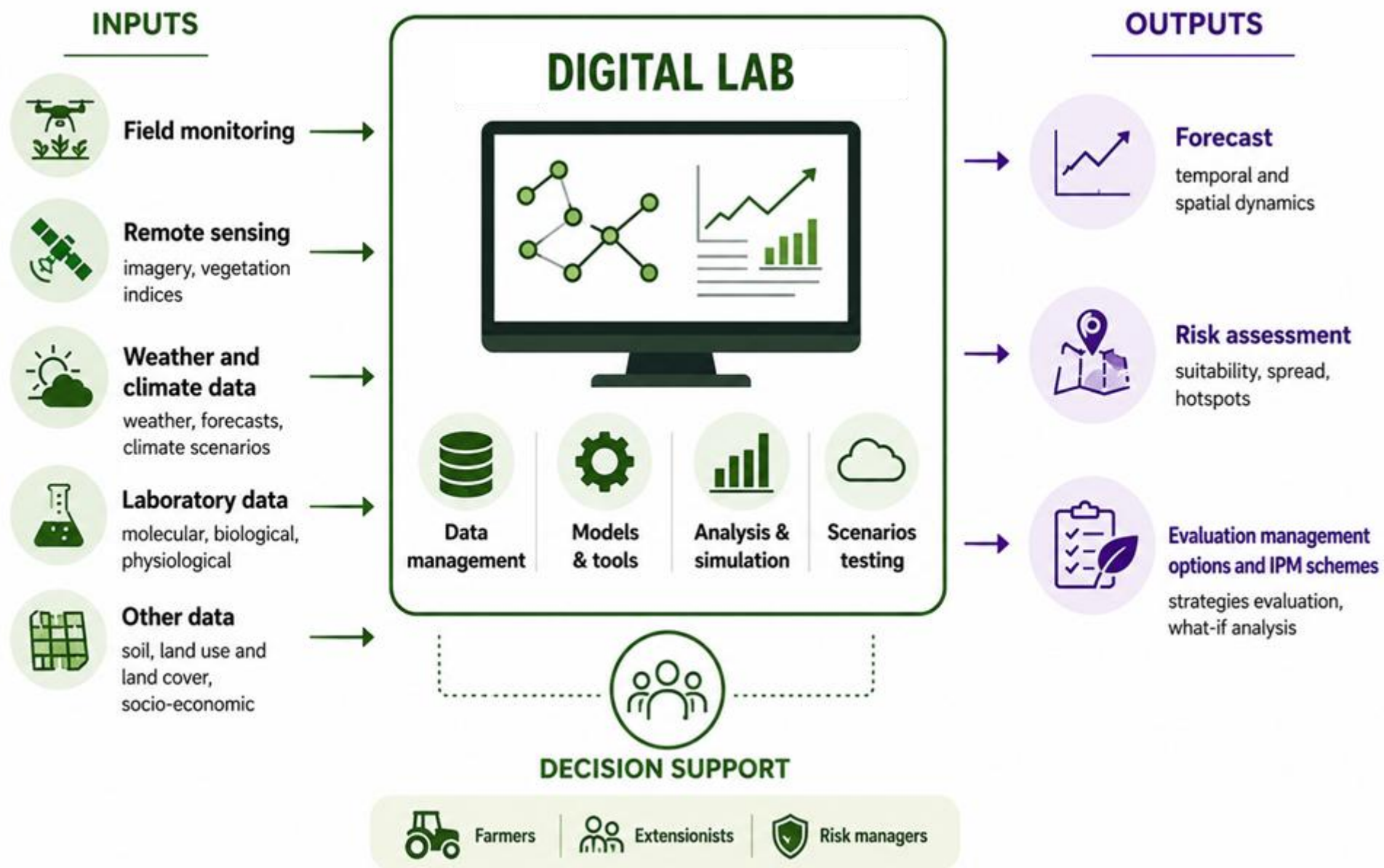
Full exploitation of lab and field results

- Connecting domains
- From observations to system dynamics
- Evaluate hypotheses and scenarios

Knowledge-based decision support

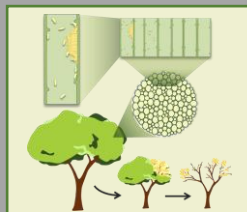
Supporting decision-making process by informing options selection

- Selection of IPM option and schemes
- Time and mode of intervention
- Performance indicators
- Adaptive and ecosystem-based management

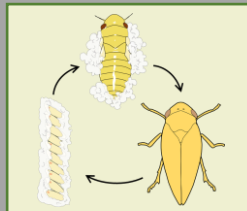


Eco-epidemiological model: a platform for knowledge integration and decision support

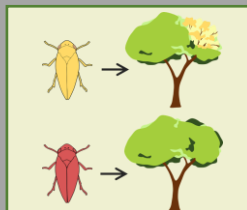
Satellite models



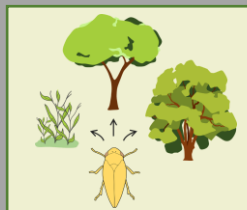
Disease
progression in
plant



Vector
population
dynamics



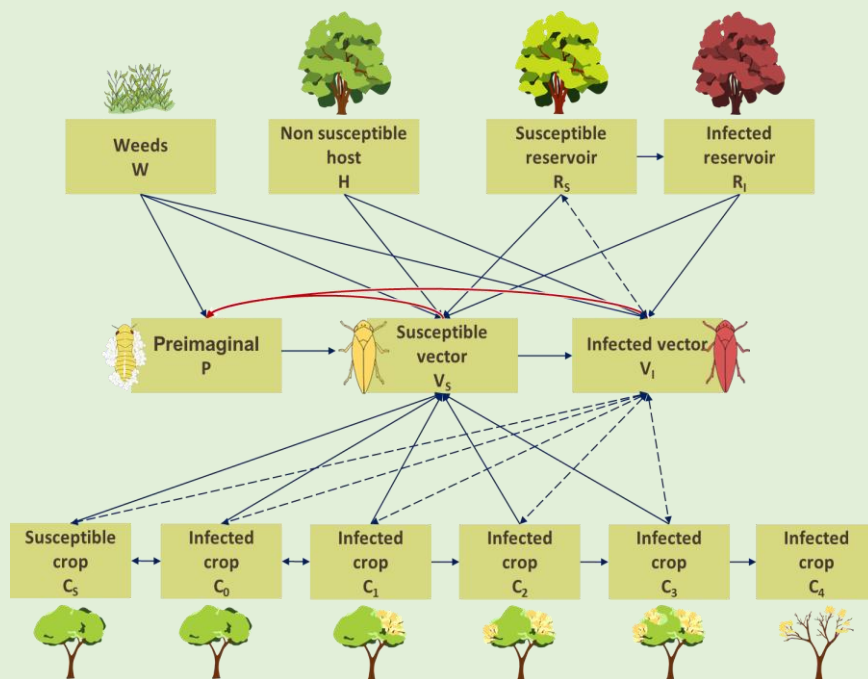
Transmission
dynamics



Vector spatial
dynamics

Core model

Local epidemiological dynamics



Spatial epidemiological dynamics

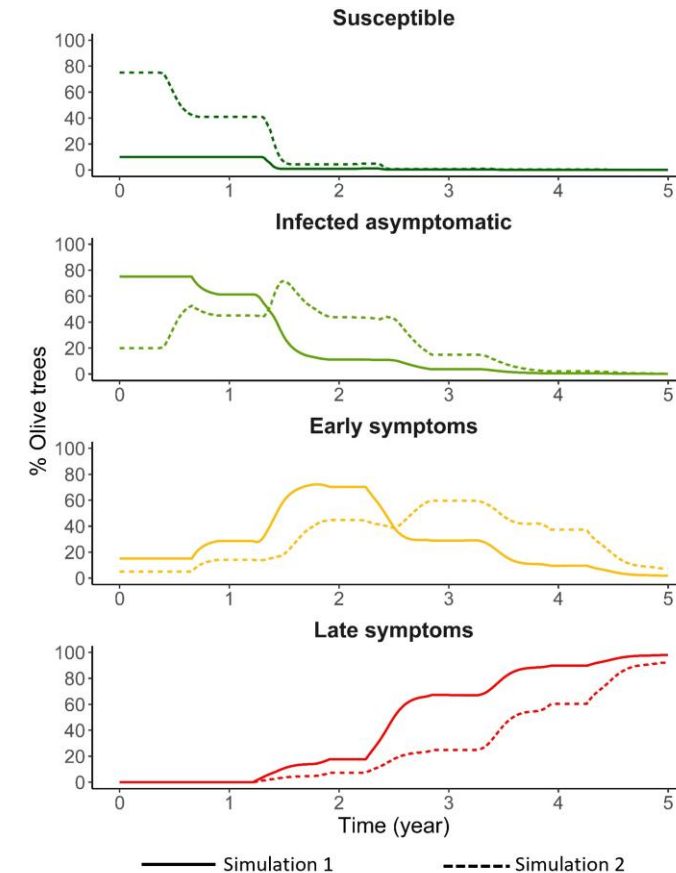
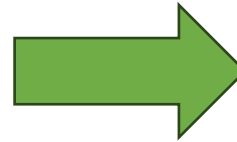
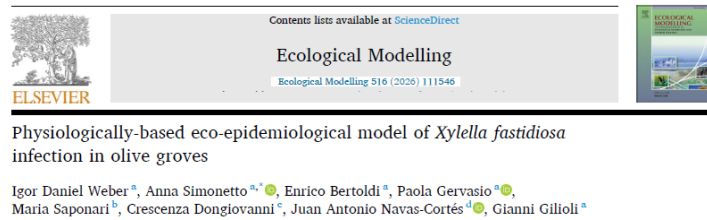


Eco-epidemiological model: a platform for knowledge integration and decision support

Current status of the framework

A common modelling architecture

 **Olive** → framework largely completed



 **Grapevine** → advanced development stage

See Poster 120

Submitted paper to Phytopathology

 **Almond** → next target for integration

From understanding epidemics to supporting decisions

- **What we learnt in this 13 years journey:**
 - **Modelling did not exploit their potentiality**
 - **Need for a wider and structured modelling activity supporting knowledge integration and guiding decision support**
 - Modelling can create new **opportunities for dialogue** between basic researchers, risk managers and IPM practitioners,
→ transforming scientific knowledge into actionable information
- **One framework → Multiple scales → Better decisions**



Università
di Brescia
AgroFood Research Hub



Funded by the
European Union



*Research is a long journey,
and the right companions
make it worthwhile*



Anna Simonetto
anna.simonetto@unibs.it
Università di Brescia



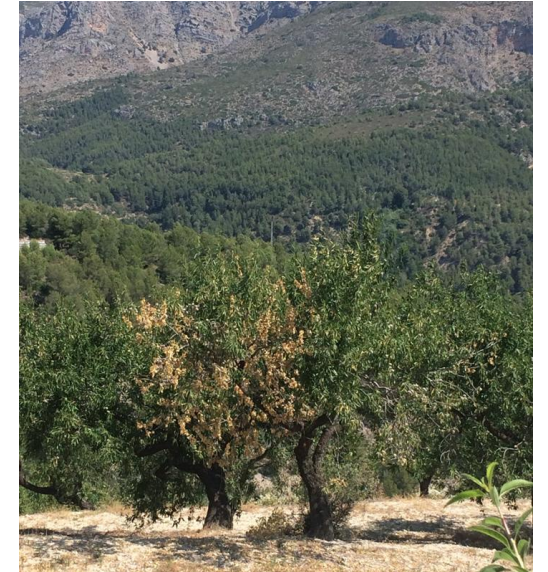
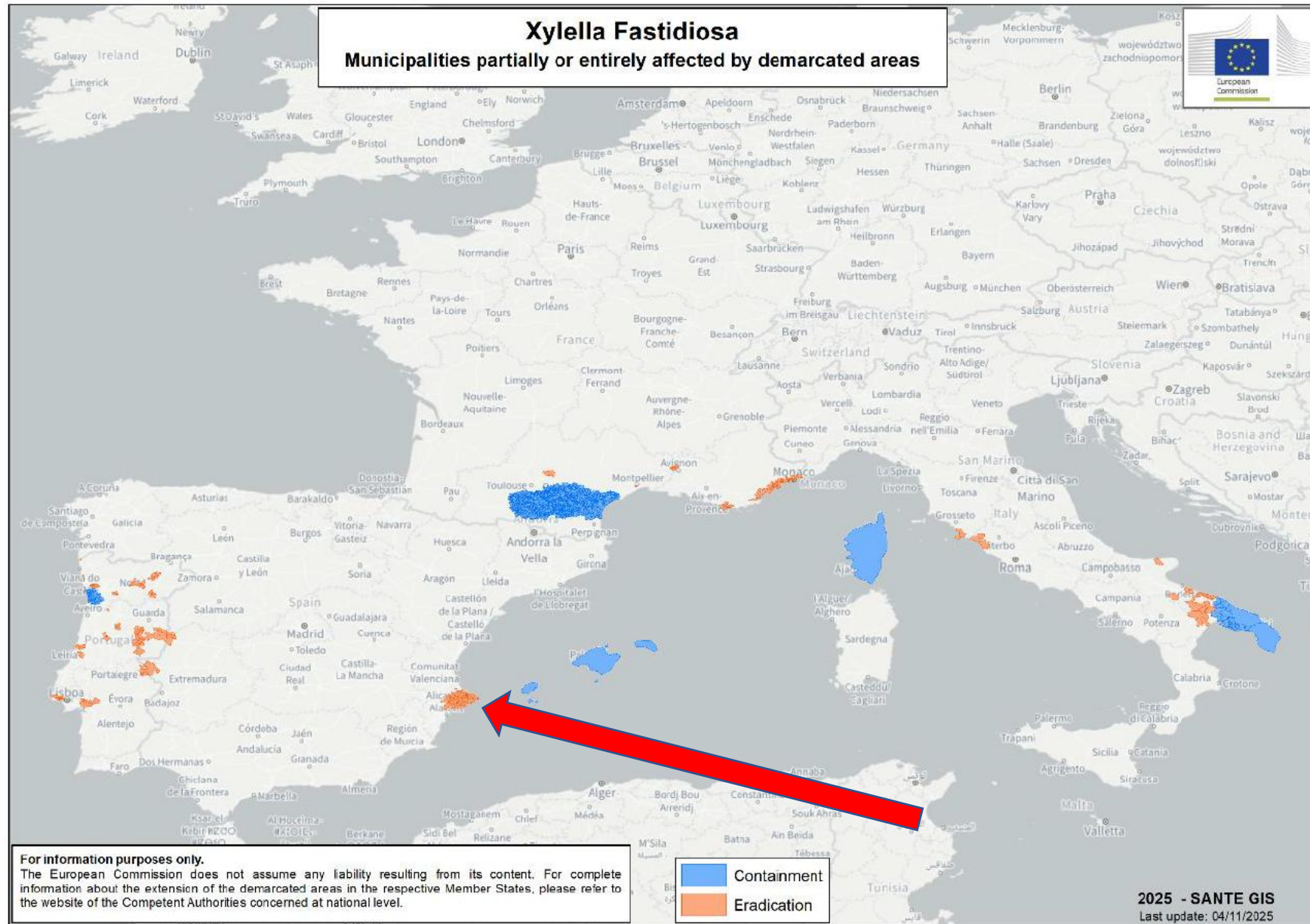
Evolution and consequences of nine years of application of phytosanitary measures to control *Xylella fastidiosa* subsp. *multiplex* outbreak in Alicante

