



Xylella fastidiosa

5th European conference

Bari, Italy | 22-26 June 2026



Pierce's disease of grapevines: climate, diversity, and novel risks

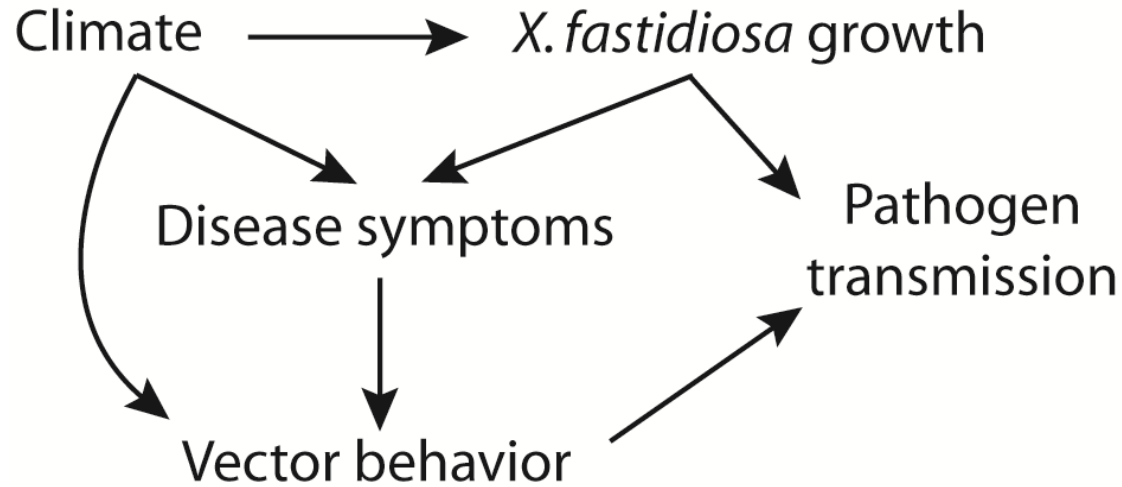
-Rodrigo Almeida, University of California, Berkeley-



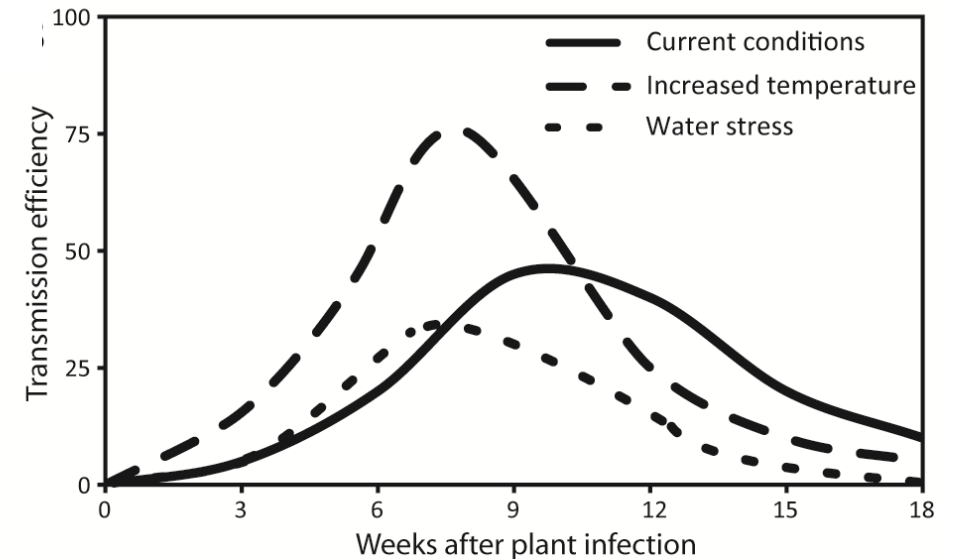
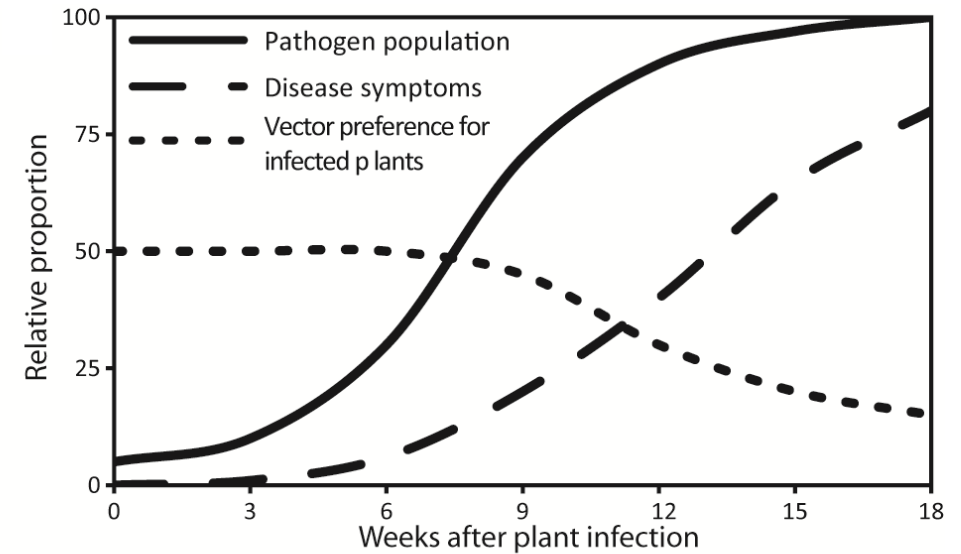
Work in collaboration with:
Monica Cooper, UCCE Napa
Matthew Daugherty, UC Riverside
Leonardo De La Fuente, Auburn U.



Climate, Diversity, and Novel Risks



Daugherty et al. 2017. Phytobiomes → essentially demonstrates that the hypothesis is well supported (model + experimental data).



Climate, Diversity, and Novel Risks

Overwinter recovery of Pierce's disease

- . known since the 1970s
- . experimentally reproducible
- . explains a lot about PD ecology and range

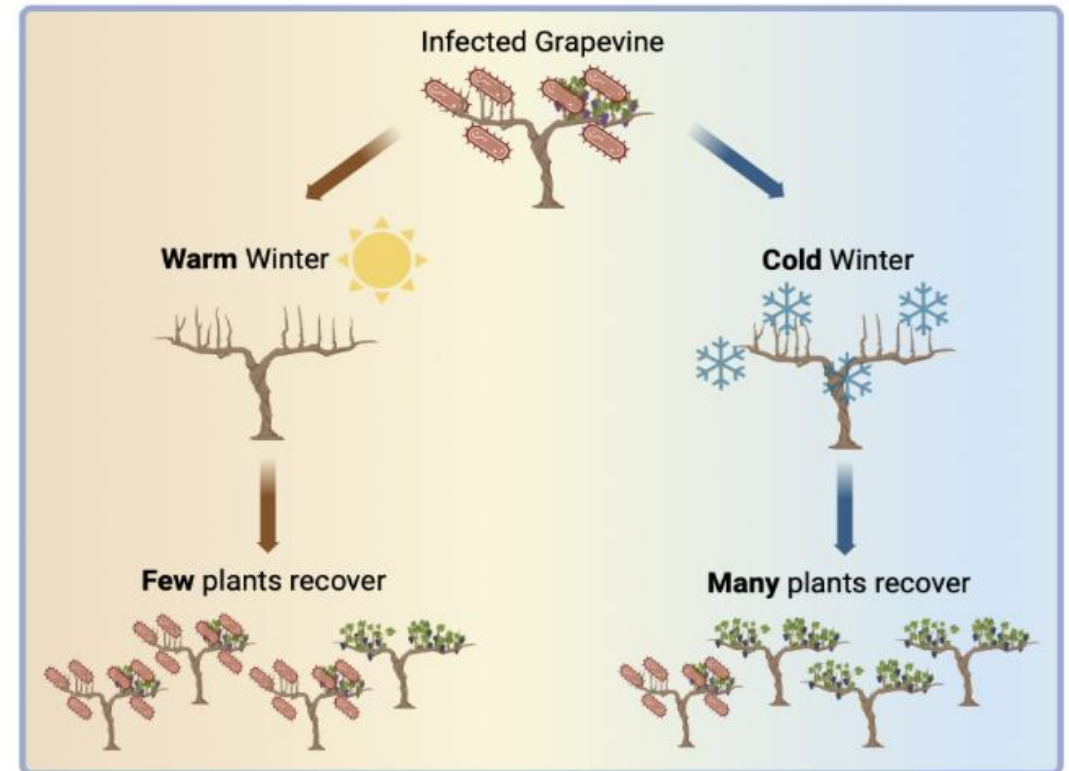
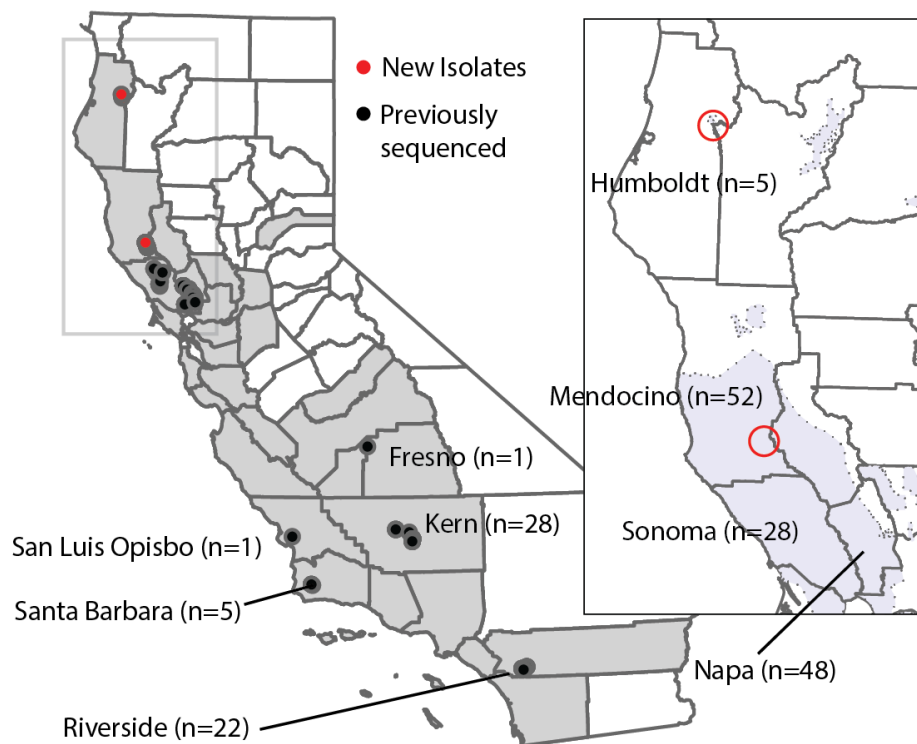


Figure 1: Grapevines infected with *X. fastidiosa* recover from their infections over cold winters. Vineyards in cooler regions therefore avoid chronic infections, whereas in warmer climates the bacteria persist through winter. Created with BioRender.com.

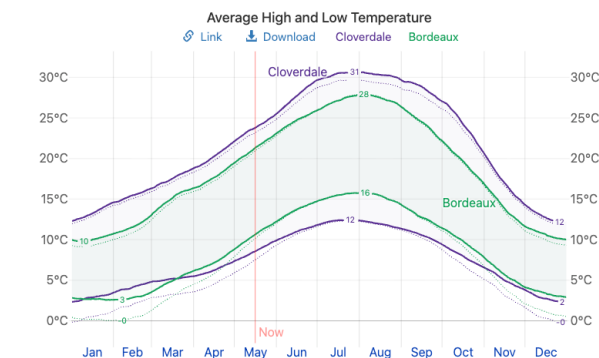
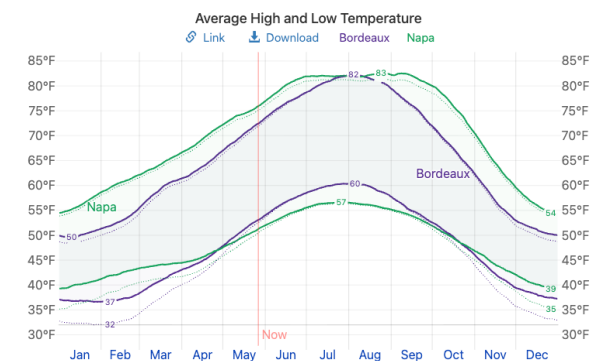
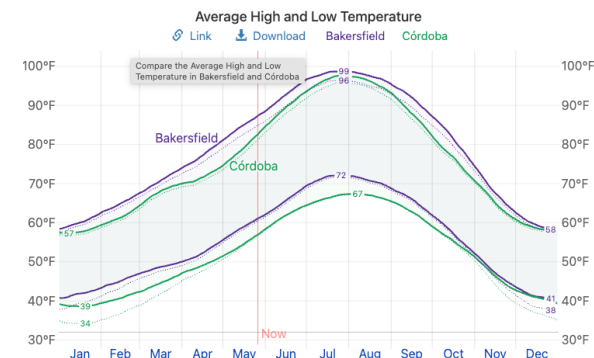
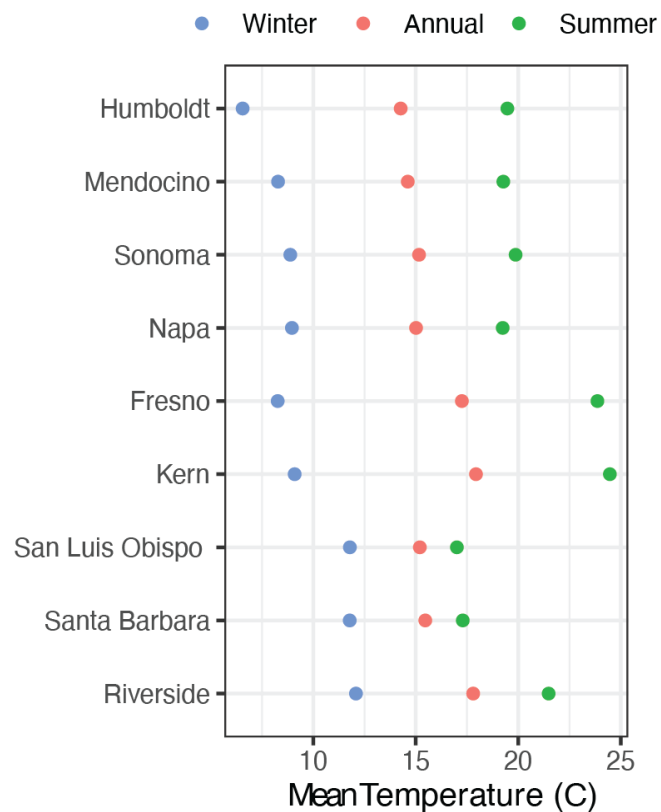
Figure: Andrea Brown