5th European Conference on *Xylella fastidiosa*
Bari, 24/06/2026

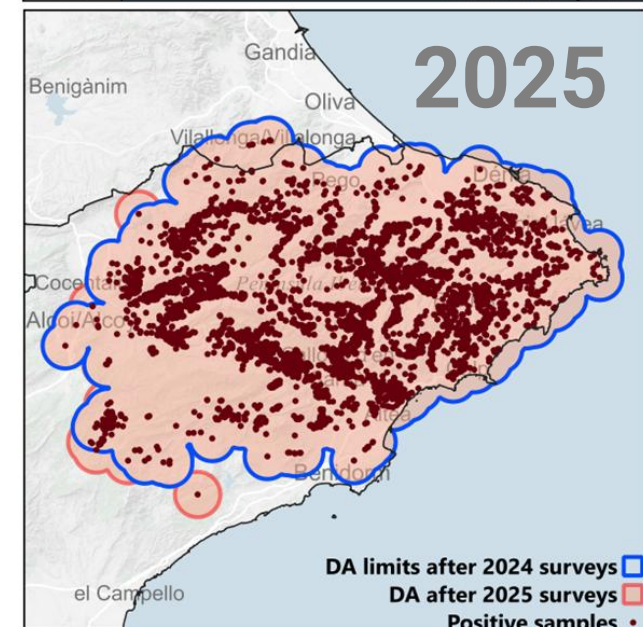
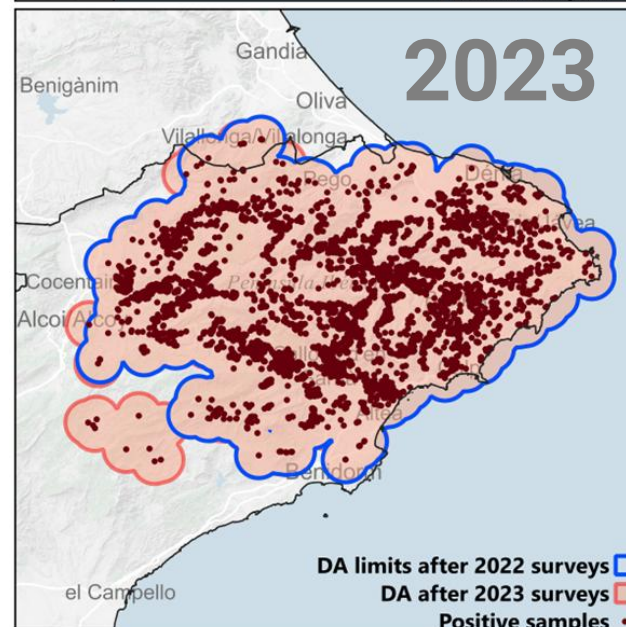
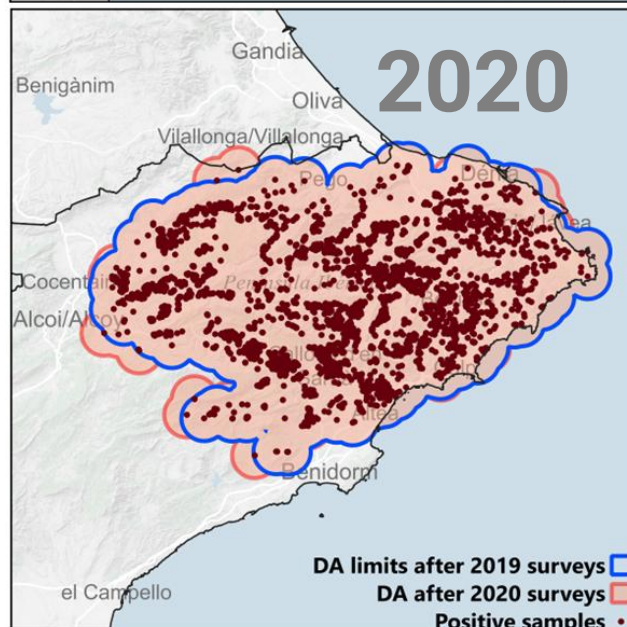
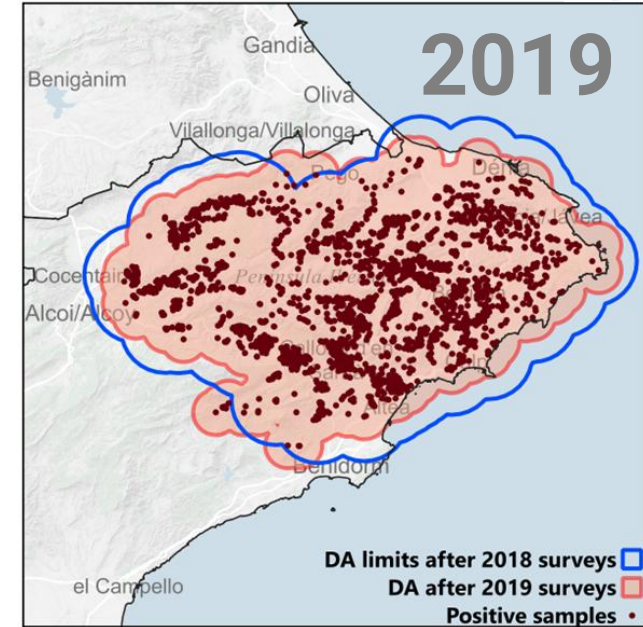
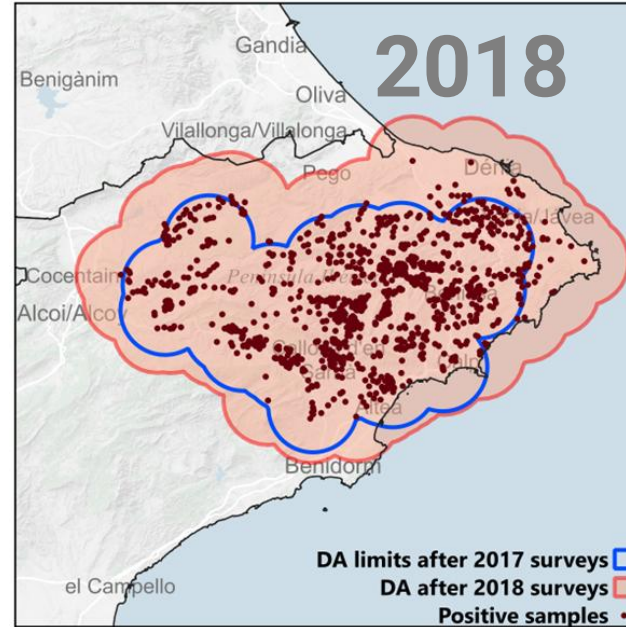
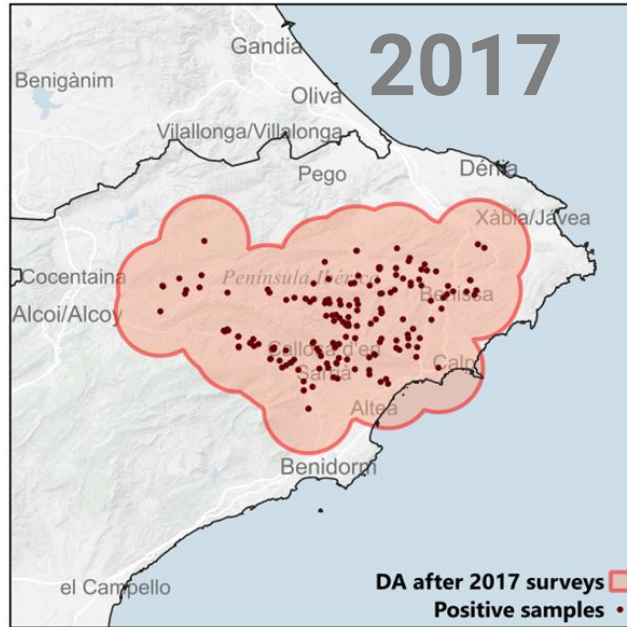
Vicente DALMAU SORLÍ
dalmau_vic@gva.es

Servicio de Sanidad Vegetal de la Generalitat Valenciana, SPAIN

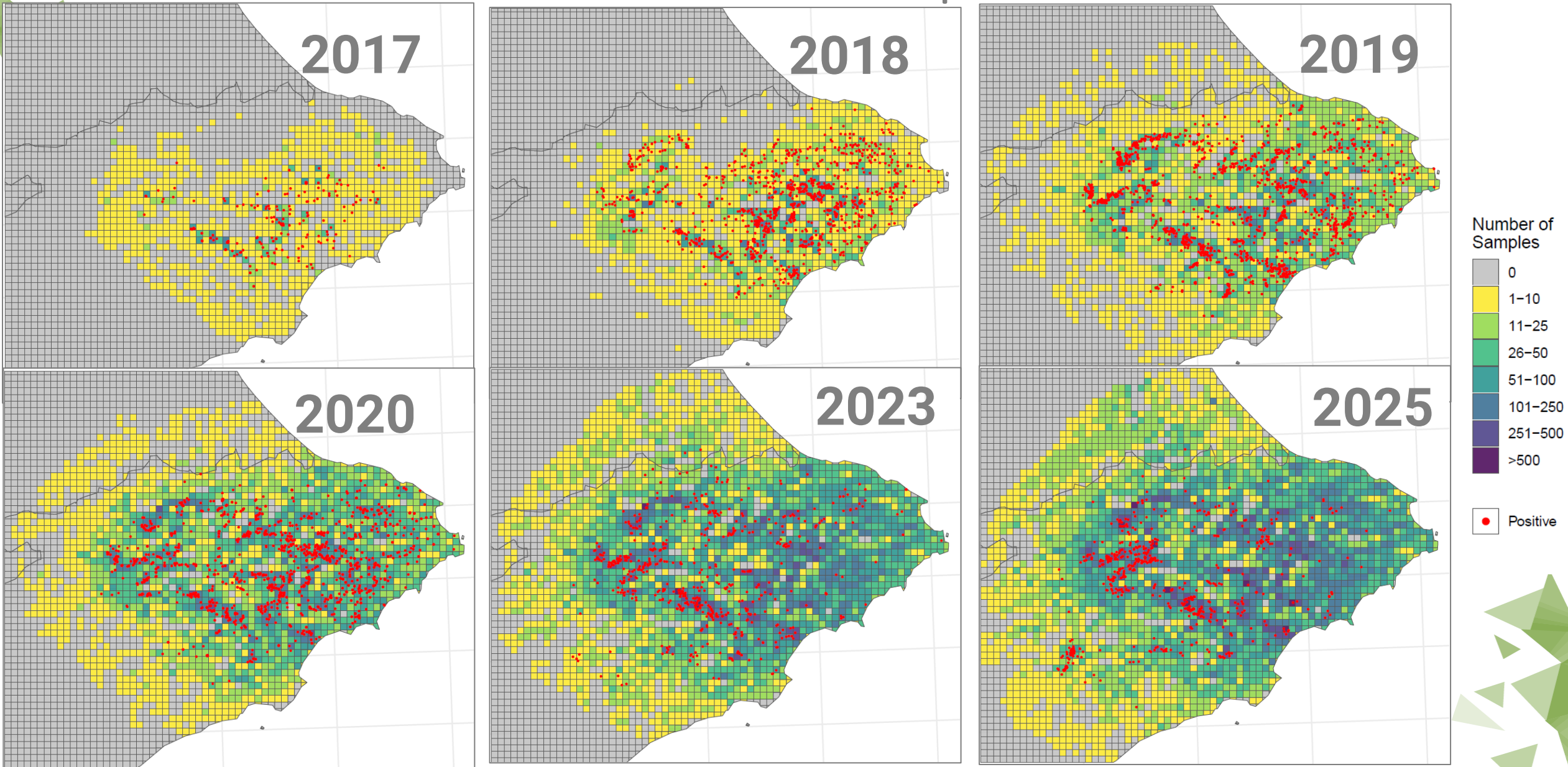
Alicante's *X. fastidiosa* outbreak detected in June 2017



X. fastidiosa Demarcated Area Evolution in Alicante



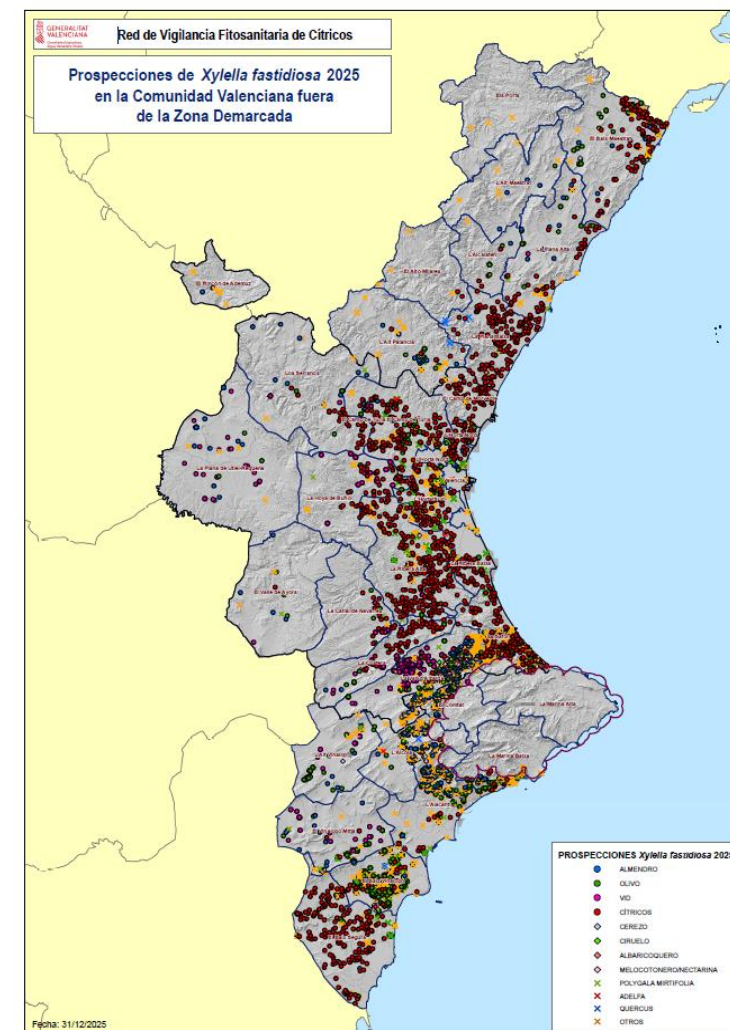
X. fastidiosa sampling evolution in the Demarcated Area and 10km envelope



Demarcated area evolution for *X. fastidiosa* in Alicante

	DA Area (ha)	Increase (ha)	Increase (%)
2017	56.256	56.256	100%
2018	109.842	53.587	95%
2019	128.080	18.238	17%
2020	135.409	7.329	6%
2021	138.002	2.593	2%
2022	145.279	7.277	5%
2023	156.864	11.585	8%
2024	165.559	8.695	6%
2025	170.722	5.163	3%

Since 2020, the annual increase is, on average,
below 5%



State of play of *X. fastidiosa* in Alicante

Demarcated area (DA)	170,721 ha , 7,3% CV and 0,3% mainland ES
DA municipalities	85
Infected Zone (IZ)	4,400 ha , 0,19% CV and 0,009% mainland ES
IZ municipalities	73
Surveys	188,000 plant analysis (123,500 DA and 64,500 ODA)
Eradicated Area	4,400 ha (3,300 ha in the 50m radius)
Insecticide treatment	5,300 ha
Plants tested positive	7,467 (all destroyed)
Plant species tested +	30
Subspecies and ST	<i>X. fastidiosa</i> subsp <i>multiplex</i> ST 6

Prevalence of *X. fastidiosa* in Demarcated Area

Plant specie **Nº analysis** **% infection**

<i>Prunus dulcis</i>	21.932	30%
<i>Polygala myrtifolia</i>	434	19%
<i>Calicotome spinosa</i>	1.303	10%
<i>Helichrysum sp.</i>	2.452	7%
<i>Lavandula sp.</i>	827	3%
<i>Phagnalon saxatile</i>	1.469	3%
<i>Cistus sp.</i>	2.919	2%
<i>Rhamnus alaternus</i>	1.948	2%
<i>Prunus armeniaca</i>	1.507	2%
<i>Prunus domestica</i>	1.336	1%
<i>Salvia rosmarinus</i>	4.904	1%
<i>Asparagus acutifolius</i>	1.655	0,2%
<i>Olea europaea</i>	26.399	0,0%
<i>Ficus carica</i>	11.109	0,0%
<i>Prunus avium</i>	7.681	0,0%
<i>Citrus sp.</i>	7.120	0,0%
<i>Vitis sp.</i>	6.167	0,0%
<i>Nerium oleander</i>	6.565	0,0%
<i>Quercus sp.</i>	5.216	0,0%
<i>Persea americana</i>	792	0,0%

Vector specie	Nº analysis	Nº positive	% positive
<i>Philaenus spumarius</i>	9,284	540	5,8%
<i>Neophilaenus campestris</i>	9,542	105	1,1%
<i>Neophilaenus lineatus</i>	1,184	0	0,0%
Total	20,010	645	3,2%



Eradicated areas



Eradicated areas



Eradicated areas orthophoto

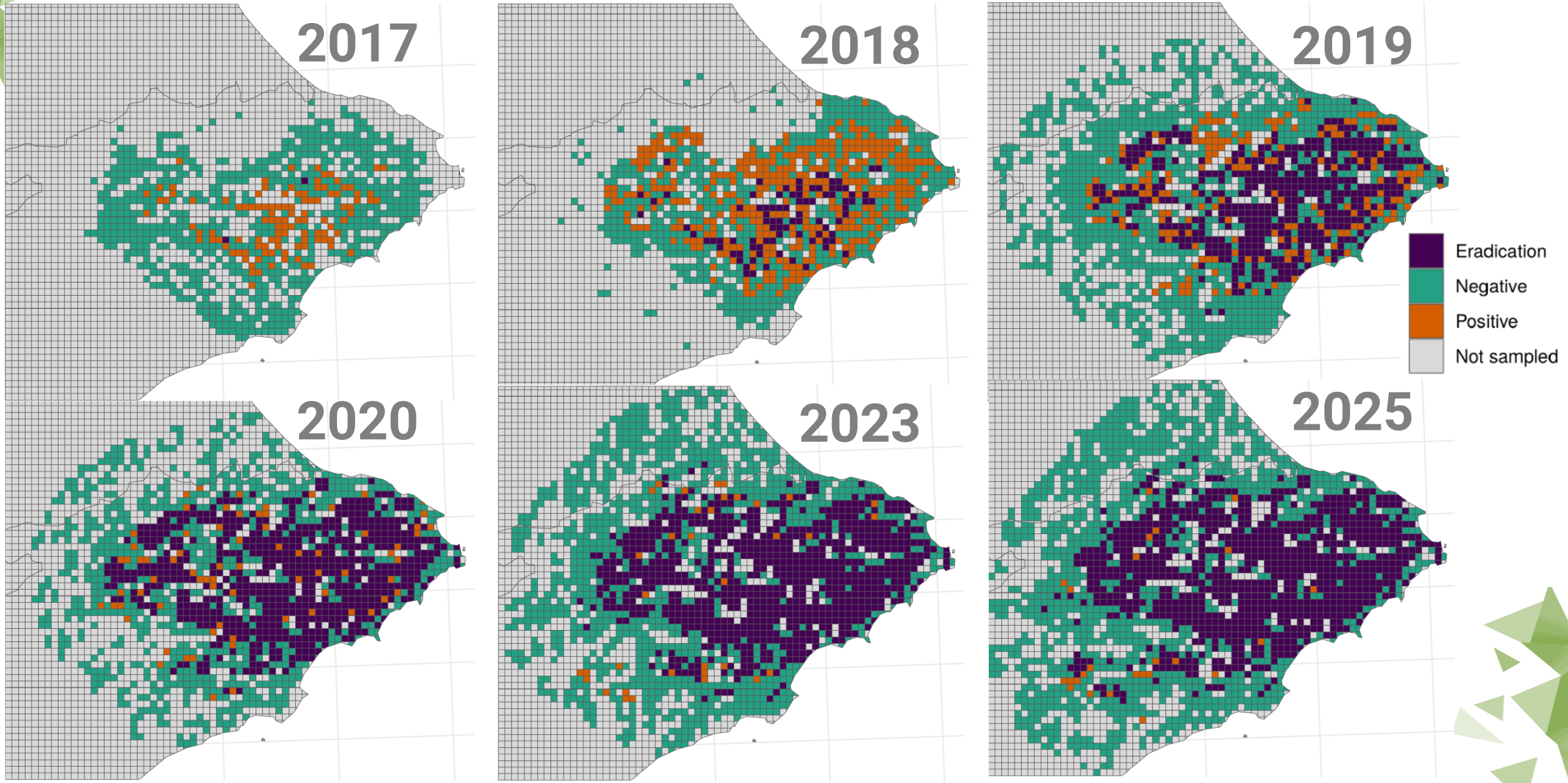


2017



2025

X. fastidiosa sampling results and eradication measures



Assays to evaluate eradication efficiency

Xylella fastidiosa detection assays in plants from eradicated forest areas

Areas with different levels of *Xf* infection incidence (levels 1–3), distributed across coastal, midland, and inland areas

Assay 1
Autumn 2020

Nine areas

Assay 2
Summer 2021

Assay 3
Autumn 2021

Four areas selected according to
Assay 1 results

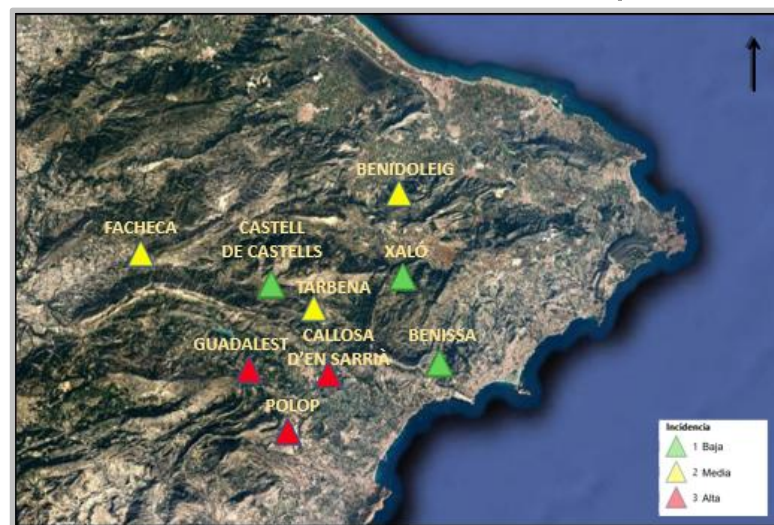
Plant material
Insect vectors

Philaenus spumarius
Neophilaenus campestris
Neophilaenus lineatus

Plant material: 10 plant species tested
+ in our DA:

- *Rhamnus alaternus*
- *Cistus sp.*
- *Calicotome spinosa*
- *Helichrysum sp*
- *Phagnalon saxatile*
- ...

Sampling was conducted in and surrounding eradicated areas, focusing on forest plant species and insect vectors.



Assays to evaluate eradication efficiency

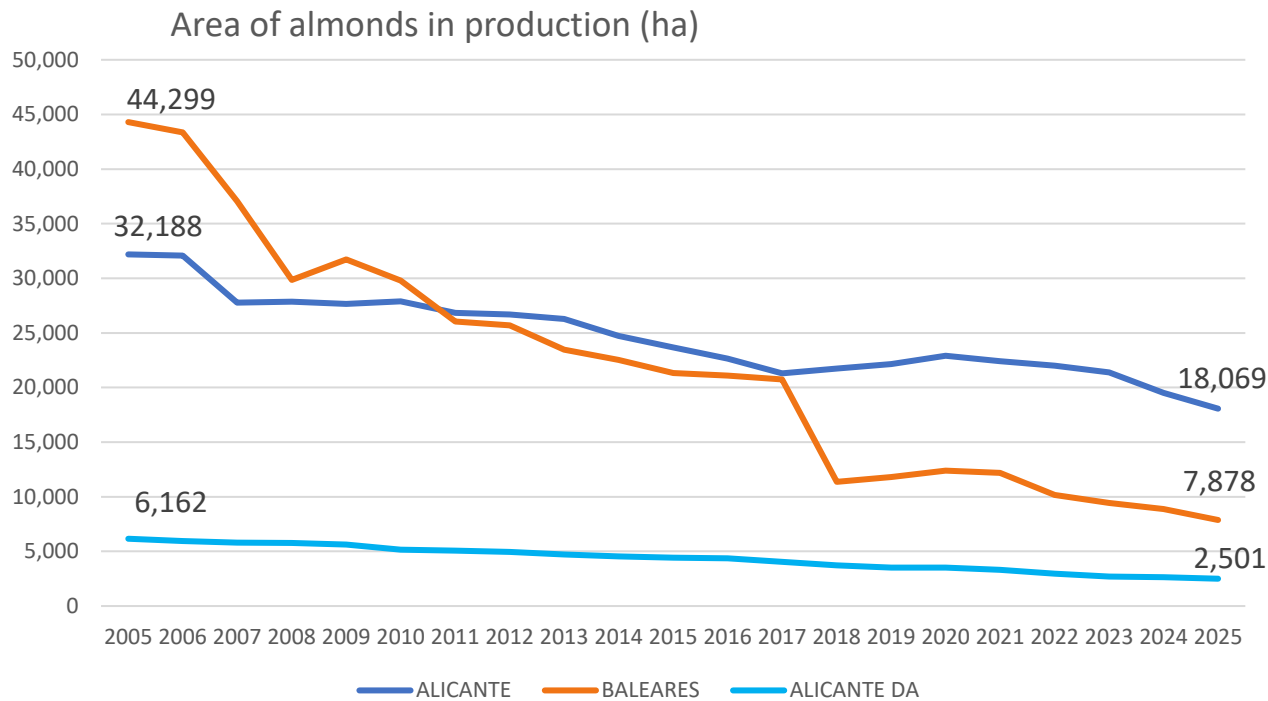
Xylella fastidiosa detection assays in plants from eradicated forest areas

Percentage of positive samples to *Xf* by qPCR

Municipality	Location	Distance from the original focus	Autumn'20		Summer'21		Autumn'21	
			Plant	Insect	Plant	Insect	Plant	Insect
Benidoleig	Midland	± 50 m	5	0	-	-	-	-
		100 – 200 m	-	-	0	0	0	0
		200 – 300 m	-	-	0	0	0	0
Castell de Castells	Inland	± 50 m	40	14	-	-	-	-
		100 – 200 m	-	-	6	8	16	0
		200 – 300 m	-	-	9	8	16	0
Callosa	Midland	± 50 m	25	17	-	-	-	-
		100 – 200 m	-	-	8	0	4	0
		200 – 300 m	-	-	0	0	0	0
Tárkena	Inland	± 50 m	80	33	-	-	-	-
		100 – 200 m	-	-	13	0	30	0
		200 – 300 m	-	-	0	0	0	0

- In autumn 2020, qPCR-positive samples were still detected in both plants and insects, with marked differences among locations.
- A substantial decline in positivity was observed during 2021:
 - No qPCR-positive insects were detected in any municipality.
 - Positive plant samples were only occasionally detected and generally at much lower prevalence than in 2020.

Almond cultivated area in Alicante and Balearic Islands



Source: ESYRCE (MAPA) and ISAV (GVA)

Since 2005, area cultivated of almonds:

82% reduction in Balearic islands

43% reduction in Alicante province

57% reduction in the 3 most affected counties of the demarcated area of Alicante

In Alicante DA 325,000 almond trees (about 1,300 ha) have been destroyed, 32% in state of abandonment

EU funding of plant health measures

Funding of Plant Health Measures

Investing in plant health is essential to ensure sustainable and competitive agriculture, horticulture and forestry industry.

EU rules on plant health aim to protect crops, fruit, vegetables, flowers, ornamentals and forests from harmful pests and diseases (harmful organisms) by preventing their introduction or spread in the EU.

The specific objectives of the Regulation (EU) No 652/2014, related to plant health expenditures, refer to the contribution for the control and prevention of organisms harmful to plants or plant products.

Survey programmes concerning the presence of pests, emergency measures and programmes concerning the control of pests in outermost regions of the Union are co-funded through Regulation (EU) No 652/2014.