Climate, Diversity, and Novel Risks

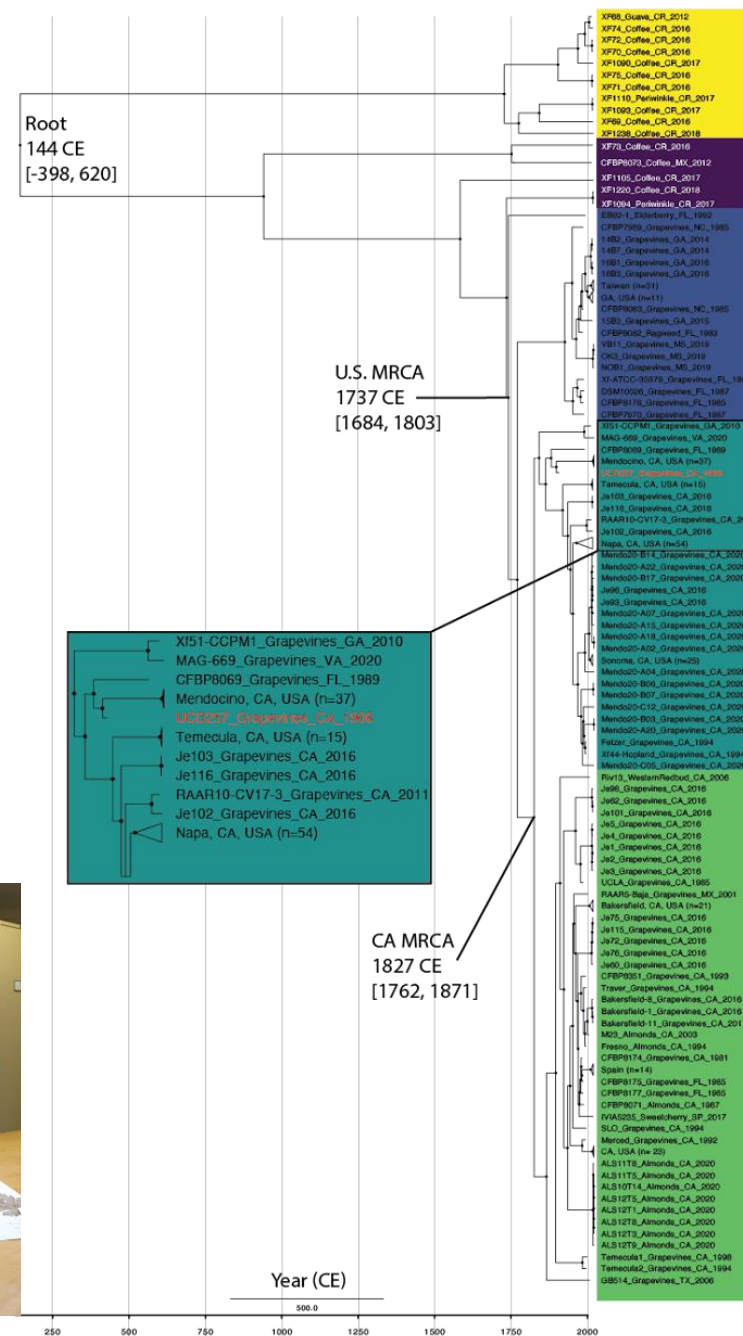
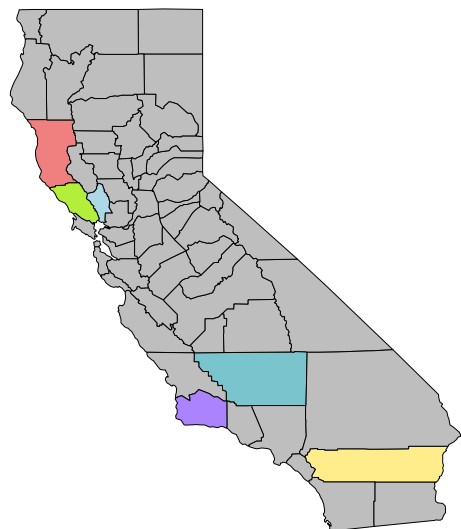
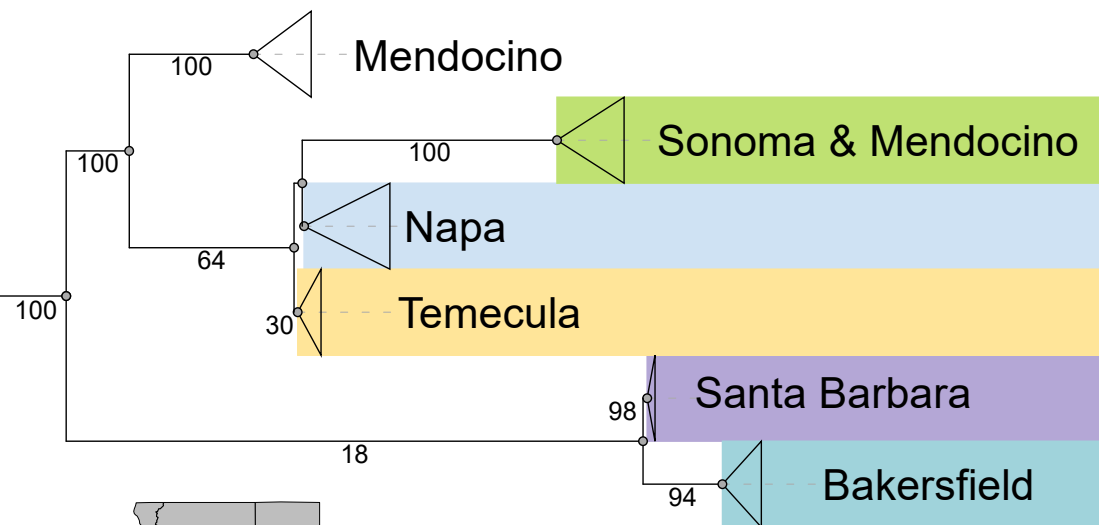
Counties with PD



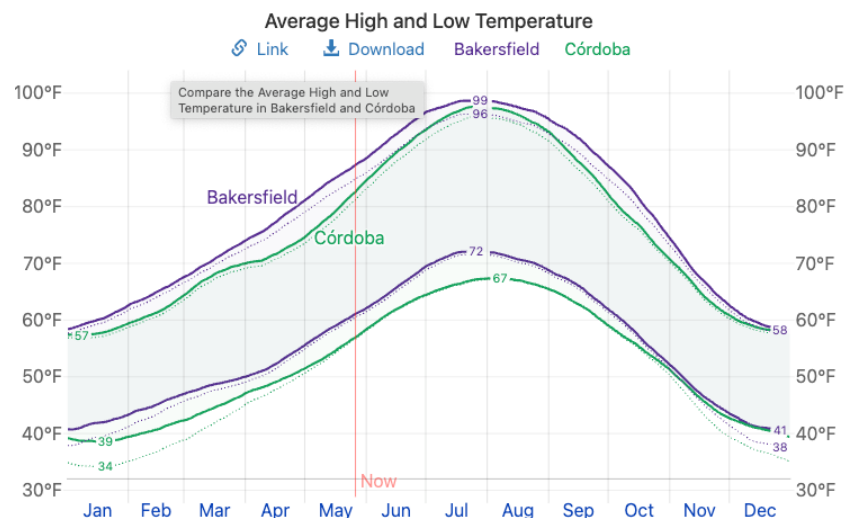
Viticultural Areas



Climate, Diversity, and Novel Risks



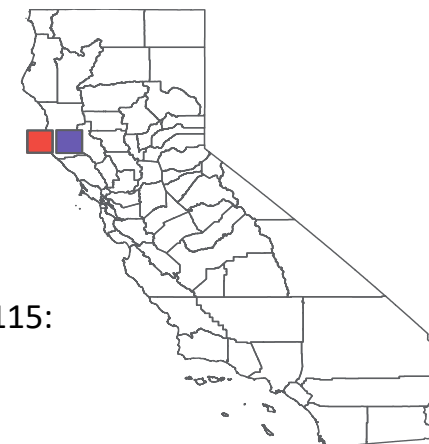
Climate, Diversity, and Novel Risks



Local D06:
Hopland

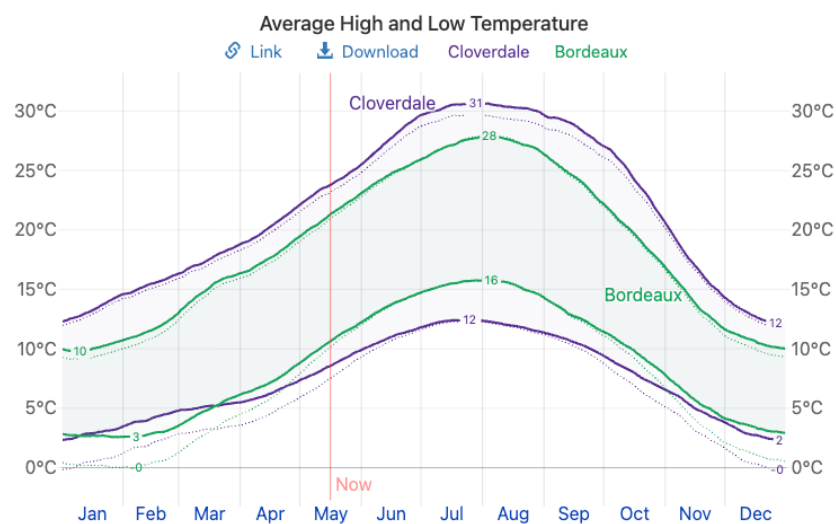


Non-Local Je115:
Bakersfield



Strain Origin

Experiment Location



Local D06:
Hopland



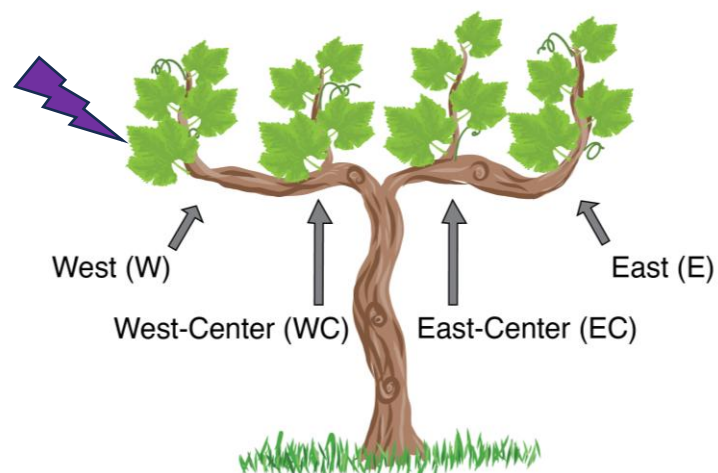
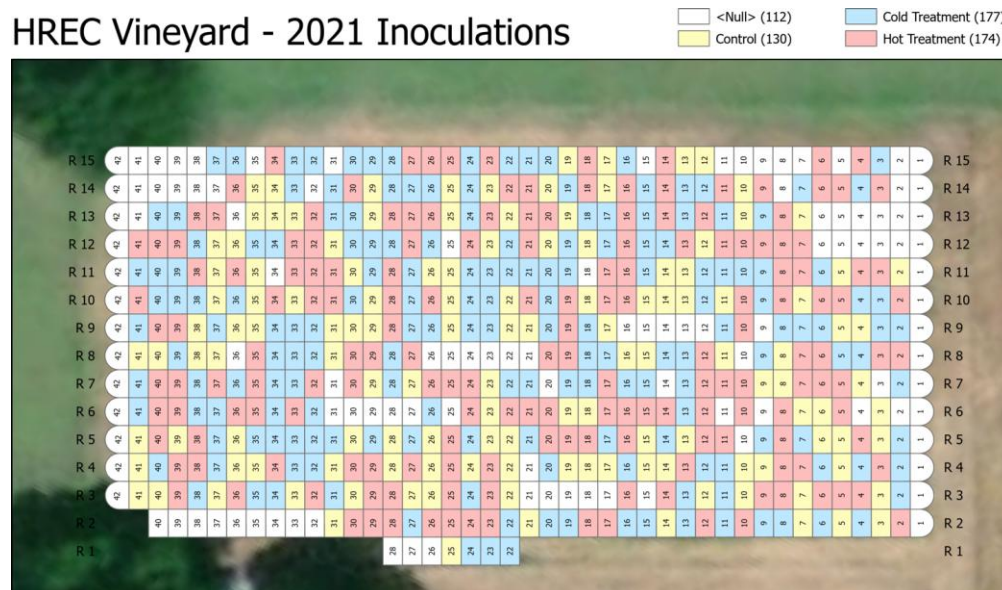
Greater winter survival, slower growth, reduced virulence