More information on:

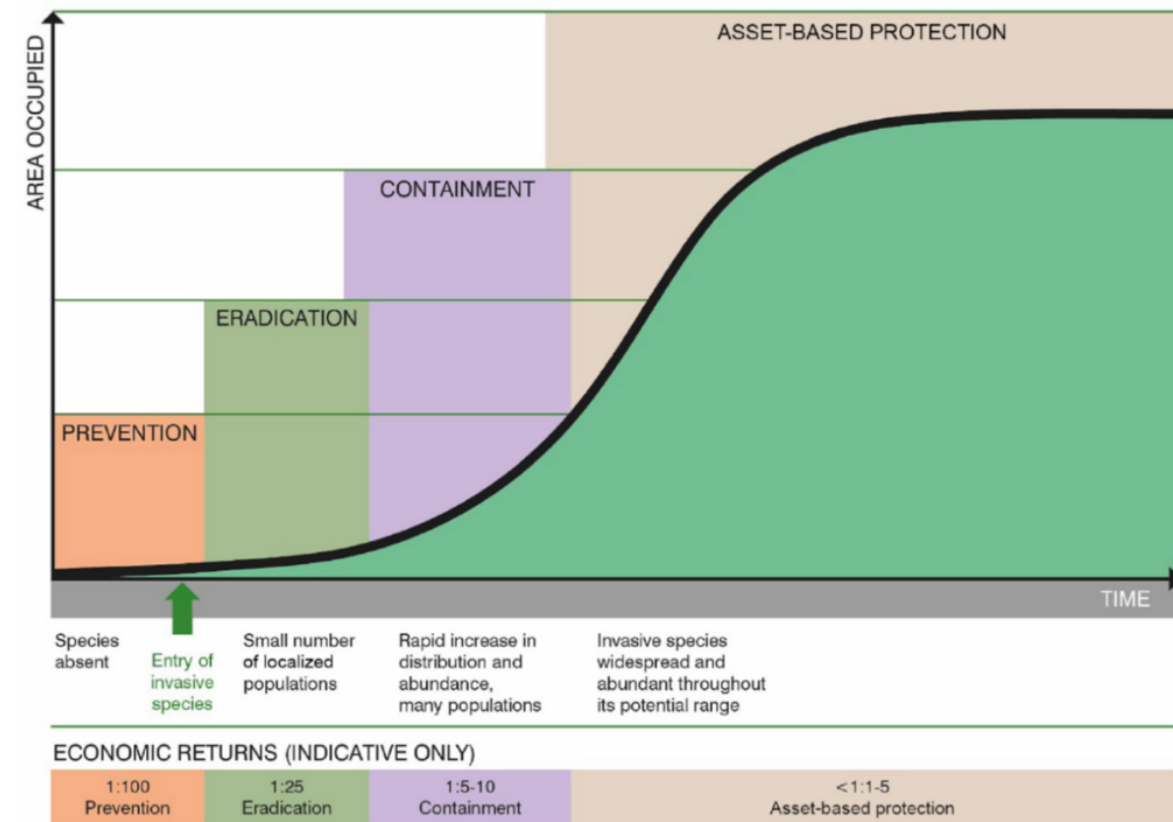
- [Survey Programmes](#)
- [Emergency Measures](#)
- [Outermost regions programmes](#)

Additional information:

- [Commission policies on plant health](#)

https://food.ec.europa.eu/horizontal-topics/funding-procurement-grants/food-chain-funding/funding-plant-health-measures_en

Investing in plant health is essential to ensure sustainable and competitive agriculture, horticulture and forestry industry.



Pest invasion curve and actions at different stages. (Source: PARM (2017)).

Impact indicator for EU priority pests

JRC TECHNICAL REPORTS

The Impact Indicator for Priority Pests (I2P2): a tool for ranking pests according to Regulation (EU) No 2016/2031

Sánchez, Berta
Barreiro-Hurle, Jesús
Soto Embodas, Iria
Rodríguez-Cerezo, Emilio

2019



EUR 29793 EN

JRC (2019) Sánchez, B; Barreiro-Hurle, J; Soto Embodas, I; Rodríguez-Cerezo, E, 29793 2019, ISBN 978-92-76-08785-4, doi:10.2760/585182, JRC116973.

Potential impact Xf:

value of production losses: **5,496 million €**

value of production losses: **7,057 million €**

But also job losses, export losses, impact on the environment...

Ranking of Union Quarantine Pests based on their potential economic, social and environmental impacts to support the identification of “priority pests”

An update of the Integrated Indication for Priority Pests (I2P2)

Schneider, K., Barreiro-Hurle, J., Vazquez-Torres, E., Di Cori, V., Rodríguez-Cerezo, E.
2025



Schneider, K., Barreiro-Hurle, J., Vazquez-Torres, E., Di Cori, V. and Rodríguez-Cerezo, E., Publications Office of the European Union, Luxembourg, 2025, <https://data.europa.eu/doi/10.2760/3350558>, JRC141239

EU funding of plant health measures

Conduct **surveys** for **400 quarantine pests** and implement **control measures** in the case of an outbreak for 27 EU MS for crops and forest



Brussels, 28.3.2023
C(2023) 2280 final
ANNEX

ANNEX
to the
COMMISSION IMPLEMENTING DECISION
amending Implementing Decision C(2022) 3467 as regards the co-financing rates of
veterinary programmes for animal diseases and zoonoses and phytosanitary
programmes for plant pests for the year 2024

'Table 2: Budget distribution per category (e.g. for a total amount of EUR 8 000 000) for the phytosanitary programmes for 2024

	Category A: Surveys in areas where the pest is not known to be present		Category B: Measures , including surveys, in the demarcated areas*	
	% of the budget	<i>Euros</i>	% of the budget	<i>Euros</i>
Priority 1: Priority pests	30%	2 400 000	45%	3 600 000
Priority 2: Pest subject to EU measures and pests present in the EU	20%	1 600 000	5%	400 000
Total	50%	4 000 000	50%	4 000 000

Phytosanitary measures for *X. fastidiosa* in Alicante

More than 57 Million € spent in 9 years (GVA, ES, EU)

Expenditures: 57.238.567,77 € (2017-2026* up to 31st may)

EU: 15.683.149,66 € (27%) (Last EU funds April 26)

Remaining: 41.555.418,11 € (73%) 50% ES and 50% GVA

A staff of up to **142 individuals** works on *Xylella* controls (surveys, labs, eradication, plant movements, administrative and legal support), deploying up to **35 teams and machines** for eradication measures



**PLAN DE CONTINGENCIA DE LA C.
VALENCIANA FRENTE A *Xylella fastidiosa***



Diciembre 2020

Phytosanitary measures for *X. fastidiosa* in Alicante

Expenditures for *Xylella fastidiosa* in 2024

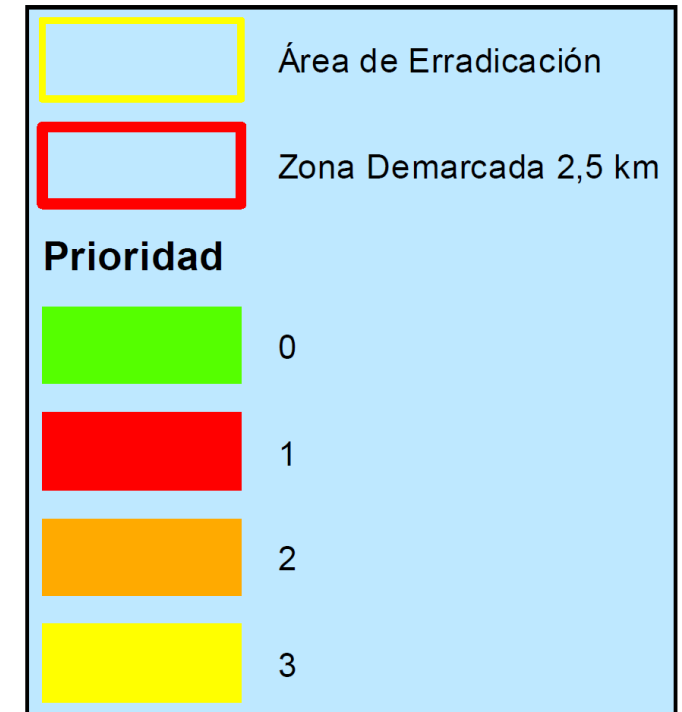
Expenditures:	7.772.292,74 €
EU eligible costs:	5.867.243,63 € (77,0%)
EU co-funding:	1.059.940,09 € € (13,6%)



PLAN DE CONTINGENCIA DE LA C.
VALENCIANA FRENTE A *Xylella fastidiosa*



Diciembre 2020

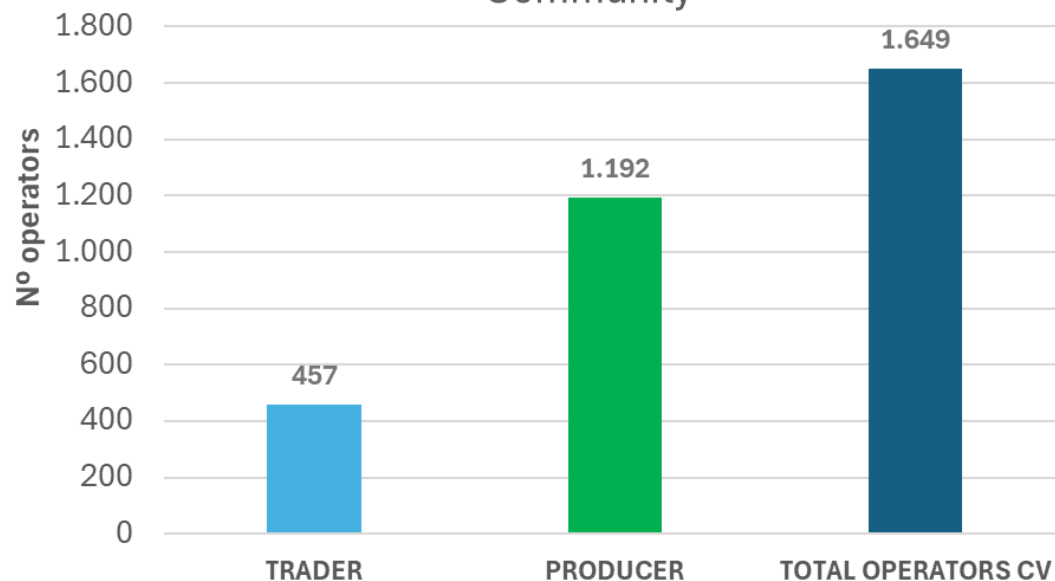


Professional operators of plants for planting

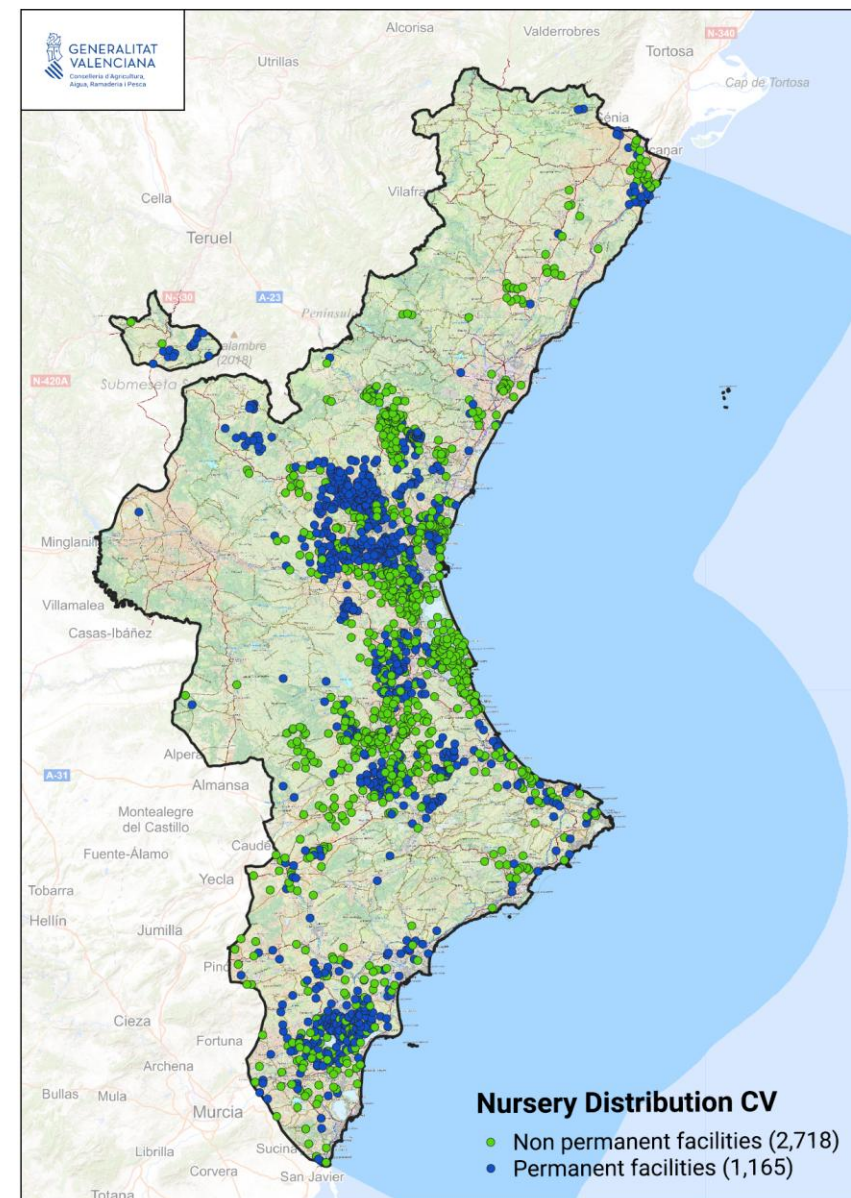
Spain has the 3rd highest production value for flowers and living plants in the EU:

EU:	24,600 million €
Spain:	4,188 million € (17%)
C. Valenciana:	684 million € (16%), main region for living plants

Professional Operators of Plants registered in Valencian Community



Source: SSV-GVA



Restrictions for Plant Propagation Material movement



Strong restrictions for the movement out of a demarcated area for PPM of **specified plants**:

- Site of production physically protected
- Phytosanitary treatments
- Intense molecular tests before movement
- PPM produced In vitro
- Thermotherapy treated

Xylella fastidiosa subsp. *multiplex*, has the highest impact (higher number of specified plants) for movement restrictions

Source: Adapted from annex II Regulation 2020/1201 and EPPO Global Database

Restrictions for Plant Propagation Material movement

Royaume du Maroc

Office National de Sécurité Sanitaire
des Produits Alimentaires



المملكة المغربية
المكتب الوطني للسلامة الصحية
للمنتجات الغذائية

2- Cas des pays où *X. fastidiosa* est présente :

A- Matériel végétal fruitier destiné à la plantation

Le matériel végétal fruitier destiné à la plantation originaire d'un pays infecté par *X. fastidiosa* peut être importé au Maroc si toutes les conditions suivantes sont remplies :

- la zone de production est indemne de *X. fastidiosa* ;
- l'ONPV du pays exportateur communique au préalable par écrit à l'ONSSA la liste des zones indemnes de *X. fastidiosa* selon les normes internationales des mesures phytosanitaires et la liste des pépinières enregistrées pour l'exportation vers le Maroc ;
- le matériel végétal objet de l'envoi est accompagné d'un certificat phytosanitaire, indiquant sous la rubrique «Déclaration supplémentaire» que :
 - le matériel végétal est produit dans une pépinière contrôlée par l'ONPV et située dans une zone indemne de *X. fastidiosa* selon les normes internationales des mesures phytosanitaires ;
 - le matériel végétal a été analysé officiellement au laboratoire et trouvé indemne de *X. fastidiosa* ;
 - le matériel végétal a été inspecté et trouvé indemne des vecteurs de la bactérie *X. fastidiosa* ;
 - le matériel végétal a été traité par un insecticide à large spectre d'action juste avant son exportation au Maroc.

Autorisation technique d'importation

Importation autorisée []

Importation refusée [X]

28 JAN 2021

N° de l'autorisation : 28 JAN 2021

Motif du refus : La pépinière de production des plants destinée à être utilisée dans une région (Valencia) infectée par la bactérie *Xylella fastidiosa*.

Date/Cachet et signature du Chef de Service
Chef du service du contrôle et de la protection des végétaux d'EL Hajeh (PO)
YAHYA Saâd

SOCIETA' VITICOLA ITALIANA
RC: 139791 - IF: 37629347
TP: 25103492
ICE: 002175955000078

Direction Régionale F&S - Malaga

* Cette ATI n'est valide que jusqu'au 31 Mars 2020.

* La validité de cette ATI est subordonnée au respect des exigences mentionnées en annexe 3.1-joint

Third countries are imposing pest-free areas much larger than the official ones without scientific basis



Vitis sp, not specified plant for *X.f. subsp multiplex*
Thermotherapy available but not authorized as alternative



ivia
Institut Valencià
d'Investigacions Agràries





Evolution and consequences of nine years of application of phytosanitary measures to control *Xylella fastidiosa* subsp. *multiplex* outbreak in Alicante

5th European Conference on *Xylella fastidiosa*
Bari, 24/06/2026

Vicente DALMAU SORLÍ
dalmau_vic@gva.es

Servicio de Sanidad Vegetal de la Generalitat Valenciana, SPAIN



Integrated Surveillance and Phytosanitary Measures against *Xylella fastidiosa* **subsp. fastidiosa ST1**

Ragone G., Zaza C., Cantatore M., Palmisano F., Percoco A., Infantino S.
Regional Plant Health Service, Puglia Region (IT)

XYLELLA EMERGENCY

25.000 ha

Table grape production in Apulia

60%

Italian national production

€400M

Annual value

The detection of *Xylella fastidiosa* subsp. *fastidiosa* **ST1** raised immediate concerns for the economic stability of the regional agricultural sector.



REGULATORY FRAMEWORK

Regulation (EU) 2016/2031

Regulation (EU) 2020/1201

Decree 22A01653/2022

D.G.R. n. 1075/2025

EFSA, 2019; EFSA, 2023; EFSA, 2025



EARLY DETECTION 2023

190

MONITORING SITES (2023)
Xylella fastidiosa *pauca* ST53

2.667

SPITTLEBUGS ANALYSED

13

POSITIVE VECTORS (*P. spumarius*)

Xylella fastidiosa was first detected in PEST-FREE AREA in insect vectors, not in plants.



DELIMITING SURVEY

BEGINNING - 2024

432 PLANT SAMPLES

Artemisia spp (2)

Asparagus acutifolius (3)

Olea europea (397)

Laurus nobilis (1)

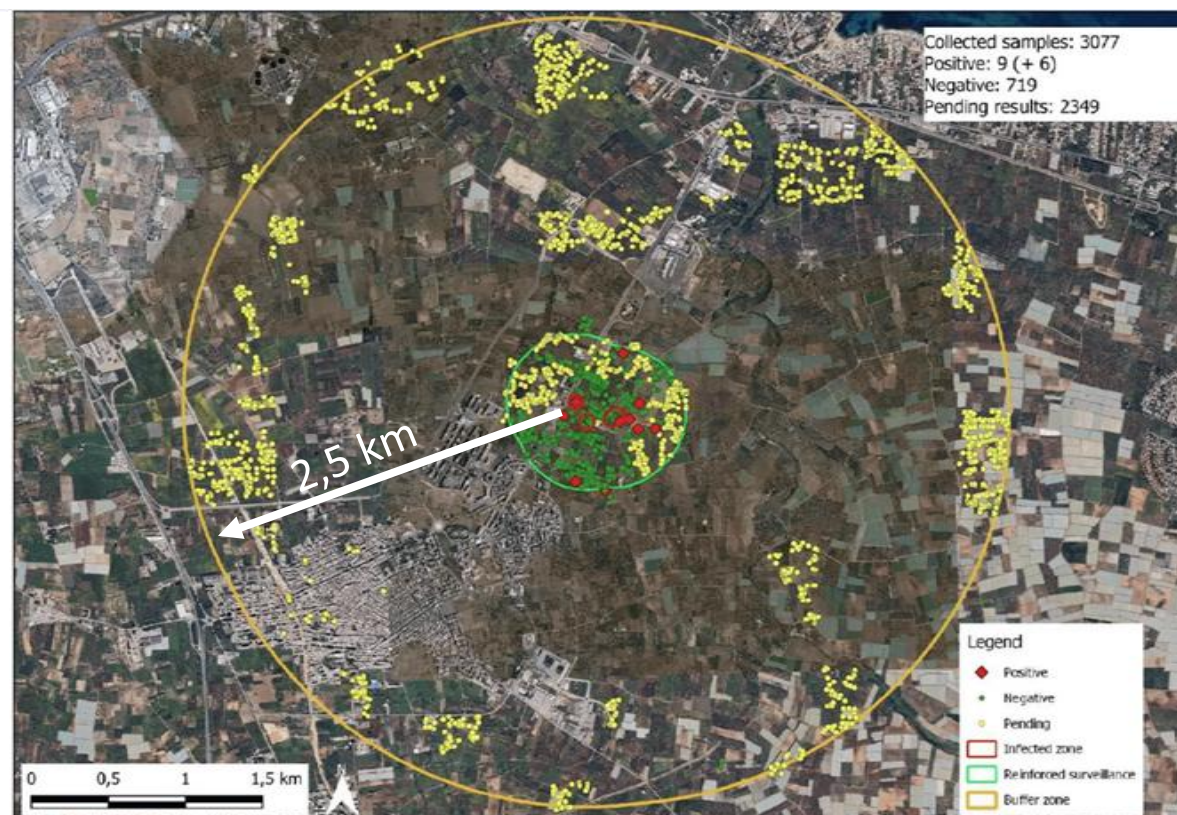
Prunus avium (3)

Prunus dulcis (20)

Prunus spp (4)

Rubus spp (1)

Salvia rosmarinus (1)



Molecular characterization of plant isolates confirmed that the detected strain belong to ***X. fastidiosa fastidiosa* ST1**