Non-Local Je115: Bakersfield

Low winter survival, faster growth, higher virulence

Climate, Diversity, and Novel Risks

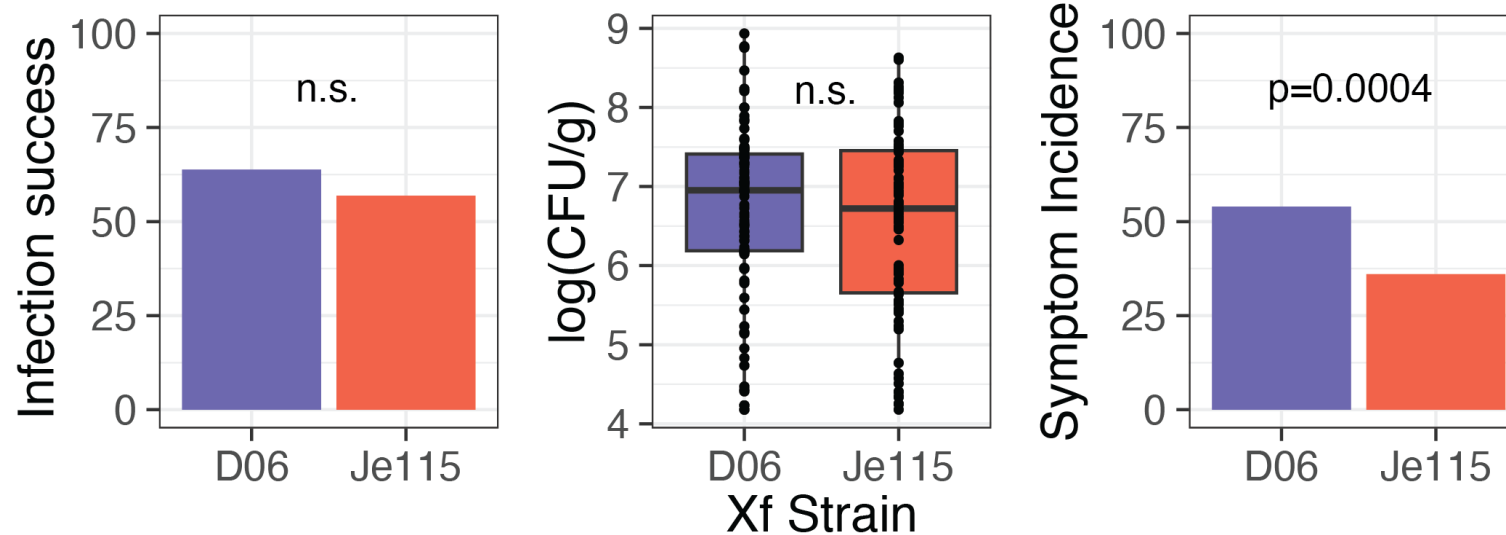
HREC Vineyard - 2021 Inoculations



174 D06-infected vines
 174 Je115-infected vines
 129 control vines
477 total vines

Climate, Diversity, and Novel Risks

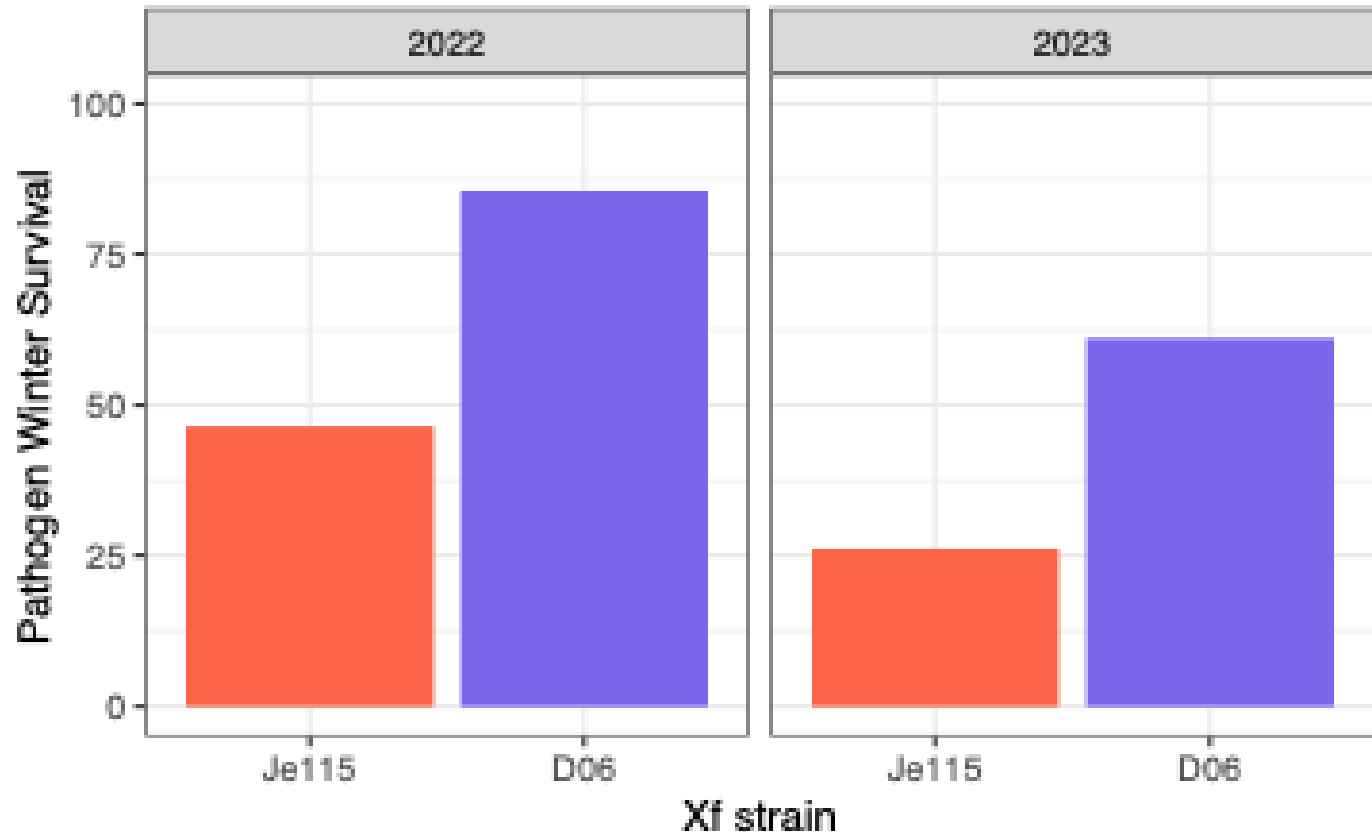
Infections by strain before the winter



Climate, Diversity, and Novel Risks

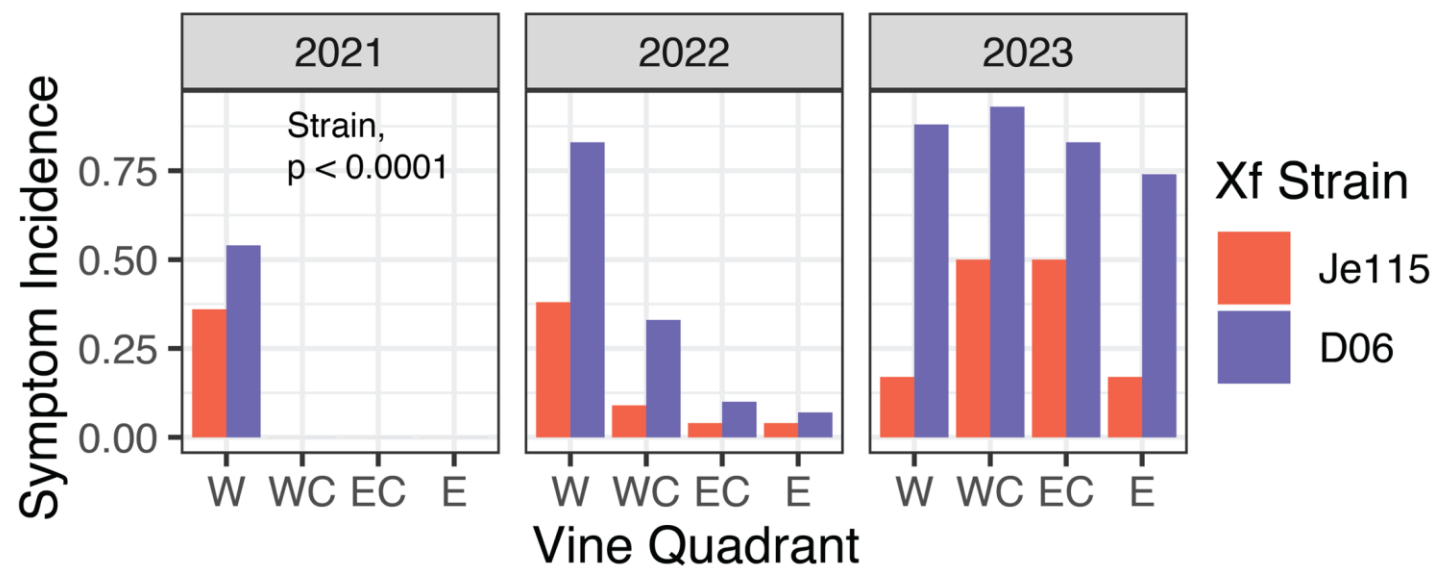
Higher winter survival in local strain

- 2021-2022
 - D06 86% (95 / 111)
 - Je115 46% (46 / 99)
- 2022-2023
 - D06 61% (58 / 95)
 - Je115 26% (12 / 46)

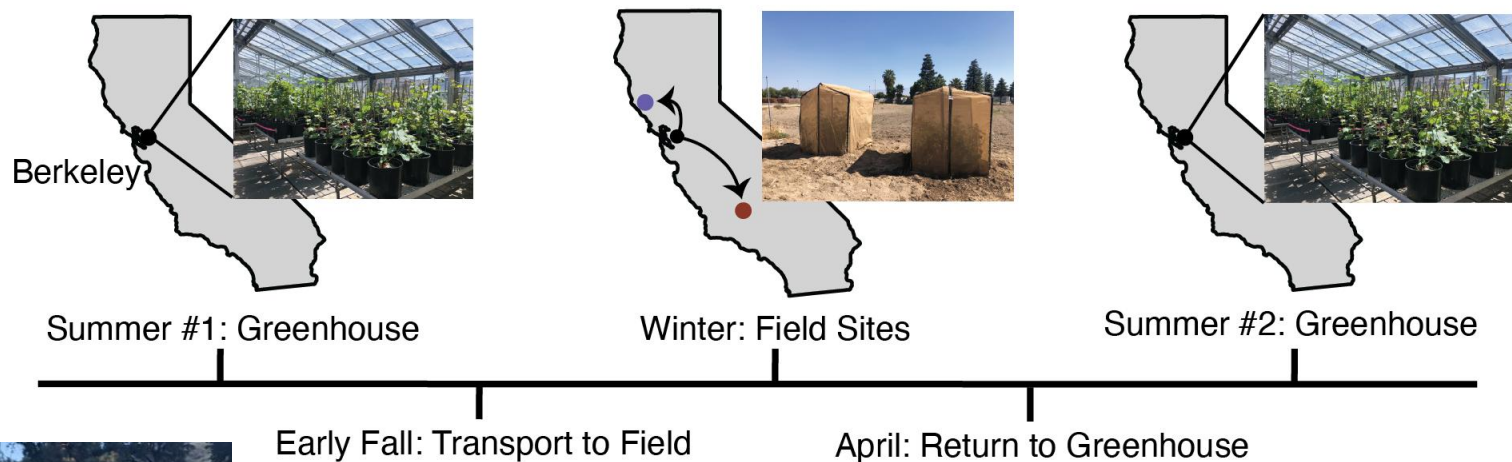
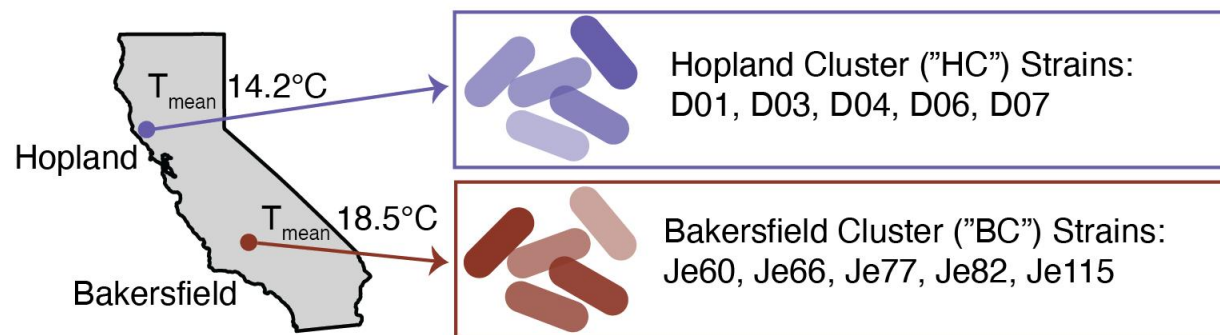


Climate, Diversity, and Novel Risks

Symptom incidence varied by strain
-and variety (not shown here)-

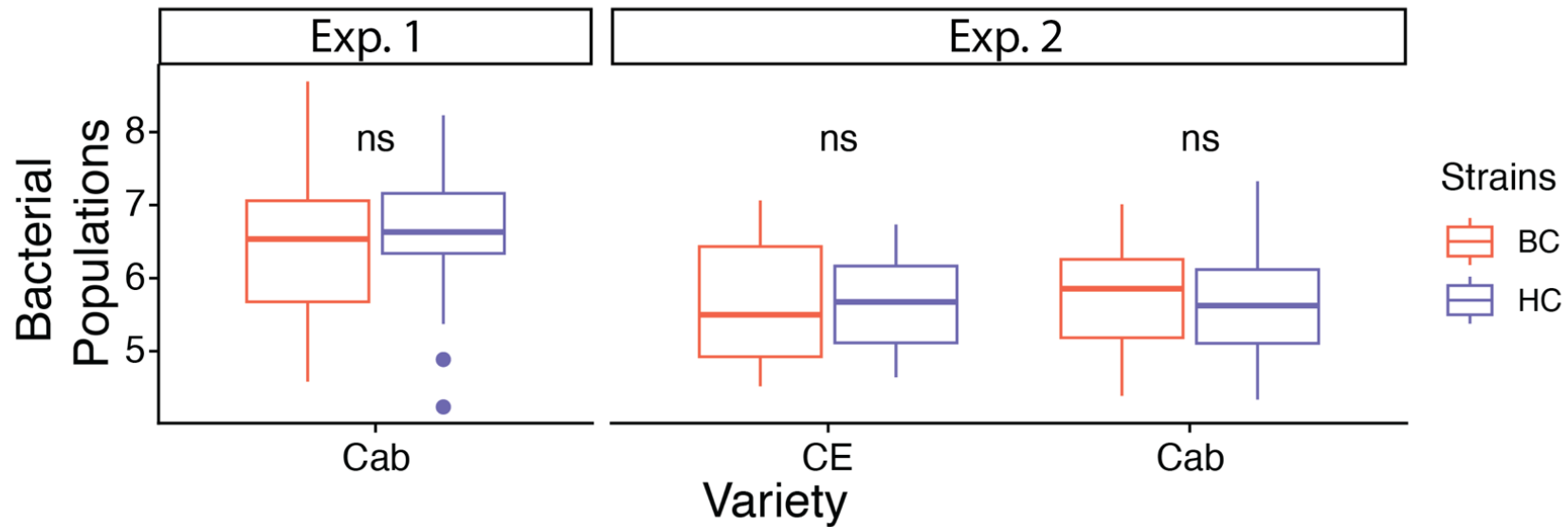


Climate, Diversity, and Novel Risks



Climate, Diversity, and Novel Risks

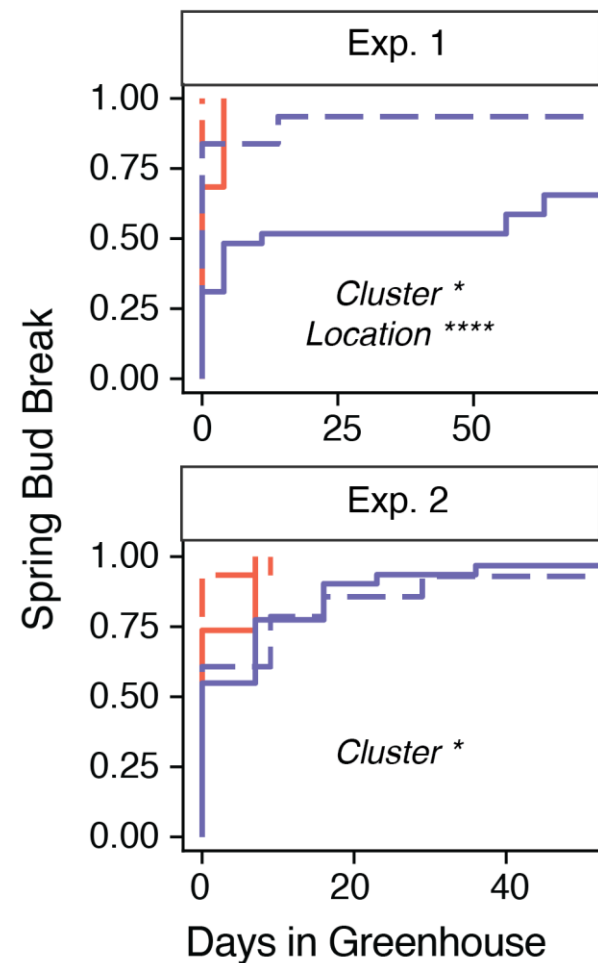
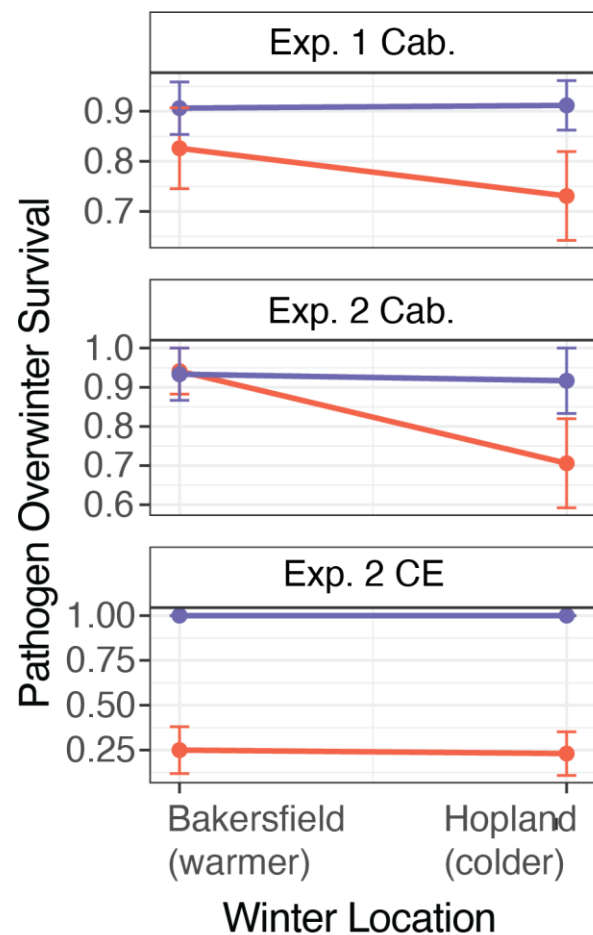
Similar populations before the winter



Climate, Diversity, and Novel Risks

In Cabernet Sauvignon vines, warm-climate strains have lower survival under colder winters.

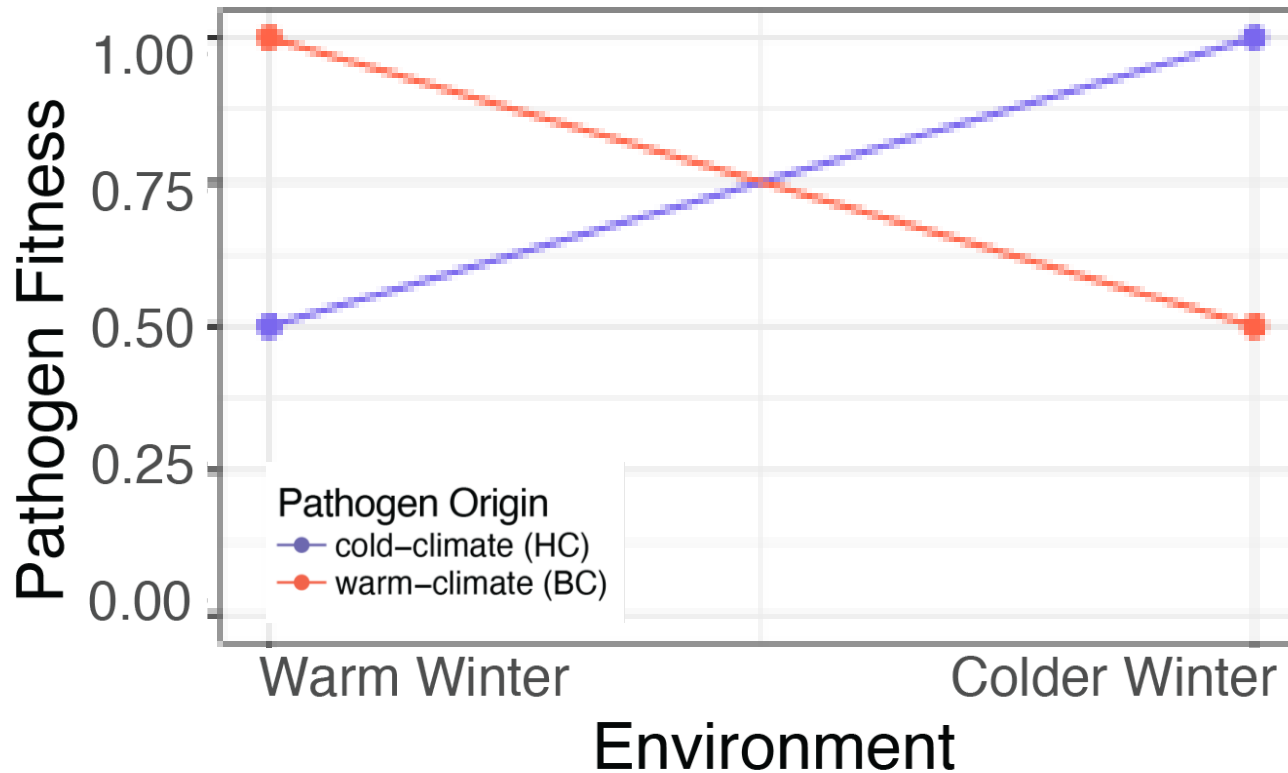
In Ciliegiolo vines, warm-climate strains don't survive the winter well in either climate.



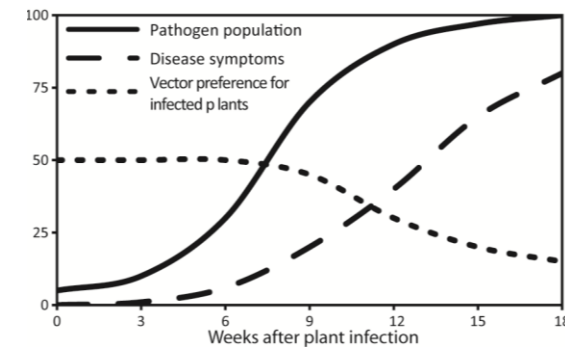
Bud break is delayed in vines infected with cold-climate strains.

And virulence for cold-climate strains – data not shown here

Climate, Diversity, and Novel Risks



Cold-climate (HC) strains are hypervirulent in warm climates after the winter.

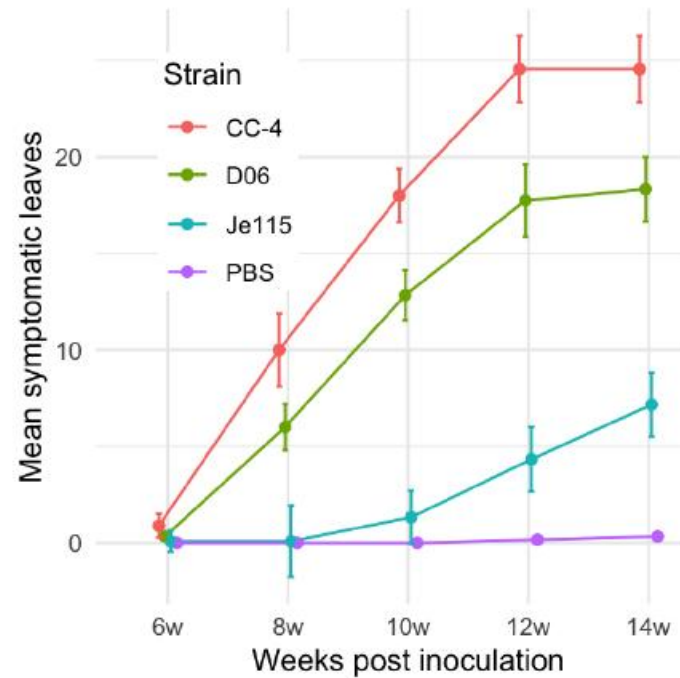


Warm-climate (BC) strains have lower survival and fitness under colder winters.



Are those results unique?

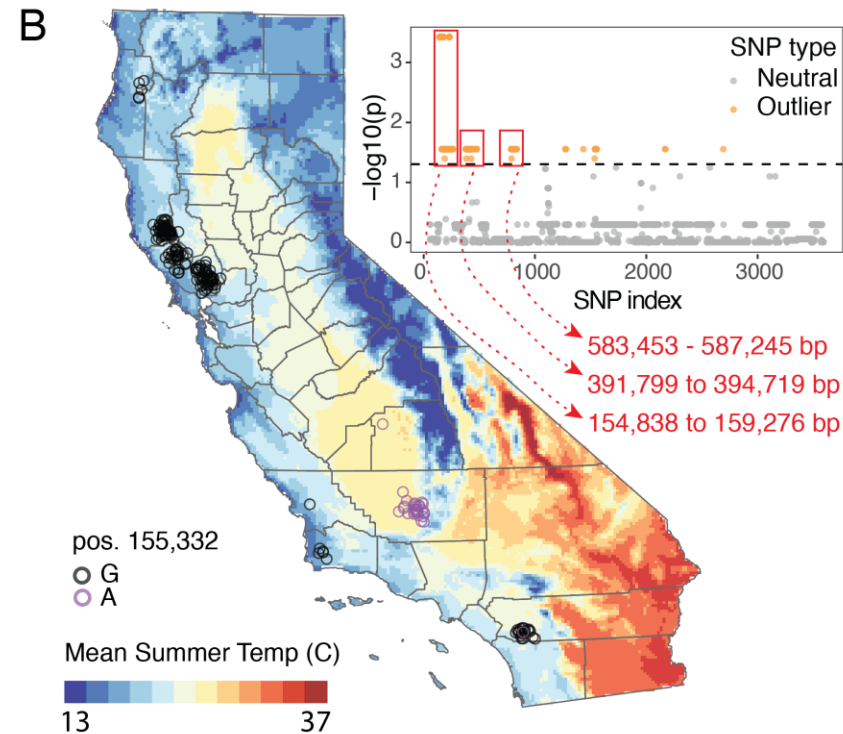
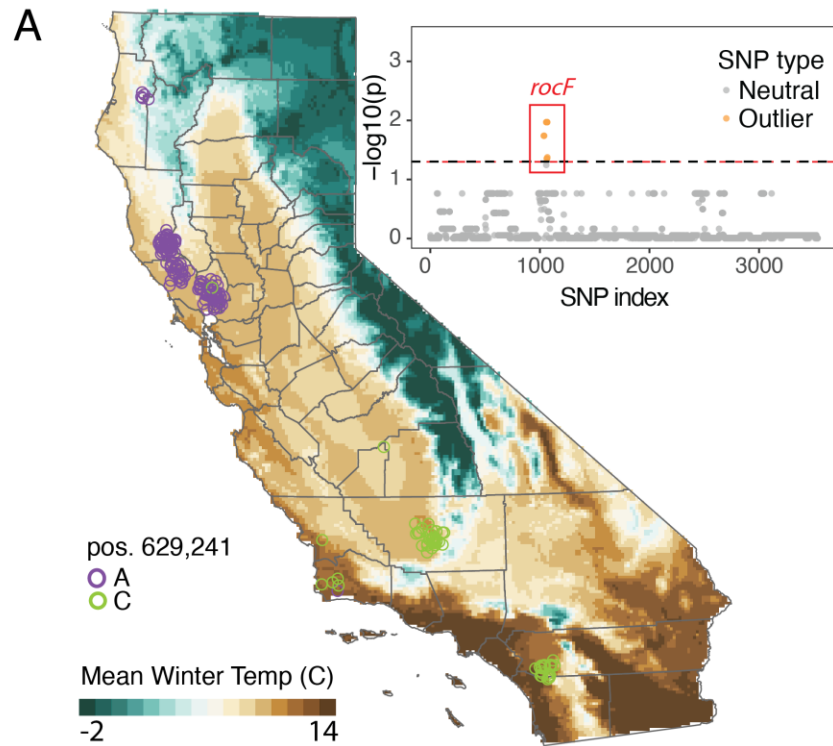
- different person, one more strain, different variety -



Karyn Newman, unpublished data

Climate, Diversity, and Novel Risks

Four genes/regions with temperature-associated mutations

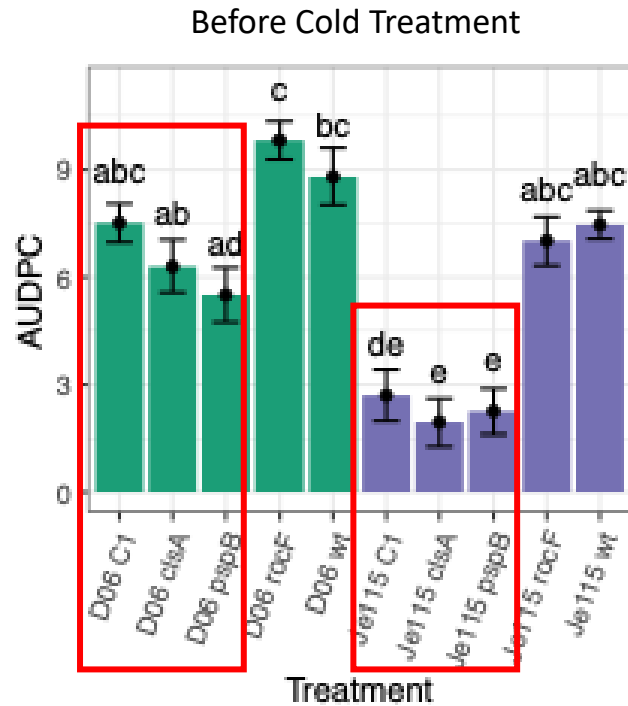


188 genomes

98% of significant mutations result from homologous recombination

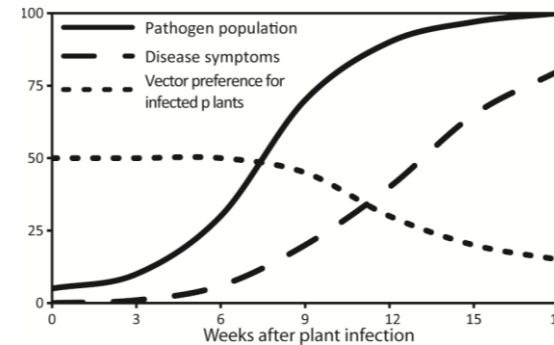
Climate, Diversity, and Novel Risks

Summer genes impact virulence



Horizontal gene transfer of *multiplex* alleles in summer genes may prevent hypervirulence