DELIMITING SURVEY

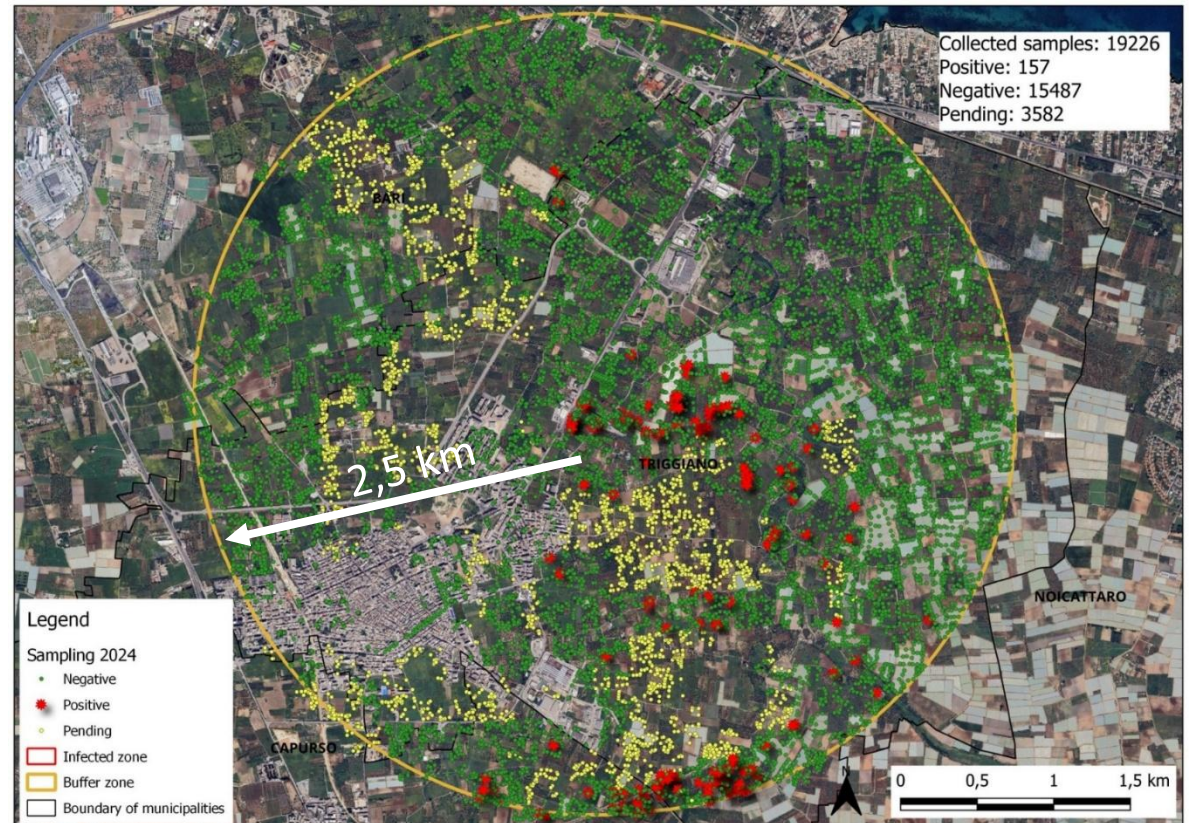
2024

SAMPLING STRATEGY

In demarcated area (2,5 km buffer) **all hectares** were sampled

SAMPLING UNIT

Each single ha in the buffer zone was surveyed
1 pool (ha) = 4-7 samples



DELIMITING SURVEY

2024

44.100

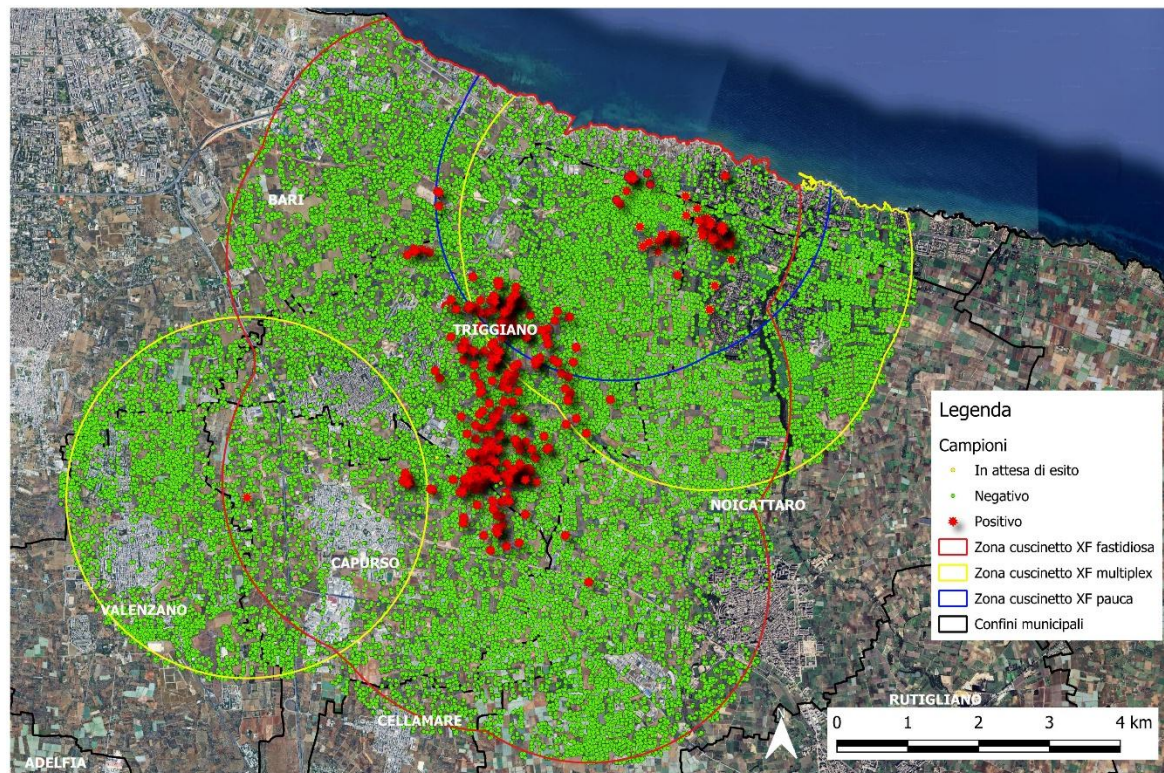
SAMPLES COLLECTED

43.694

NEGATIVE PLANTS

406

POSITIVE PLANTS



DELIMITING SURVEY

2024

339

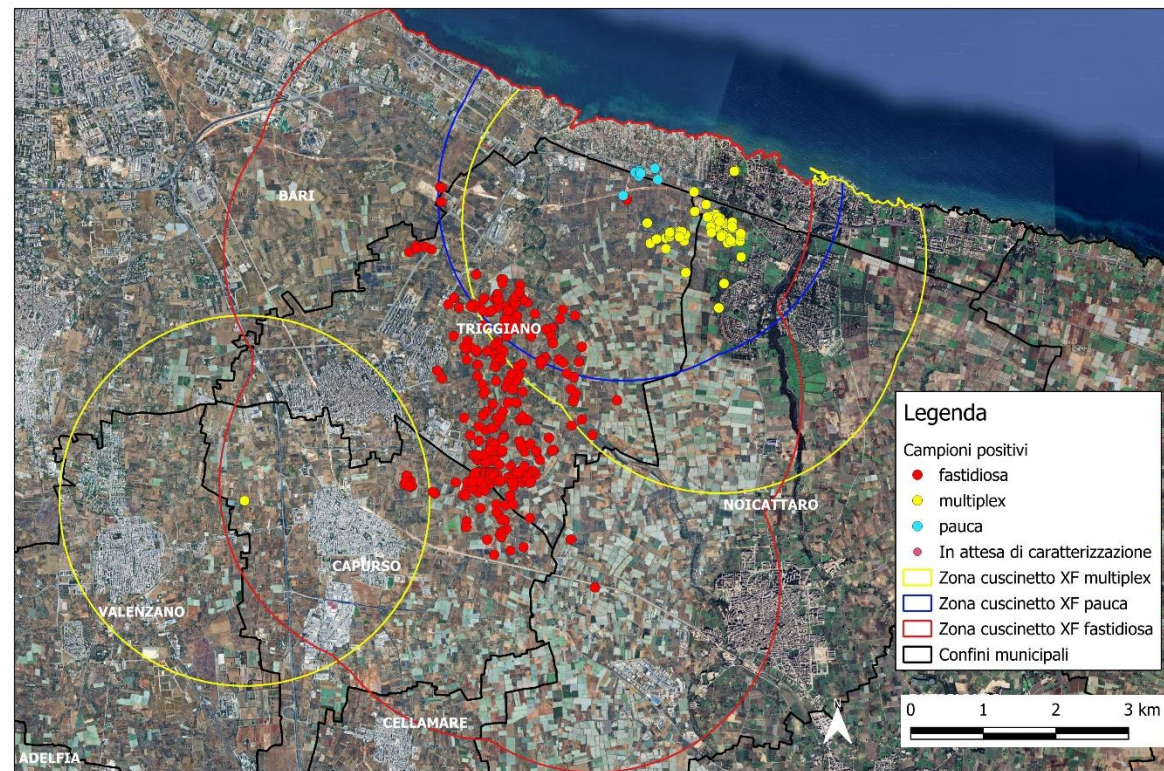
X. fastidiosa fastidiosa ST1

58

X. fastidiosa multiplex ST26

9

X. fastidiosa pauca ST53



MONITORING SURVEY XFF

2025

61

POSITIVE PLANTS

20

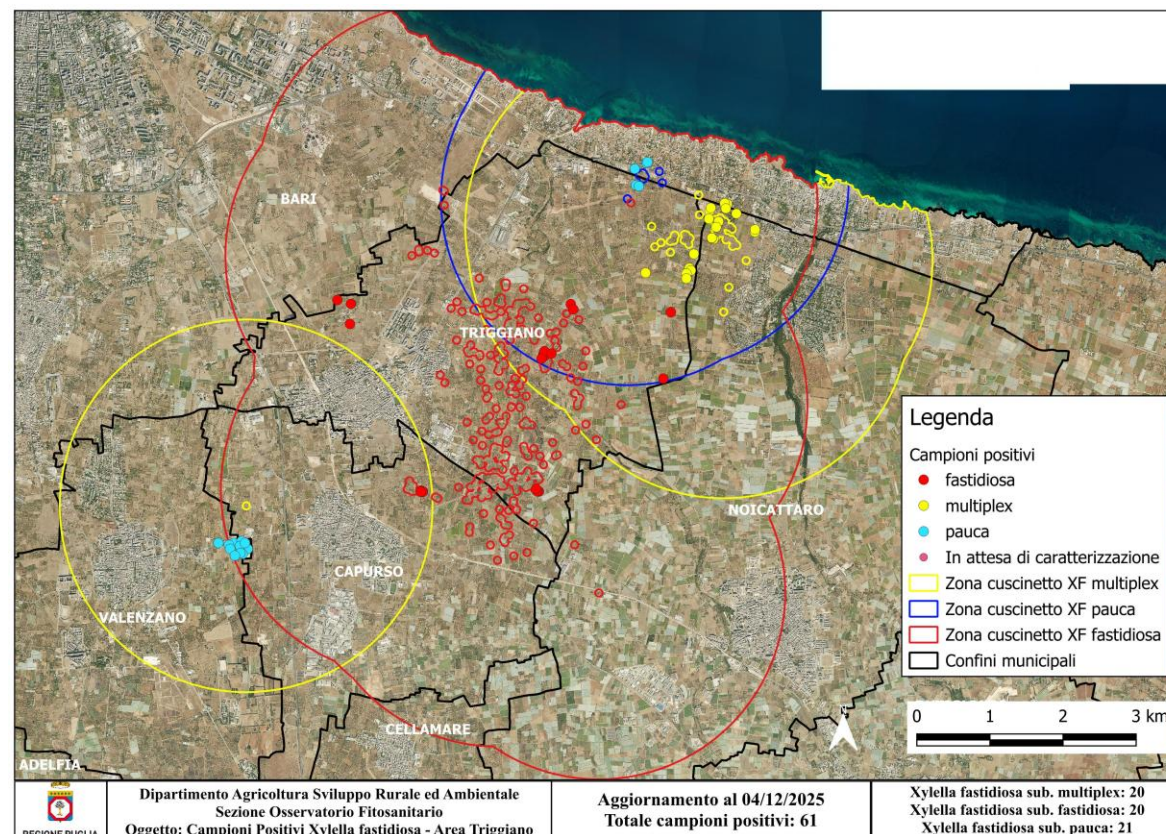
X. fastidiosa fastidiosa ST1

20

X. fastidiosa multiplex ST26

21

X. fastidiosa pauca ST53



MONITORING SURVEY XFF

2026

22

POSITIVE PLANTS

13

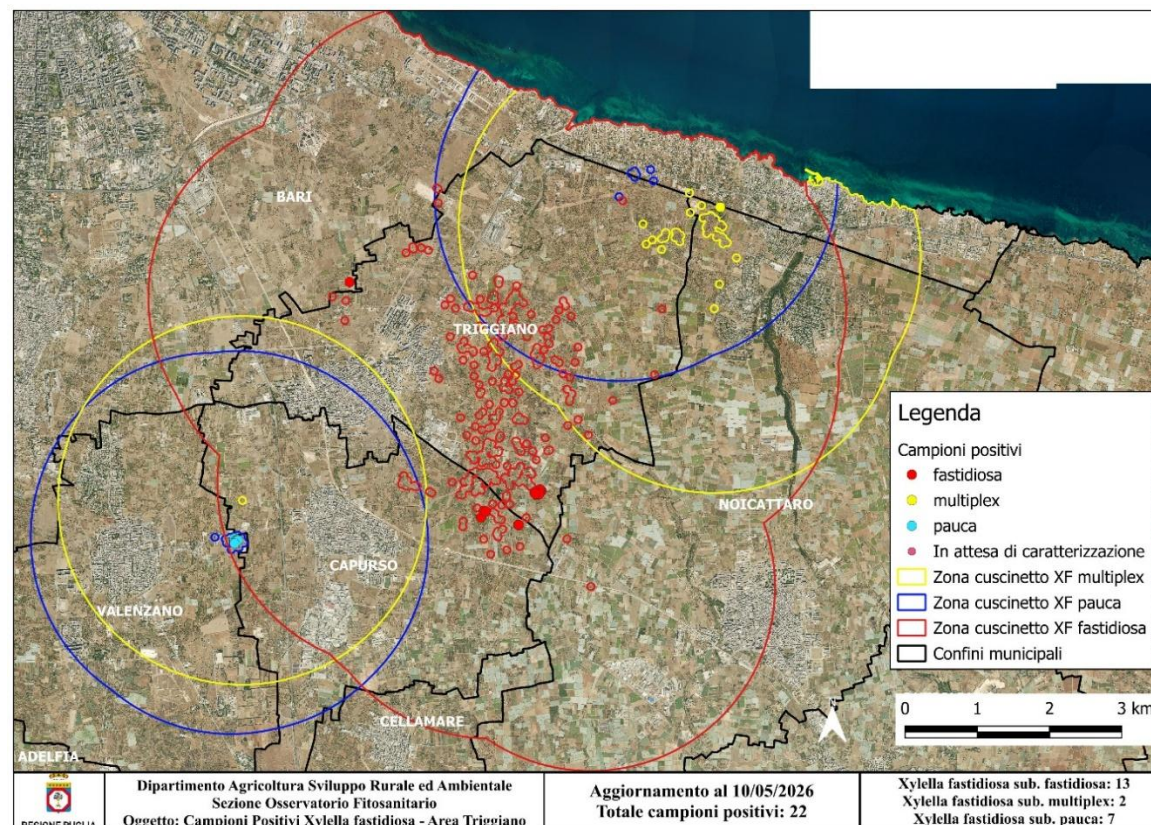
X. fastidiosa fastidiosa ST1

2

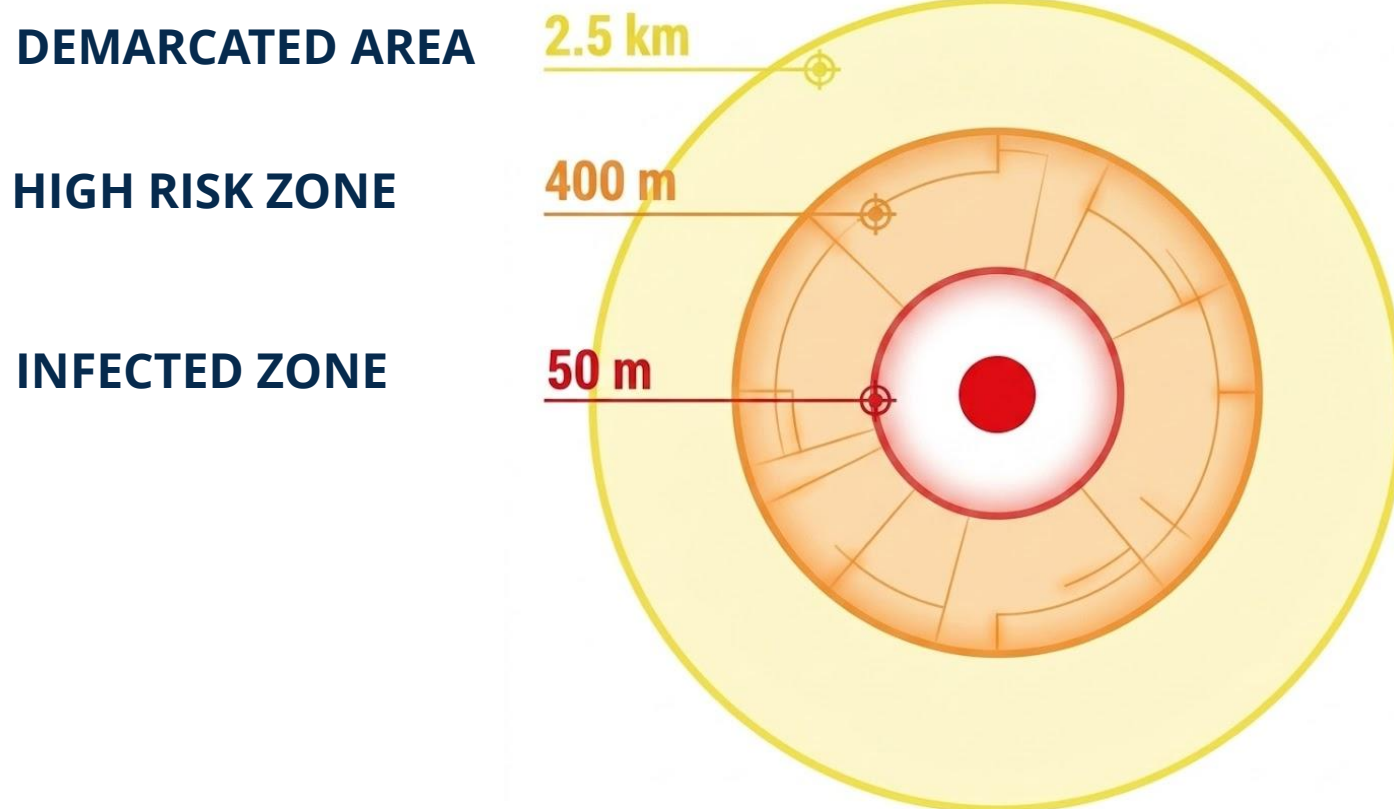
X. fastidiosa multiplex ST26

7

X. fastidiosa pauca ST53



ERADICATION MEASURES



⊗ **MANDATORY ERADICATION**

Immediate removal of infected plants and all host plants within a 50 m radius.

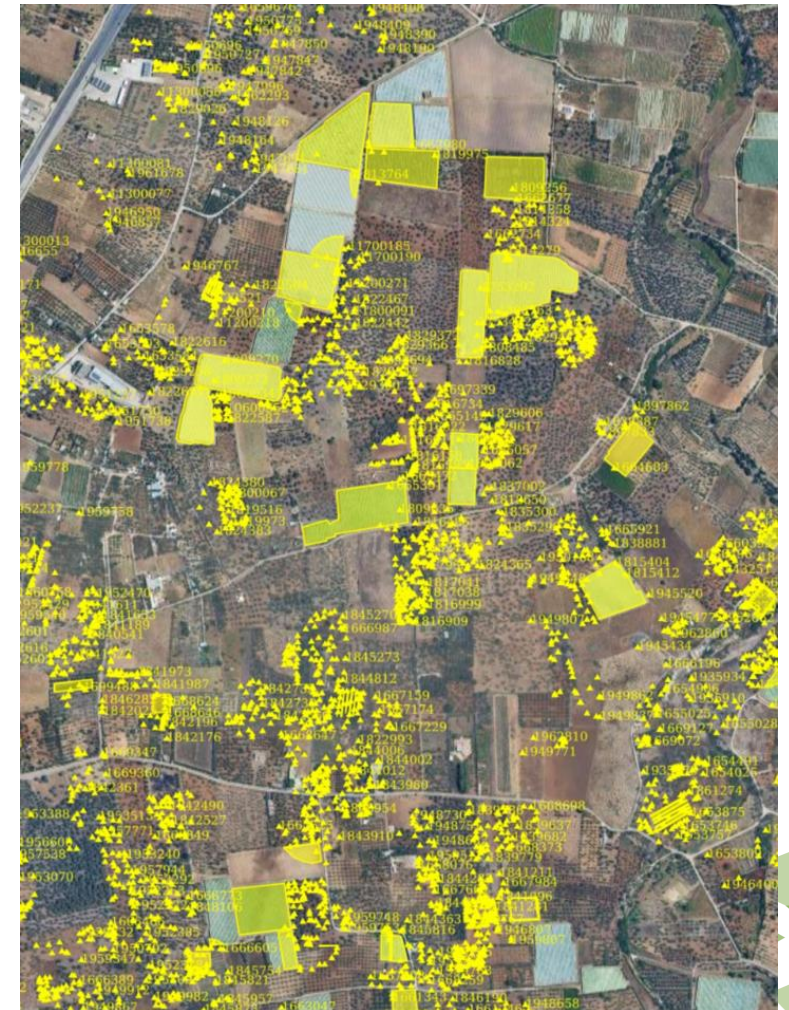
⚠ **SUPPLEMENTARY MEASURE**

Removal of marginal or abandoned almond trees within 400 m to reduce local inoculum pressure and limit spread.

📄 **VOLUNTARY EXTENSION**

Farmers may voluntarily extend eradication to vineyard plantings within a maximum radius of 400 m.

ERADICATION MEASURES



ERADICATION MEASURES



SOCIO-ECONOMIC MITIGATION

Economic Framework (DGR n. 903/2026):
Compensation for "loss of income" calculated
as **gross production value - production costs**.

 Table grape	€ 58.174 / ha
 Cherry	€ 22.438 / ha
 Almond	€ 10.323 / ha

Uprooting costs: €3,000/ha for vineyards. 