↓virulence = slower symptom progression = ↑vector spread



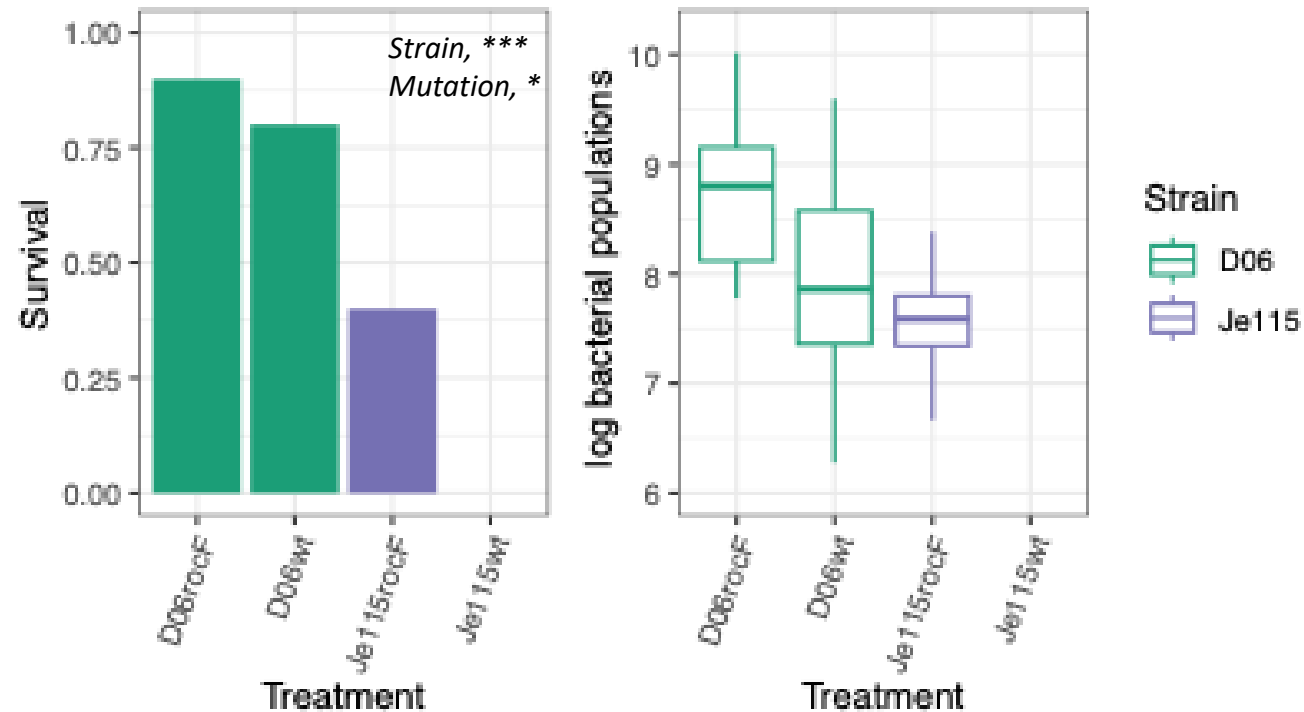
Modulation of disease is present in *X. fastidiosa* through cell-cell signaling.

high cell density → shut down of plant colonization factors

Climate, Diversity, and Novel Risks

Winter gene impacts cold survival

After Cold Treatment



Climate, Diversity, and Novel Risks

Subspecies *multiplex* in grapevines? Yes
Cold climates? Yes

Where does PD occur in the US?
What genotypes cause PD in the US?

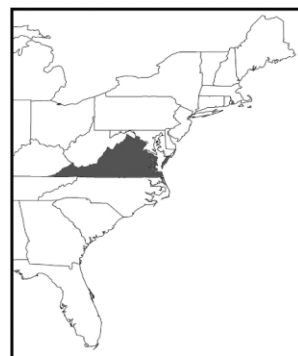
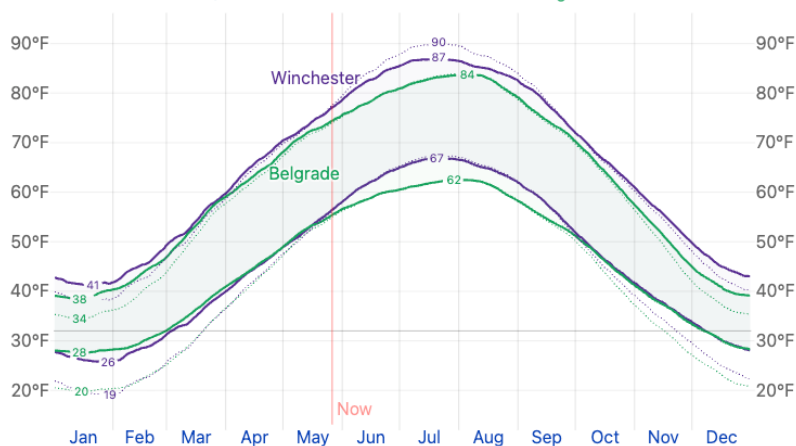
Nunney et al. 2019



Fig. 1. Leaves from a Merlot grapevine infected with ALS003 (Dixon) showing characteristic scorch symptoms. Symptomatic leaves from Pinot Noir are shown on the front cover of this issue.

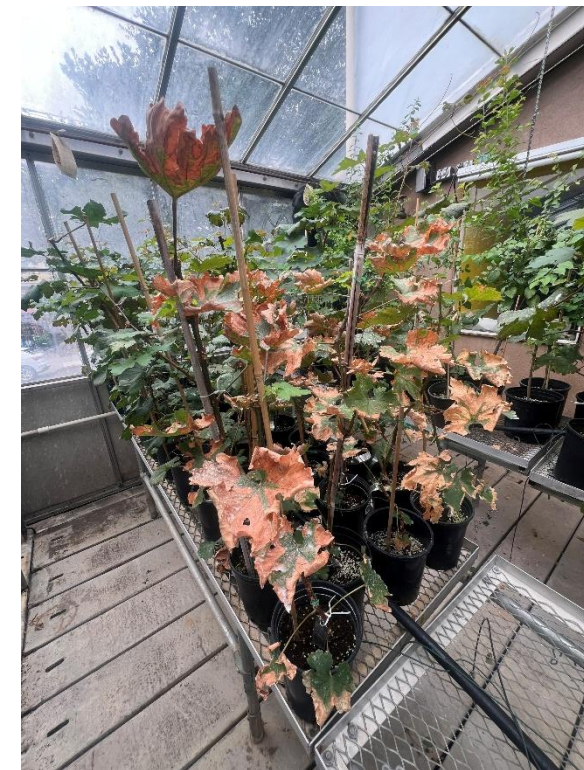
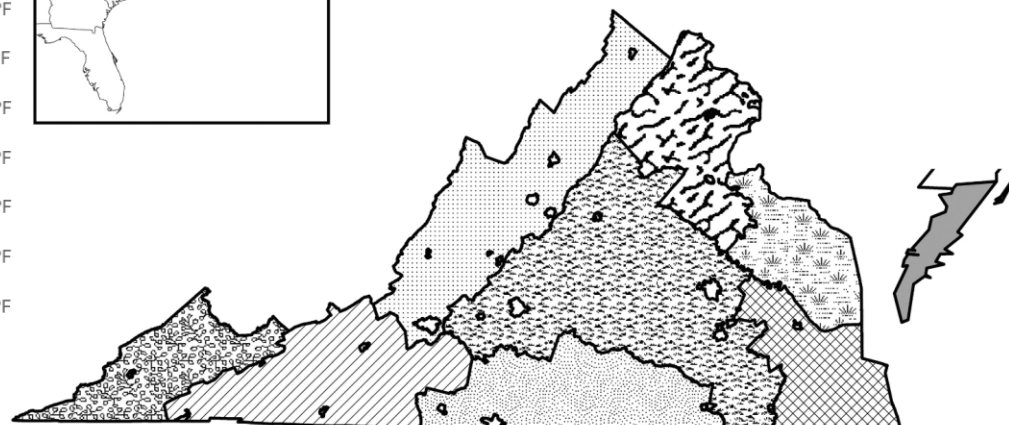
Fig. 1. Location of Virginia and nine Virginia winegrowing regions.

Average High and Low Temperature
[Link](#) [Download](#) Winchester Belgrade



Wine Regions

- Blue Ridge
- Central Virginia
- Chesapeake Bay
- Eastern Virginia
- Hampton Roads
- Heart of Appalachia
- Northern Virginia
- Shenandoah Valley
- Southern Virginia



Patrick Lee, unpublished data

Abdelrazek et al. 2024

Climate, Diversity, and Novel Risks

First Report of *Xylella fastidiosa* Infection and Pierce's Disease in Resistant Grape Cultivars in Texas, U.S.A.

Jacy L. Lewis,^{1,†}  Pedro Uribe,² David N. Appel,²
Alexandra K. Kahn,³ and Rodrigo P. P. Almeida³

- . Texas has high PD pressure
- . PD is a production limiting factor in Texas
- . It remains unclear why plants were symptomatic
- . These varieties labeled as PD-resistant supported low *X. fastidiosa* populations





Take home messages

- . There is a lot of PD-causing *X. fastidiosa* diversity in the US yet to be reported
 - . There is PD in regions with summers as hot as Cordoba and winters as cold as Belgrade
 - . There is PD in commercial vineyards caused by subspecies *multiplex*, and there is evidence of *multiplex* being pathogenic to grapevines in the greenhouse
 - . Winter recovery is dependent on *X. fastidiosa* genotype, grapevine variety, climate, and yearly winter temperature variation
 - . Evidence shows that PD-causing *X. fastidiosa* in California is locally adapted
 - . Genomic regions associated with temperature in California are of recombinant origin
 - . PD risk and incidence is not necessarily going to increase or decrease with climate change, many variables will impact disease outcomes, range is likely to change though
 - . How to interpret research not done locally, with local strains and varieties, with local climates?
- 



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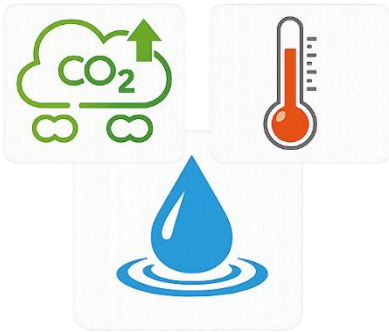
Impact of simulated climate change conditions on *Xylella fastidiosa*–grapevine interactions

M. ROMÁN-ÉCIJA, J.L. TRAPERO-CASAS, G. LEON-ROPERO, F.Z. BENHALIMA, J.C. RIVAS-ROMERO, C. OLIVARES-GARCÍA, J. A. NAVAS-CÓRTES and B.B. LANDA
Instituto de Agricultura Sostenible (IAS-CSIC)



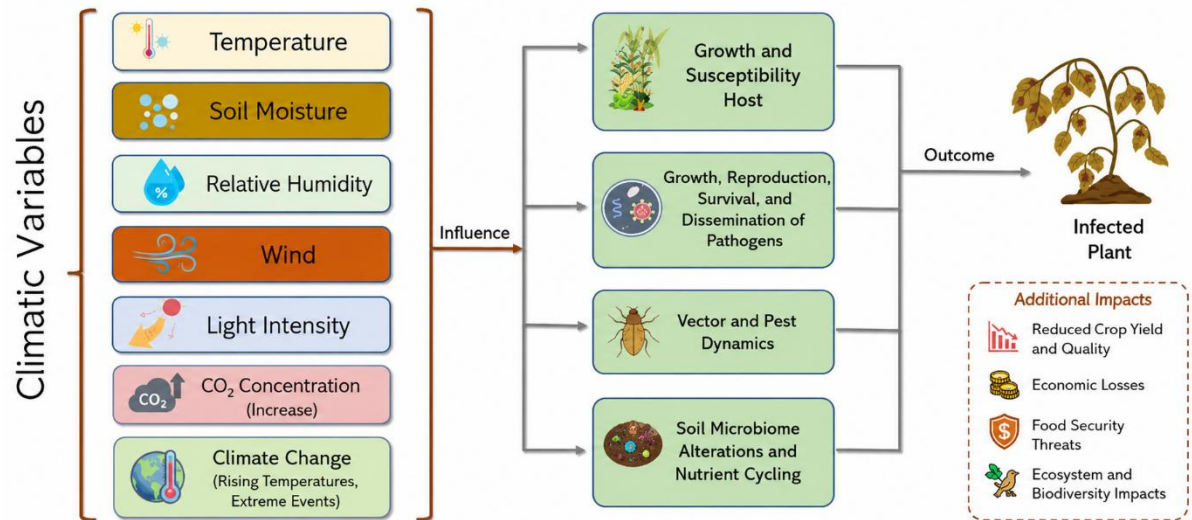
REGIONE PUGLIA

INTRODUCTION

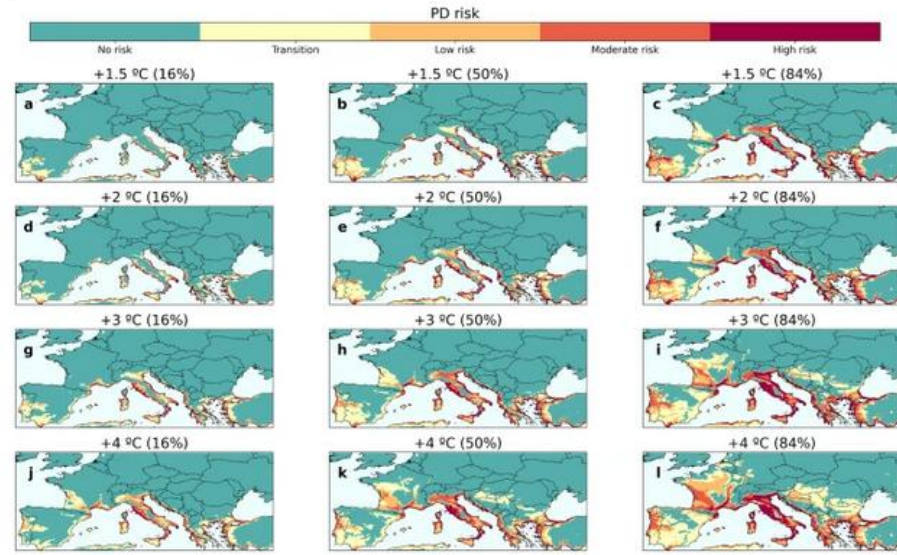


Climate change
↑ **Temperature**
↑ **CO₂ concentration**
↓ **Water availability**

Climate change is expected to alter plant-interactions



Adapted from Hossain et al.
Discover Agriculture (2024)



Giménez-Romero et al. Scientific Reports (2024)

Current models predict an increased risk of *Xylella fastidiosa* establishment and spread under future climate scenarios

Experimental validation of these predictions is limited

OBJECTIVES

Evaluate grapevine responses to *Xylella fastidiosa* infection under simulated climate change scenarios in controlled conditions

Determine the effects of temperature, elevated CO₂ concentration, irrigation regime and cultivar susceptibility on disease progression and pathogen systemic colonization