GRAPE VINE

Crop	Compensation for damage (€/ha)	Compensation for plant removal (€/ha)
Table grape vine	58.174	3.000
Common wine grape vine	30.638	3.000
Quality wine grape vine	34.319	3.000

Crop	Compensation for cost (€/ha)	Compensation for plant removal (€/ha)
Vineyard established with non-grafted rootstock/cuttings	32.394,00	1.000

OLIVE TREE

Crop	Compensation for damage (€/plant)	Compensation for plant removal (€/plant)
Olive tree > 200 plants/ha	98,00	130,5
Olive tree between 101 and 200 plants/ha	121,00	145
Olive tree <= 100 plants/ha	146,00	166,75

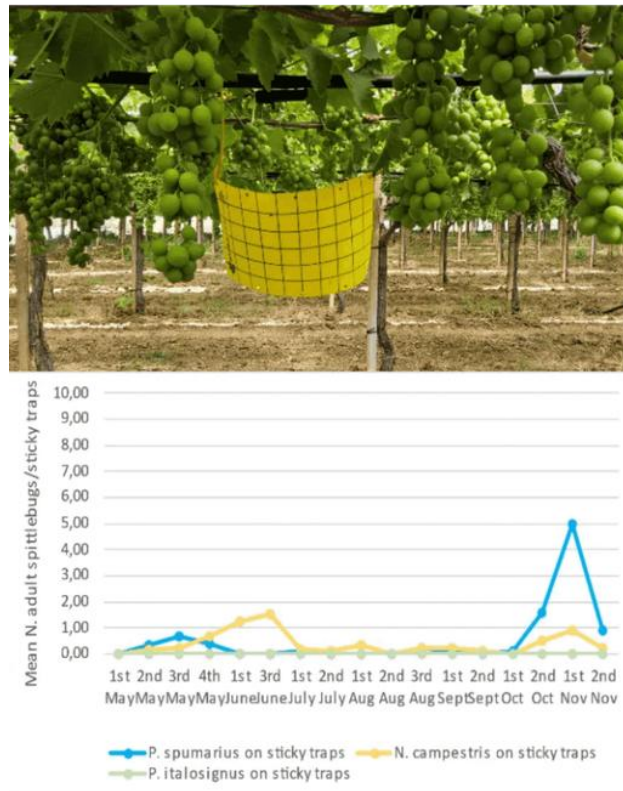
CHERRY TREE

Crop	Compensation for damage (€/ha)	Compensation for plant removal (€/plant)
Cherry tree	22.438,00	79.75

ALMOND TREE

Crop	Compensation for damage (€/ha)	Compensation for plant removal (€/plant)
Almond tree	10.323,00	69.6

VECTORS MONITORING AND PHYTOSANITARY MEASURES



MANDATORY PRACTICES:

- Tillage and weed management for juvenile control
- Insecticide operations for adult control



PROTECTION OF NURSERIES AND PROPAGATION MATERIAL

Zero Positive Detections

- Out of **>11,000 propagation** plants systematically tested in officially authorized fields and nurseries.
- Intensive monitoring program in **the grapevine nursery** sector.
- **Movement restrictions** to ensure the health of the trade sector.



CONCLUSIONS

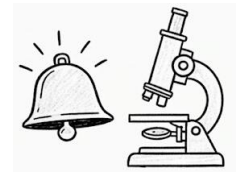
> 50.000 Tests

Spatial stability - outbreak (8 km²)



Early Warning

Vector surveillance



Mandatory practices

30 ha removed



Propagation material

Certification system



INTEGRATED METHODOLOGY TO PROTECT EUROPEAN VITICULTURE



THANK YOU!

Gianvito Ragone PhD
E-mail: g.ragone@regionepuglia.it

INSTITUTO DE
AGRICULTURA
SOSTENIBILE



Xylella *fastidiosa*



5th European conference

A HYPERSPECTRAL PHENOTYPING PLATFORM FOR EARLY DETECTION OF *XYLELLA FASTIDIOSA* INFECTION IN WOODY HOSTS

Egea-Cobrero V., Calderón R., Jiménez-Berni JA., Zarco-Tejada PJ.,
Román-Écija M., León-Ropero G., Hornero A., Navas-Cortés JA., Landa BB.





BACKGROUND

Xylella fastidiosa (*Xf*) detection is challenging due to asymptomatic infections, long incubation periods and non-specific symptoms, allowing infected plants to spread the pathogen before visible symptoms appear.

High-resolution hyperspectral imaging have demonstrated their ability to determine physiological and biochemical traits of plants and their responses to pathogens.

OBJECTIVES

- To develop a phenotyping platform to obtain plant spectral information in the visible and near infrared range (VNIR 400-1000 nm).
 - To analyze the spectral signatures of woody hosts non-infected and infected with *Xf* in pathogenicity experiments under controlled conditions.
 - Identify vegetation traits as physiological, pigments or structural indicators associated with *Xf* infection before the development of symptoms.
- 



METHODOLOGY



METHODOLOGY

01

Platform development and plant preparation

02

Hyperspectral image acquisition

03

Image preprocessing

04

Vegetation spectral feature extraction

05

Vegetation indices screening and selection

06

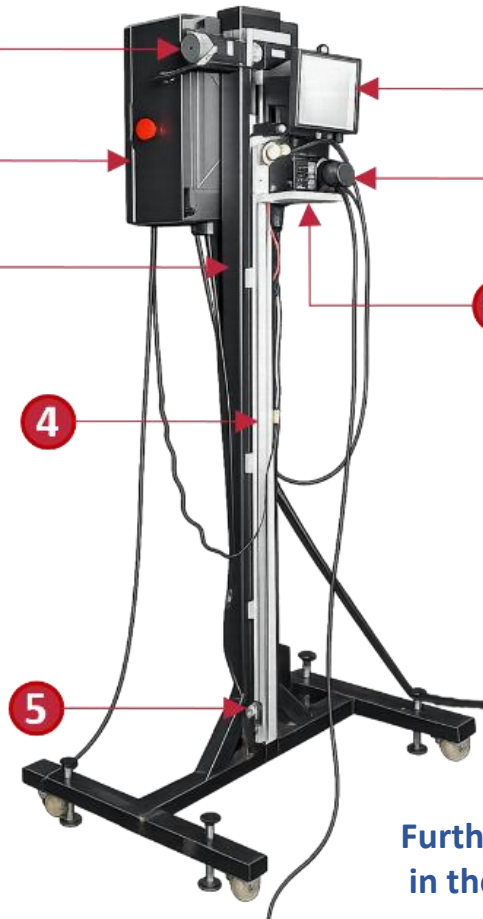
Disease classification machine learning models

07

Ensemble-based disease detection

01

CURIOUS?
SCAN TO SEE
IT IN ACTION!



- 1 Motorised linear axis module
- 2 Control and electronics box
- 3 Mobile support structure base
- 4 Vertical linear stage
- 5 Proximity and limit sensor
- 6 Halogen projector
- 7 Hyperspectral imaging sensor
- 8 Custom sensor L-bracket

02

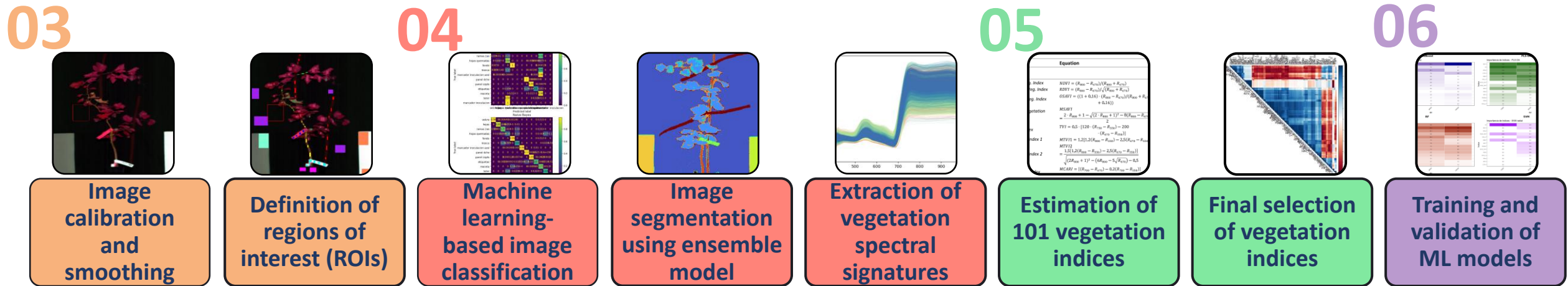
Host	Cultivars	Xf strains	Images per time	Time from inoculation (days)
Almond <i>Prunus dulcis</i>	1	1	48	60, 120 and 180
Grapevine <i>Vitis vinifera</i>	2	1	256	60 and 120
Olive <i>Olea europaea</i>	5	3	192	15, 90 and 180



MORE INFO

Further information is available in a manuscript
in the journal *Phytopathologia Mediterranea* (under review)

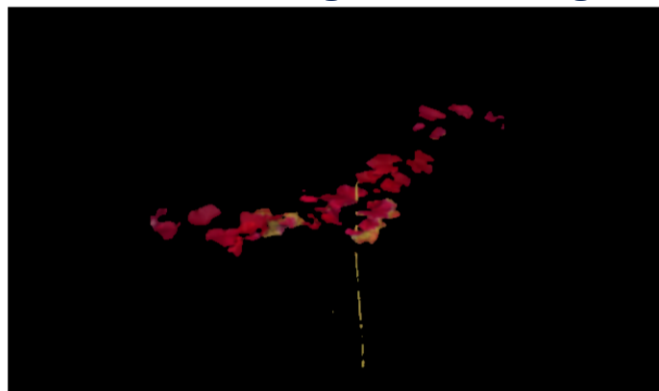
METHODOLOGY



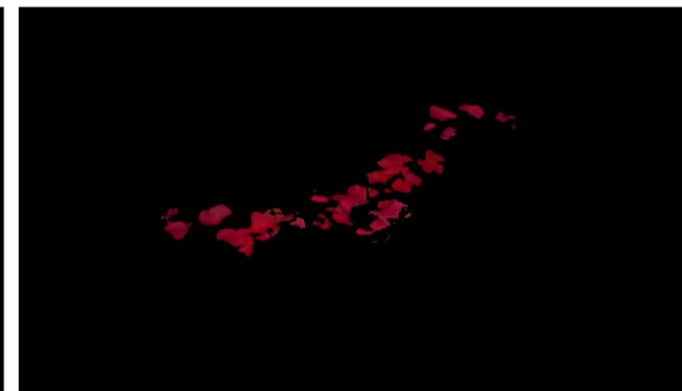
Calibrated image



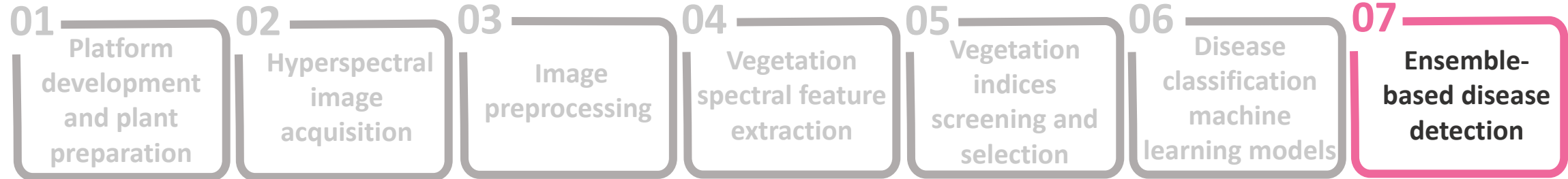
Classified vegetation image



Ensembled image



RESULTS



Random forest

PLSDA

XgBoost

Support vector machine

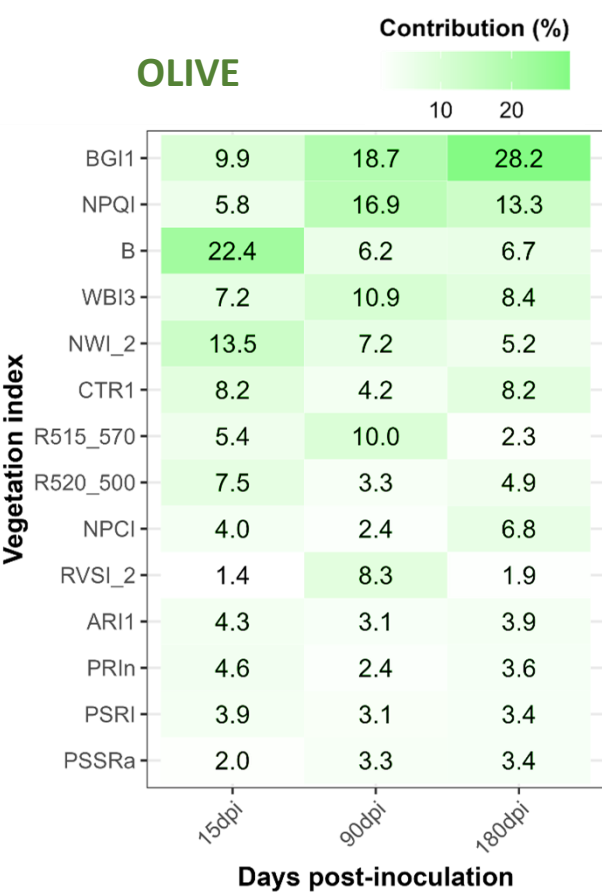
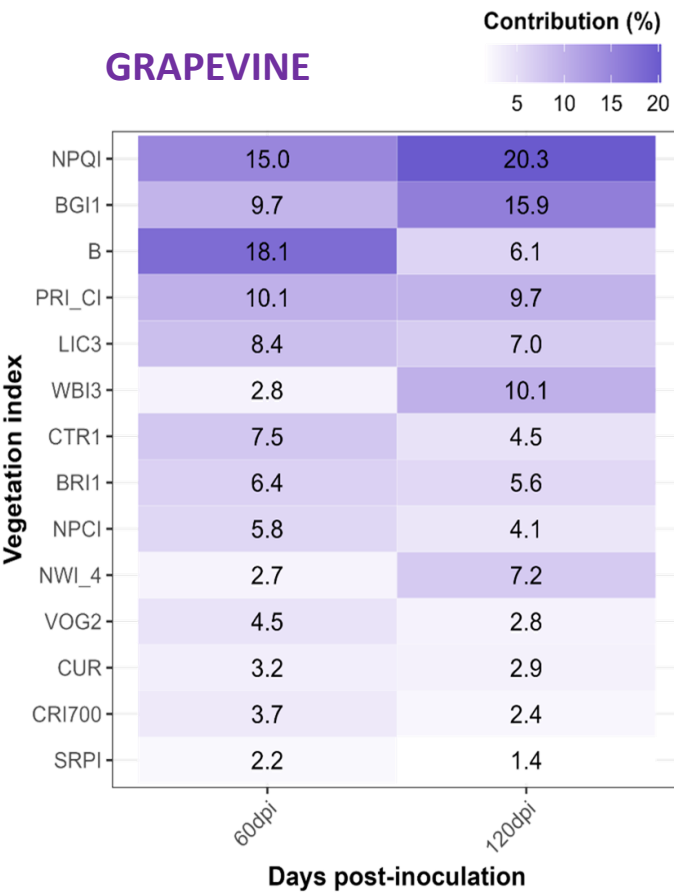
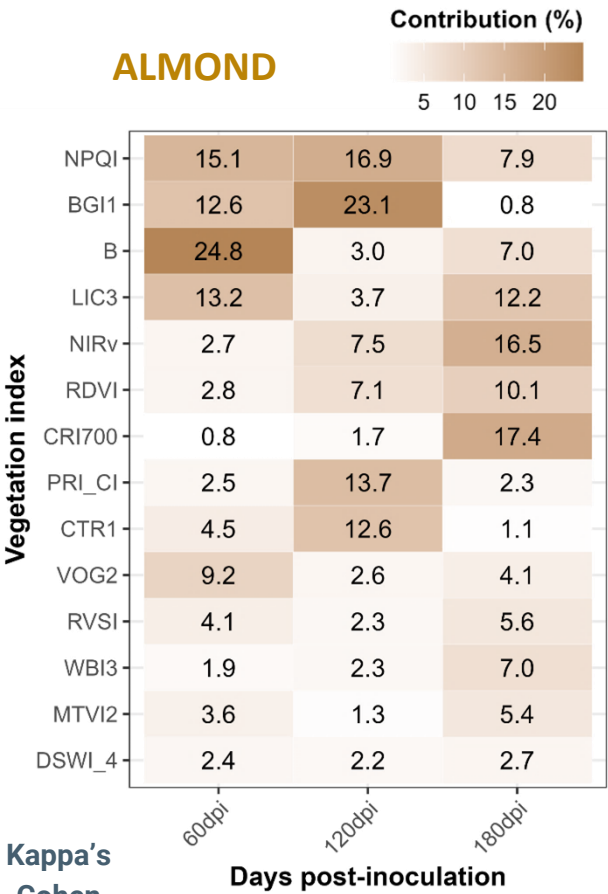
Woody host (plants per time)	Time (days post-inoculation)	Balanced accuracy	Kappa's Cohen
Almond 48 plants	60	0.79 ± 0.080	0.60 ± 0.178
	120	0.67 ± 0.118	0.36 ± 0.253
	180	0.68 ± 0.208	0.33 ± 0.411
Grapevine 256 plants	60	0.61 ± 0.085	0.21 ± 0.170
	120	0.73 ± 0.028	0.47 ± 0.056
Olive 192 plants	15	0.79 ± 0.034	0.51 ± 0.082
	90	0.85 ± 0.040	0.64 ± 0.126
	180	0.88 ± 0.039	0.71 ± 0.065