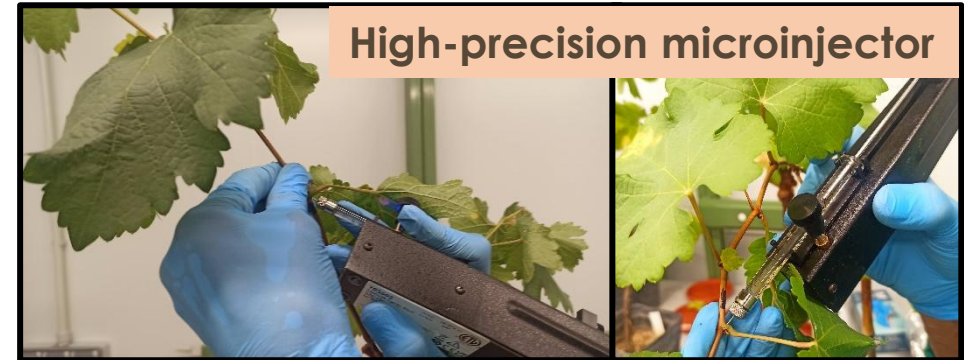
METHODOLOGY



Xylella fastidiosa subsp. *fastidiosa*
strain IVIA5770 (ST1)



3 grapevine cultivars
Sauvignon Blanc
Sirah
Chardonnay

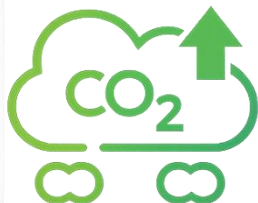
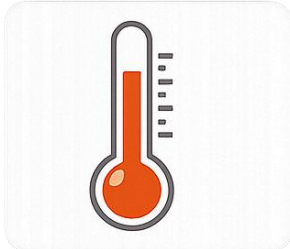


High-precision microinjector

2 climate change scenarios

3 Temperature and CO₂ levels

- 24°C / 400 ppm CO₂ (Current)
- 27°C / 550 ppm CO₂ (CC Scenario 1)
- 30°C / 750 ppm CO₂ (CC Scenario 2)



2 irrigation levels
Field capacity (FC)
50% FC



Continuous monitoring of:

Temperature and CO₂
Plant weight
Stomatal conductance
Soil moisture

METHODOLOGY

Disease evaluation

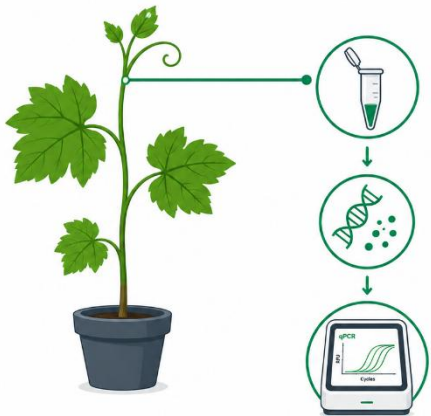


Symptom evaluation:
Severity
Incidence
sAUDPC

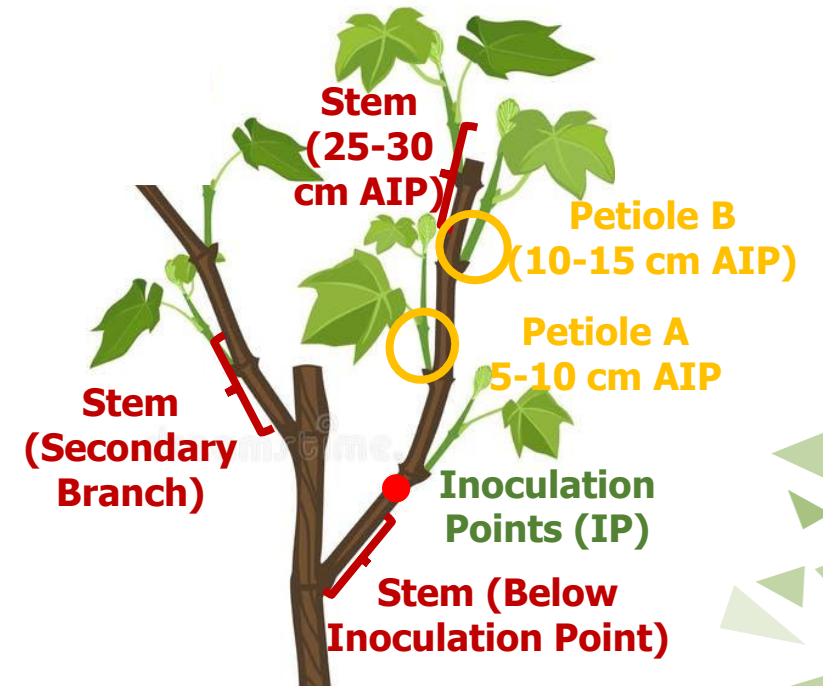


Scale severity: 0 to 5 (% plant symptoms)

Infection evaluation



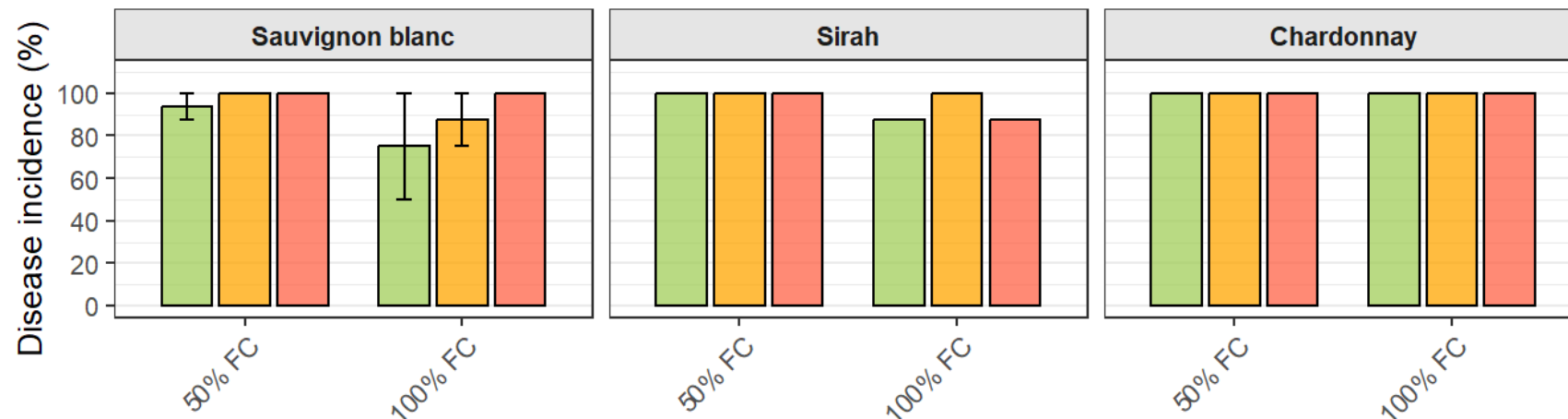
Sampling leaf petioles
at 2- and 4-mpi
Sampling stem at 6-mpi
qPCR
Isolation
Frequency of detection
Bacterial load



RESULTS. Disease development

Pierce's Disease incidence

24°C/400 ppm CO₂ 27°C/550 ppm CO₂ 30°C/750 ppm CO₂



Sauvignon blanc

30°C - 750ppm CO₂



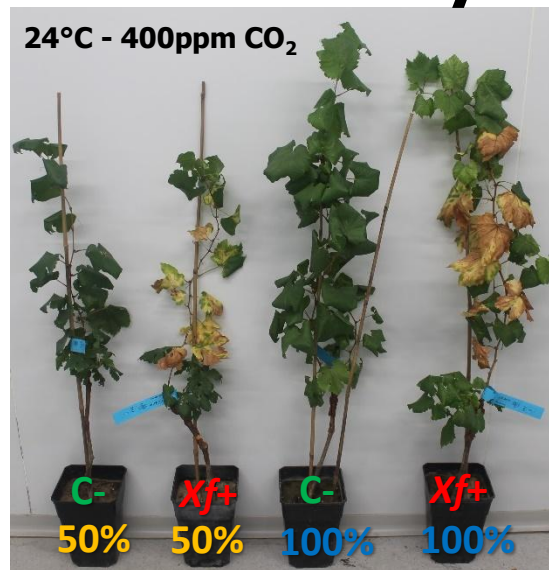
Syrah

27°C - 550ppm CO₂



Chardonnay

24°C - 400ppm CO₂



Disease incidence reached close to 100% across cultivars and climate scenarios and irrigation

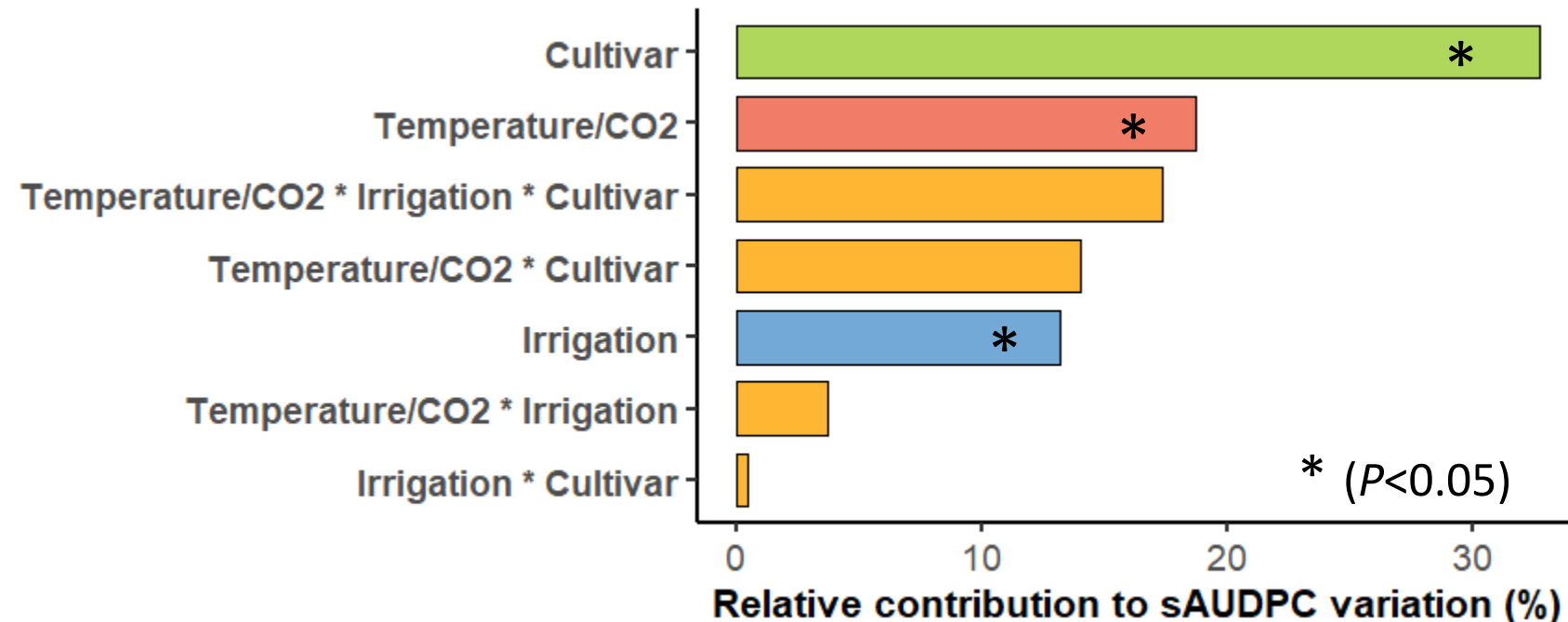
RESULTS. Disease development (sAUDPC)



Pierce's Disease was significantly influenced by:
Temperature and CO₂
Cultivar
Irrigation



↑ sAUDPC: 27°C/550 ppm CO₂, 30°C/750 ppm CO₂
↓ sAUDPC: 24°C/400 ppm CO₂



↑ sAUDPC Chardonnay
↔ sAUDPC Sirah
↓ sAUDPC Sauvignon Blanc

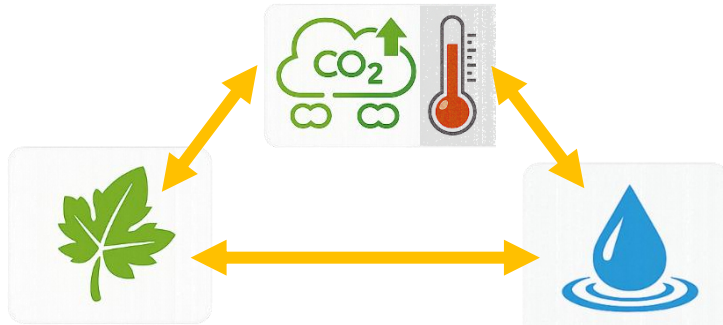


↑ sAUDPC at 50% FC
↓ sAUDPC at 100% FC

RESULTS. Disease development (sAUDPC)



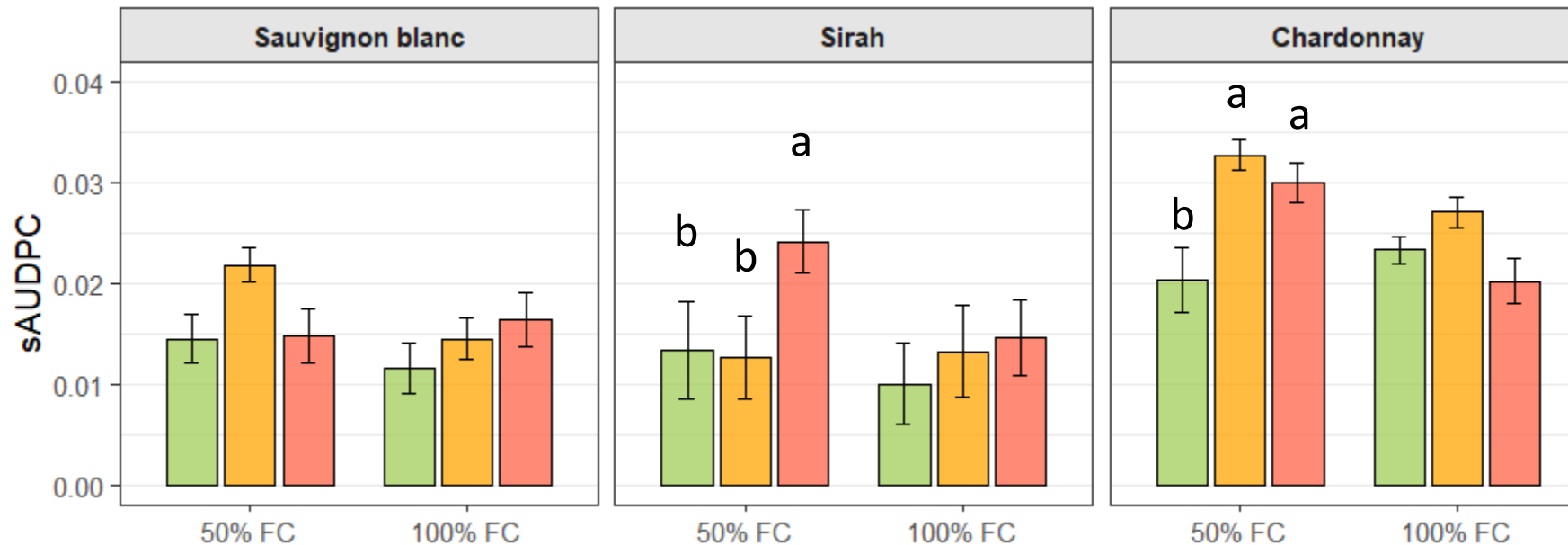
Cultivar-dependent response
to climate change scenarios
and irrigation