RESULTS

07

Ensemble-
based disease
detection



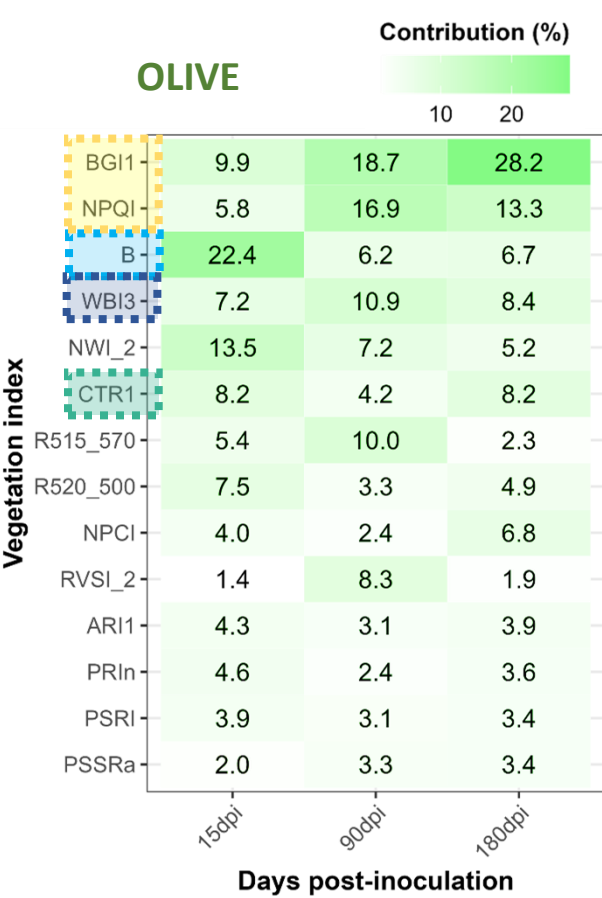
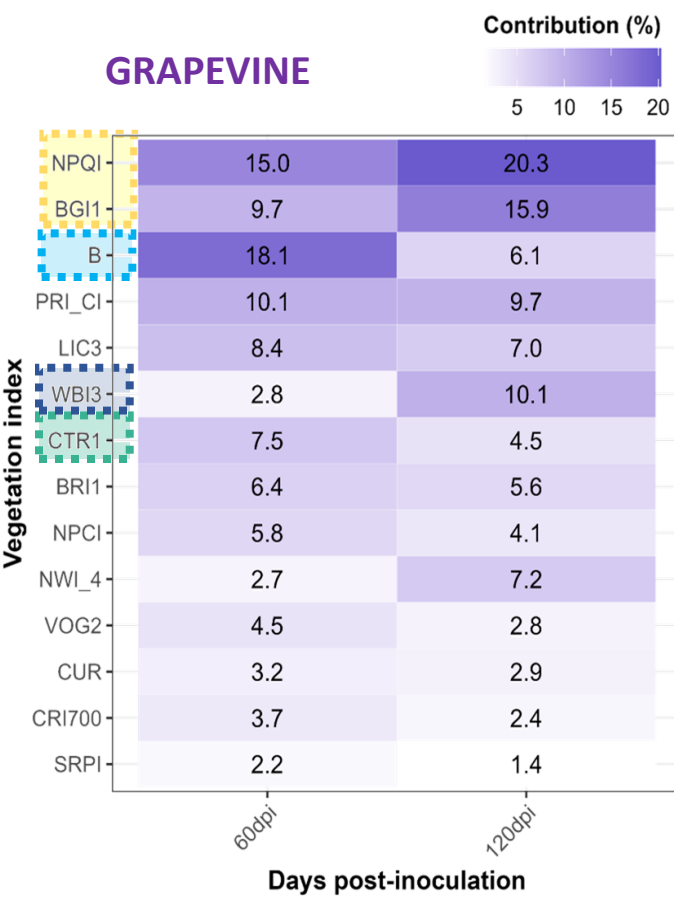
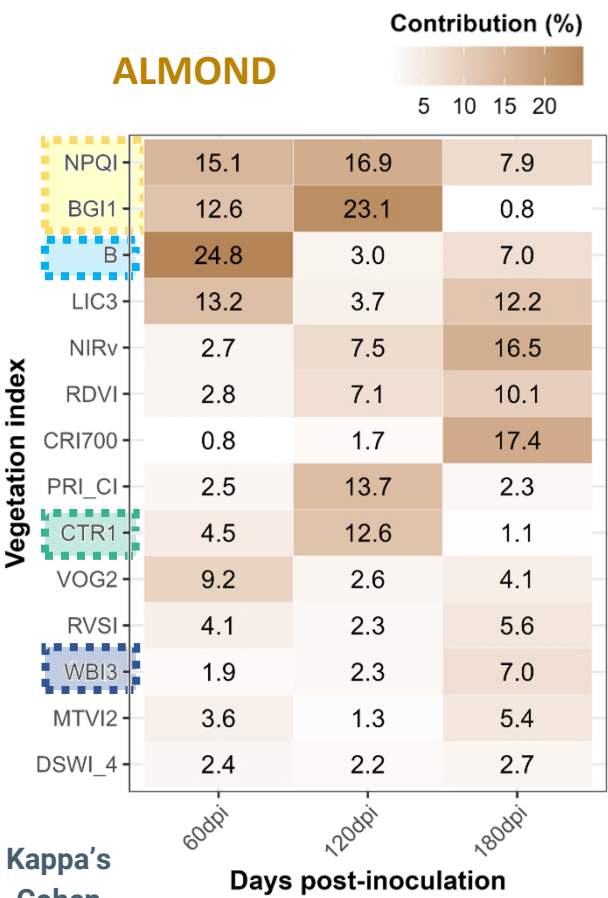
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RESULTS

07

Ensemble-
based disease
detection

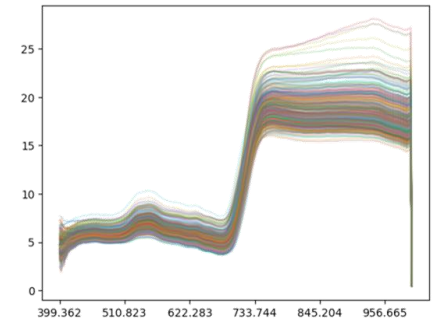
B
BGI1
NPQI
CTR1
WBI3



Woody host (plants per time)	Time (days post- inoculation)	Balanced accuracy	Kappa's Cohen
Almond 48 plants	60	0.79 ± 0,080	0.60 ± 0.178
	120	0.67 ± 0.118	0.36 ± 0.253
	180	0.68 ± 0.208	0.33 ± 0.411
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CONCLUSIONS

- ▶ A **hyperspectral phenotyping platform** has been successfully developed for imaging woody potted plants under controlled conditions.
- ▶ A robust **image-processing workflow** was established to accurately extract vegetation pixels from images of woody plants.
- ▶ Reliable **discrimination between *Xylella fastidiosa*-infected and non-infected plants** across species was achieved using ensemble machine-learning models.
- ▶ **Species-specific spectral responses** were also observed, with distinct vegetation indices contributing to disease discrimination in almond, grapevine and olive.
- ▶ Several **vegetation indices** were identified as consistent **predictors of infection**, particularly **BGI1, NPQI, B, WBI3** and **CTR1**, which highlights the importance of traits related to pigments and water for disease detection.





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A HYPERSPECTRAL PHENOTYPING PLATFORM FOR EARLY DETECTION OF *XYLELLA FASTIDIOSA* INFECTION IN WOODY HOSTS

Egea-Cabrero V.¹, Calderón R.¹, Jiménez-Berni JA.¹, Zarco-Tejada PJ.¹, Román-Écija M.¹, León-Ropero G.¹, Hornero A.¹, Navas-Cortés JA.¹, Landa BB.¹

¹ Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Córdoba, Spain. ✉ vegea@ias.csic.es



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Xylella fastidiosa (Xf) detection is hindered by asymptomatic infections, long incubation periods and non-specific symptoms, allowing infected plants to spread the pathogen before visible symptoms appear.

High-resolution hyperspectral imaging have demonstrated their ability to quantify physiological and biochemical traits of plants and their responses to pathogens.

OBJECTIVES

- To develop a phenotyping platform to acquire plant spectral information in the visible and near infrared range (VNIR 400-1000 nm).
- To analyze the spectral signatures of woody hosts inoculated and non-inoculated with Xf in pathogenicity experiments under controlled conditions.
- To identify vegetation traits as physiological or structural indicators associated with Xf infection before the development of symptoms.

METHODOLOGY

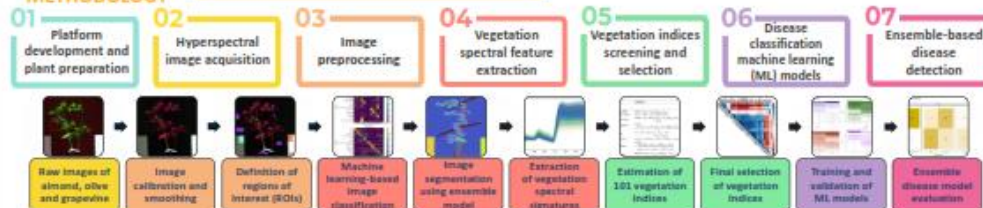


Figure 3. Workflow for processing the hyperspectral imagery generated by the phenotyping platform.

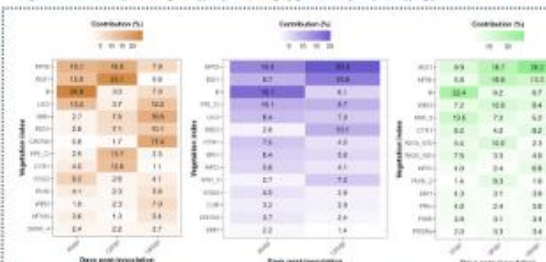


Figure 4. Relative importance of vegetation indices contributing to the discrimination between non-inoculated and *Xylella fastidiosa*-infected woody hosts (almond, grapevine and olive) across sampling times post-inoculation under controlled conditions.

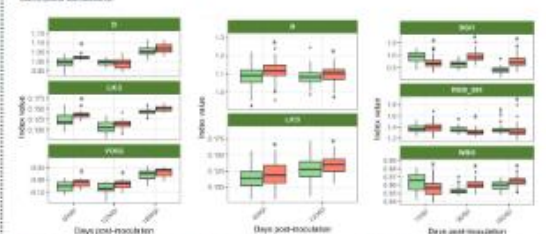


Figure 5. Temporal dynamics of the physiological significant vegetation indices identified by the ensemble model as the most informative for discriminating non-inoculated and *Xylella fastidiosa*-infected woody hosts (almond, grapevine and olive).

RESULTS

Table 1. Classification performance metrics of the ensemble models for the detection of *Xylella fastidiosa* infection in woody hosts at different times (days post-inoculation) under controlled conditions using hyperspectral phenotyping platform.

Woody host (plants per time)	Time (days post-inoculation)	Balanced accuracy	Kappa's Cohen	Sensitivity	Specificity	ROC AUC
Almond	60	0.79 ± 0.080	0.60 ± 0.178	0.68	0.70	0.85 ± 0.114
	48 plants	0.67 ± 0.118	0.36 ± 0.253	0.68	0.66	0.82 ± 0.176
Grapevine	180	0.68 ± 0.208	0.33 ± 0.411	0.70	0.67	0.80 ± 0.212
	258 plants	0.41 ± 0.283	0.21 ± 0.130	0.45	0.38	0.68 ± 0.287
Olive	120	0.73 ± 0.028	0.47 ± 0.296	0.74	0.73	0.85 ± 0.048
	162 plants	0.78 ± 0.024	0.51 ± 0.082	0.81	0.76	0.85 ± 0.041
		0.85 ± 0.040	0.64 ± 0.126	0.86	0.85	0.95 ± 0.044
		0.88 ± 0.029	0.71 ± 0.025	0.89	0.88	0.93 ± 0.040

CONCLUSIONS

- A hyperspectral phenotyping platform has been successfully developed for imaging woody potted plants under controlled conditions.
- A robust image-processing workflow was established to accurately extract vegetation pixels from images of woody plants.
- Reliable discrimination between *Xylella fastidiosa*-inoculated and non-inoculated plants across species was achieved using ensemble machine-learning models.
- Several vegetation indices were identified as consistent predictors of infection, particularly BG1, NPQI, B, WB13 and CTR1, which highlights the importance of traits related to pigments, chlorophyll and water for disease detection.
- Species-specific spectral responses were also observed, with distinct vegetation indices contributing to disease discrimination in almond, grapevine and olive.

MORE INFO Further information is available in a manuscript in the journal *Phytopathologia Mediterranea* (under review)