Limited response in
'Sauvignon blanc'

'Syrah' and 'Chardonnay'
exhibited higher sAUDPC
values under 50% FC and
30°C/750ppm

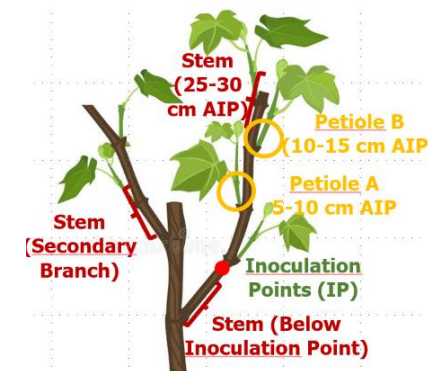
Higher PD
→ elevated temperature
and CO₂
→ water deficit



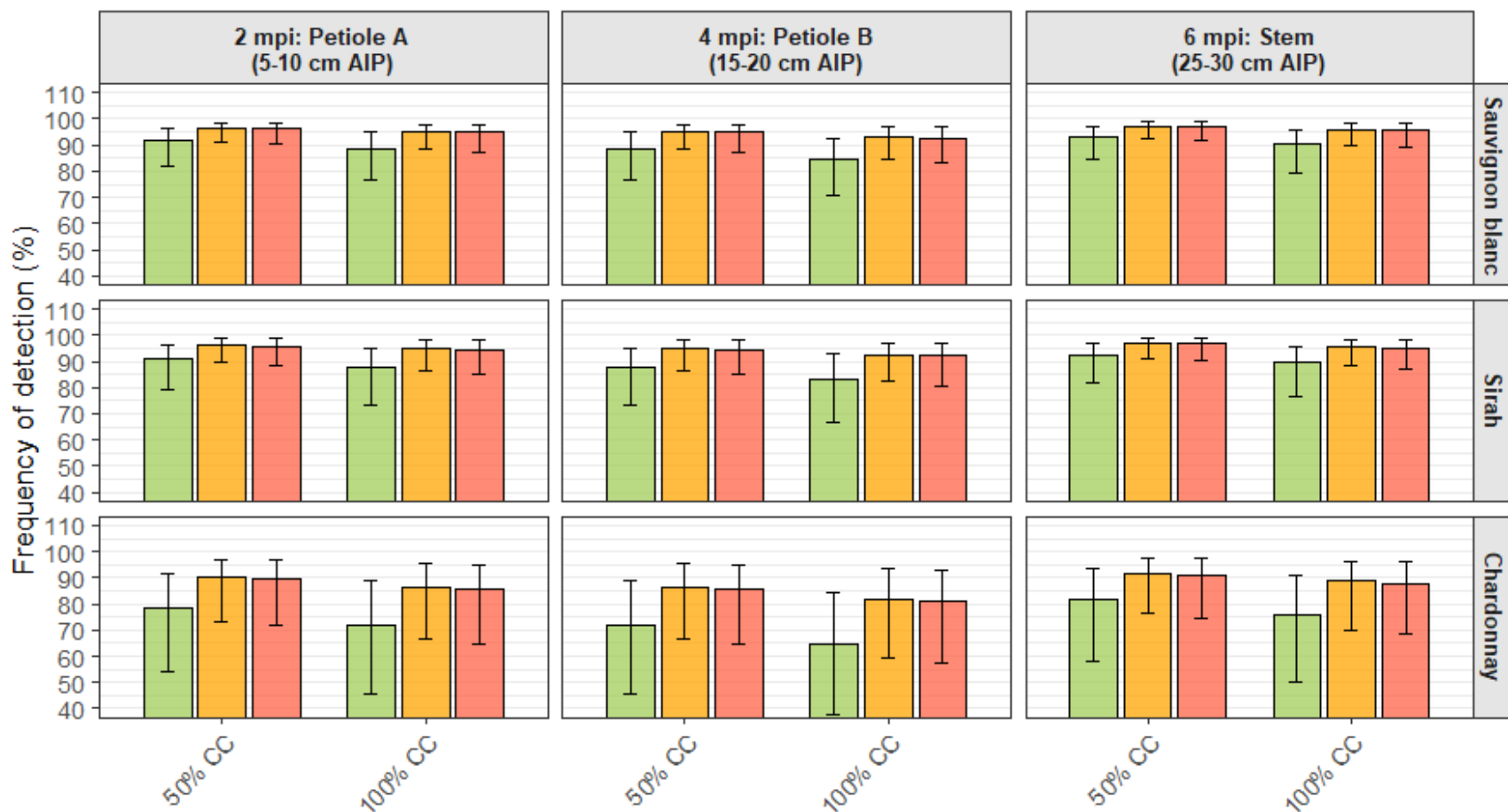
RESULTS. Bacterial detection

Frequency of detection by qPCR

Main effect of climatic conditions



24°C/400 ppm CO₂ 27°C/550 ppm CO₂ 30°C/750 ppm CO₂



Higher *Xf* detection frequencies
27°C/550 ppm CO₂
30°C/700 ppm CO₂

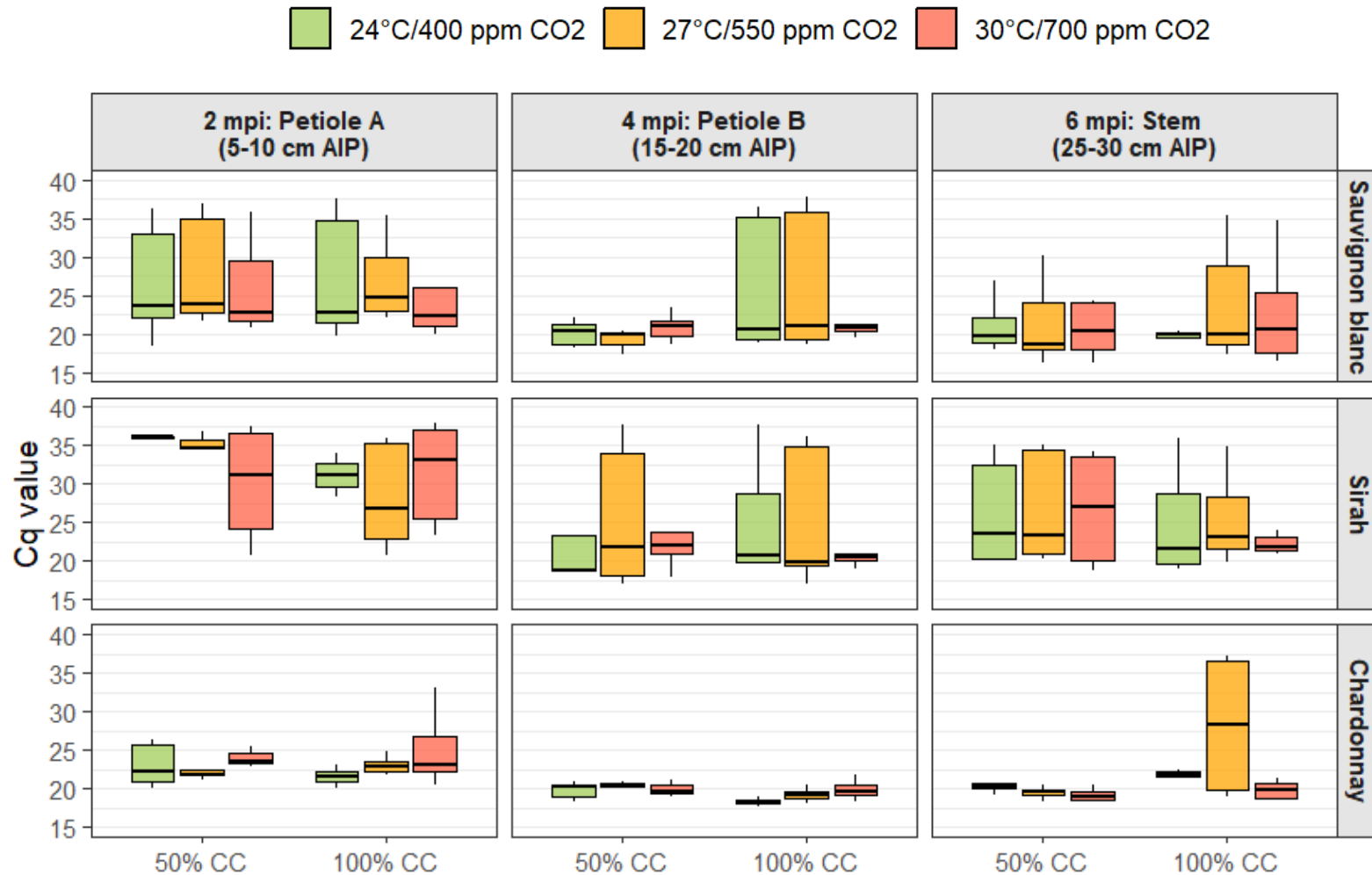
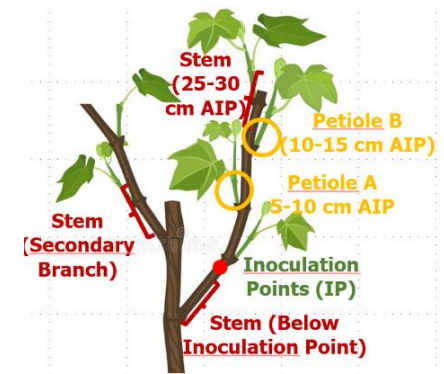
Consistent trends across tissues, cultivars and sampling times

RESULTS. Bacterial detection

Bacterial load by qPCR (Cq value)

Main effect of plant section sampled

Higher at 4- and 6-mpi
and at 20-30 cm AIP



Significant interaction
were detected:
temperature/CO with
irrigation or cultivar

Bacterial loads remained
relatively stable across
climate and irrigation
treatments

Can *Xf* survive winter in Spain wine-producing areas?

To evaluate possibility of winter recovery in three protected denomination of origin in Spain

TT 4°C

Jerez (Cádiz)

TT -2°C

Montilla
(Córdoba)

TT -5°C

La Rioja

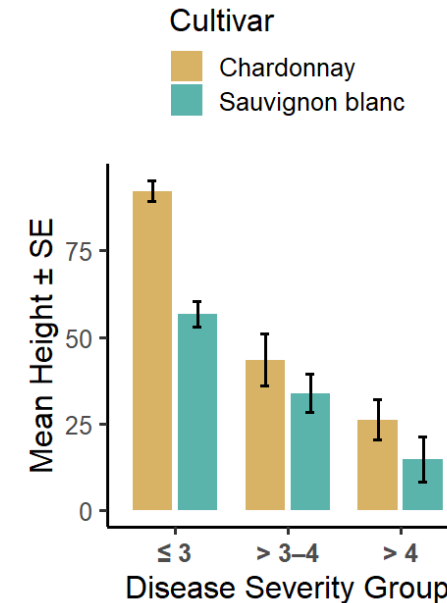
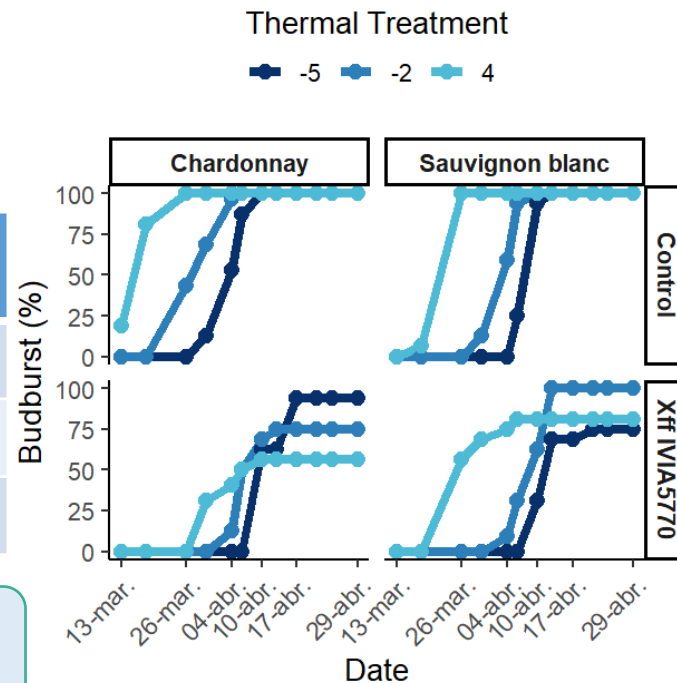
X. fastidiosa artificially-inoculated grapevine plants with different levels of disease severity in the previous season were subjected to different cold scenarios

Effect of cold treatments on plant height and budburst

Effect of cold treatments on *Xf* isolation from inoculated grapevines

Thermal Treatment	Isolation rate
Control (4°C)	100 %
Cold Treatment (-2°C)	77.8 %
Cold Treatment (-5°C)	72.7 %

Isolation rates decreased under freezing conditions



Symptom development and colonization pattern evaluation ongoing



CONCLUSIONS

- Elevated **temperature** and **CO₂** conditions **increased Pierce's Disease** severity, suggesting that future climate scenarios may favour the severity of *Xylella fastidiosa* infection.
 - **Water deficit** accentuated disease development under future climate conditions, with more **pronounced effect** in more **susceptible cultivars**.
 - **Bacterial detection** frequencies **increased** under **elevated temperature** and **CO₂** scenarios, but bacterial loads remained stable across treatments within the same grapevine cultivar.
 - These results will contribute to improve our understanding of **disease dynamics** and disease **risk assessment** under current and future **climate change scenarios**.
- 



This work was supported by:
BeXyl Beyond Xylella
(Grant ID 101060593, EU-Horizon Europe)

KODA-IPEC (Knowledge-based and Data-driven Agriculture tools for Irrigation of Permanent Crops)

PIE202340E021

**Qualifica Project QUAL21-023 IAS
PTI-SolXyl-CSIC**

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REGIONE PUGLIA



Pre-winter pathogen load and cold exposure impact overwinter recovery from Pierce's Disease of grapevine

Andrea Brown and Rodrigo Almeida
UC Berkeley



Outline

1. Cold exposure experiment
2. Reinfection after recovery



Overwinter recovery from PD

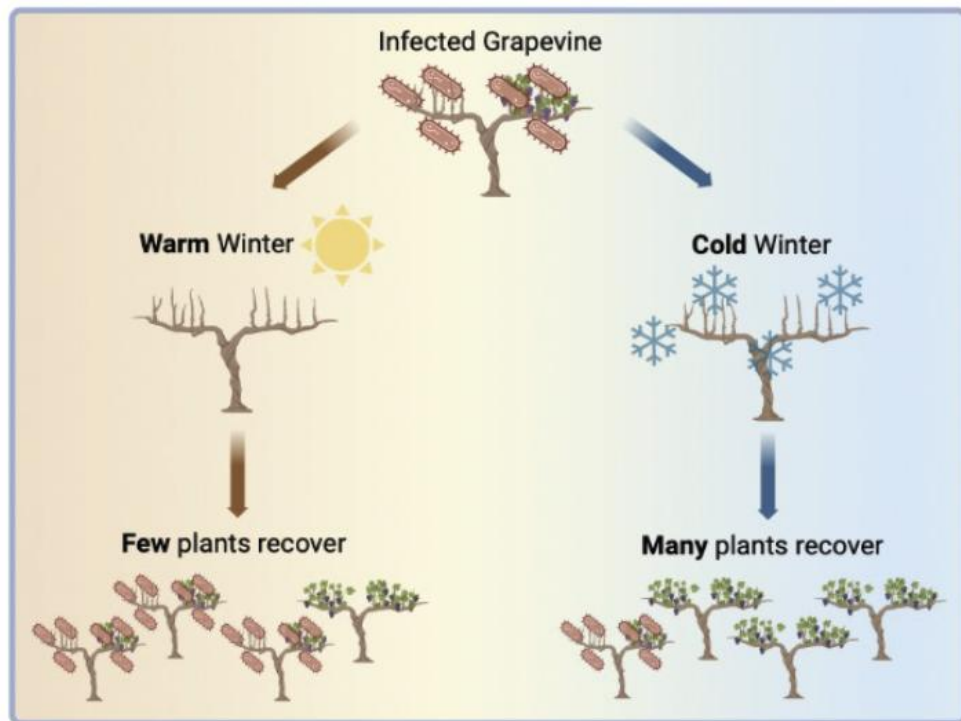


Figure 1: Grapevines infected with *X. fastidiosa* recover from their infections over cold winters. Vineyards in cooler regions therefore avoid chronic infections, whereas in warmer climates the bacteria persist through winter. Created with BioRender.com.



Counties where Pierce's disease has been reported, based on CDFA laboratory records and reports from researchers and cooperative extension agents.
[Note: the known distribution of Pierce's disease in each county is not reflected on the map, and not all counties have been surveyed for Pierce's disease.]

January 30, 2023

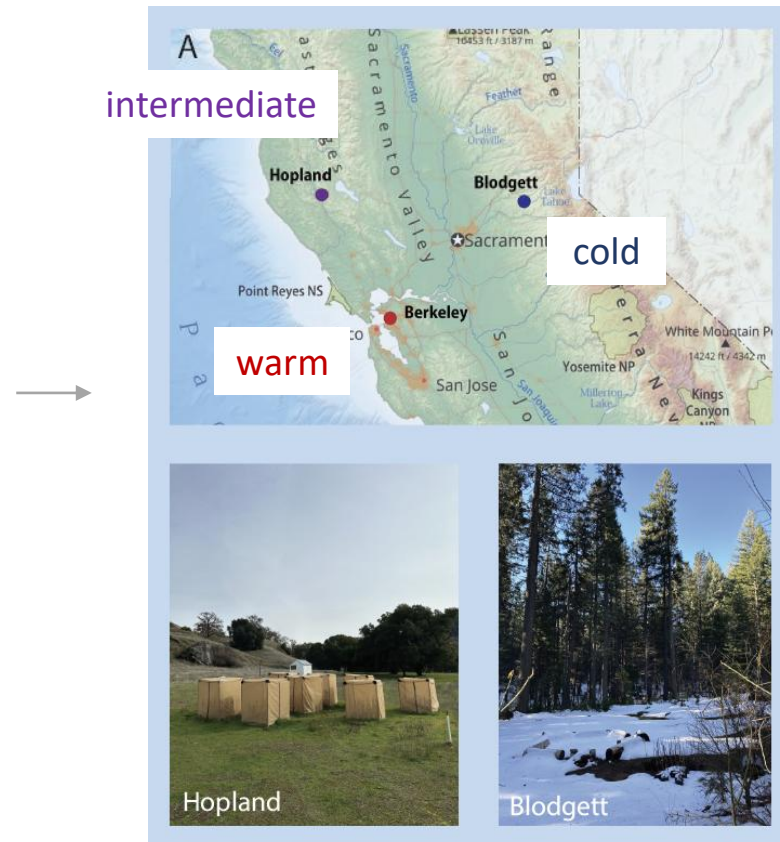
Recovered plants: Infected plants are qPCR negative and symptom-free after winter

1. Cold exposure experiment

Question: What cold exposure is necessary for recovery to occur in California?



Summer: Greenhouse

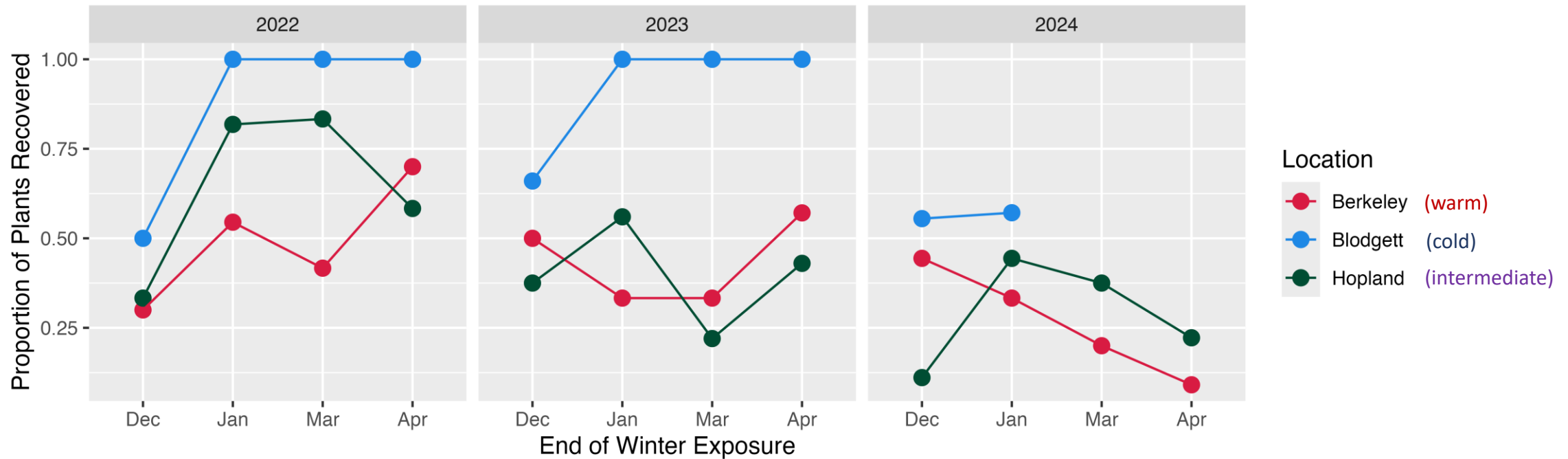


Winter: Field, four removals



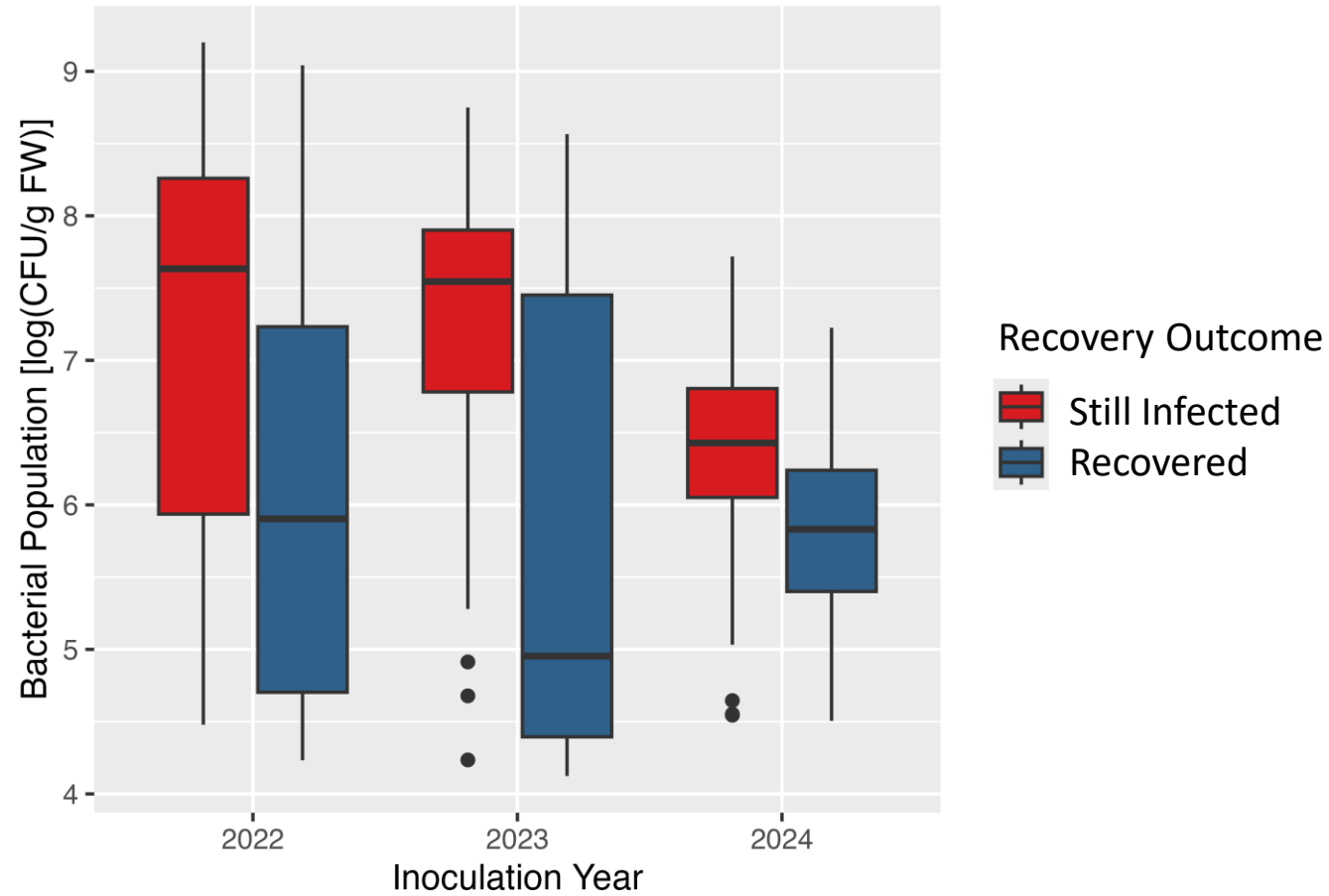
Summer: Greenhouse

1. Cold exposure experiment



Recovery did not increase predictably with overwinter exposure time

1. Cold exposure experiment

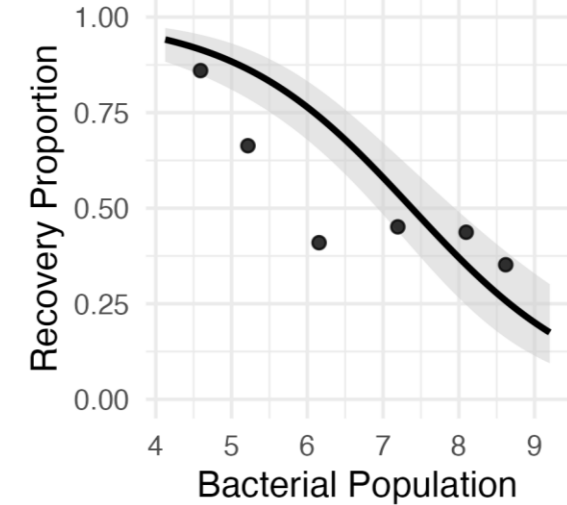
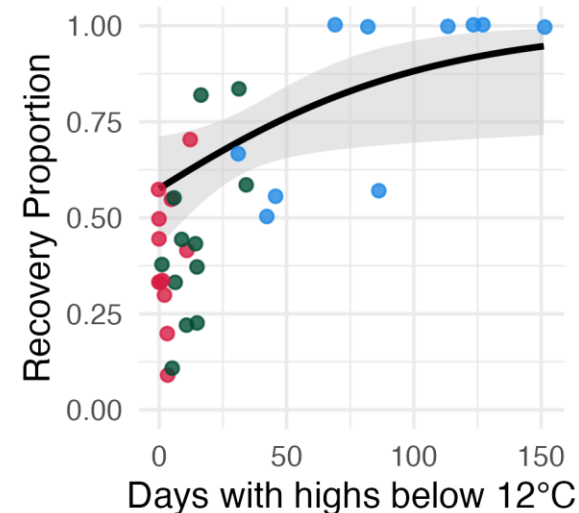
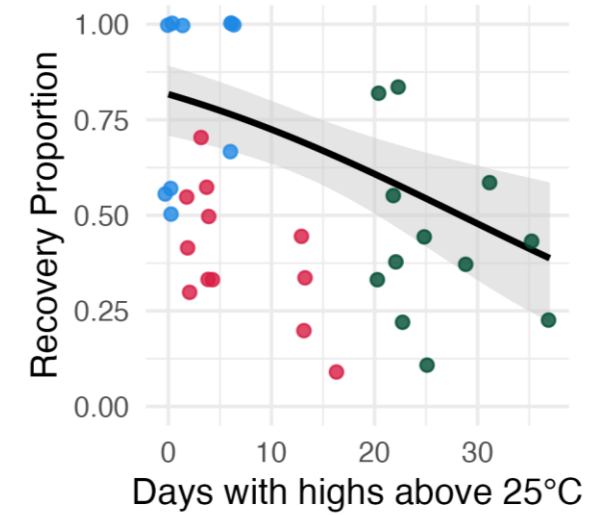
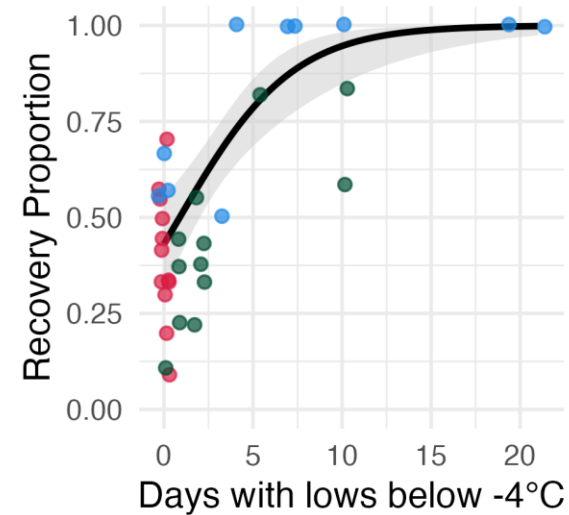


Plants with higher bacterial populations were less likely to recover over the winter

Model: $Recovery \sim \beta_0 + \beta_1(population) + \beta_2(lows < -4^{\circ}C) + \beta_3(highs < 12^{\circ}C) + \beta_4(highs > 25^{\circ}C) + (1|cohort)$

Binomial model of recovery per plant (n=326) with scaled temperature variables selected using cross-validation

Predictors	Recovery impact
Bacterial Population	-
Lows < -4°C	+
Days Max Temp < 12°C	+
Days Max Temp > 25°C	-



location

- Berkeley
- Blodgett
- Hopland

Model Fit

Accuracy: 79.1%

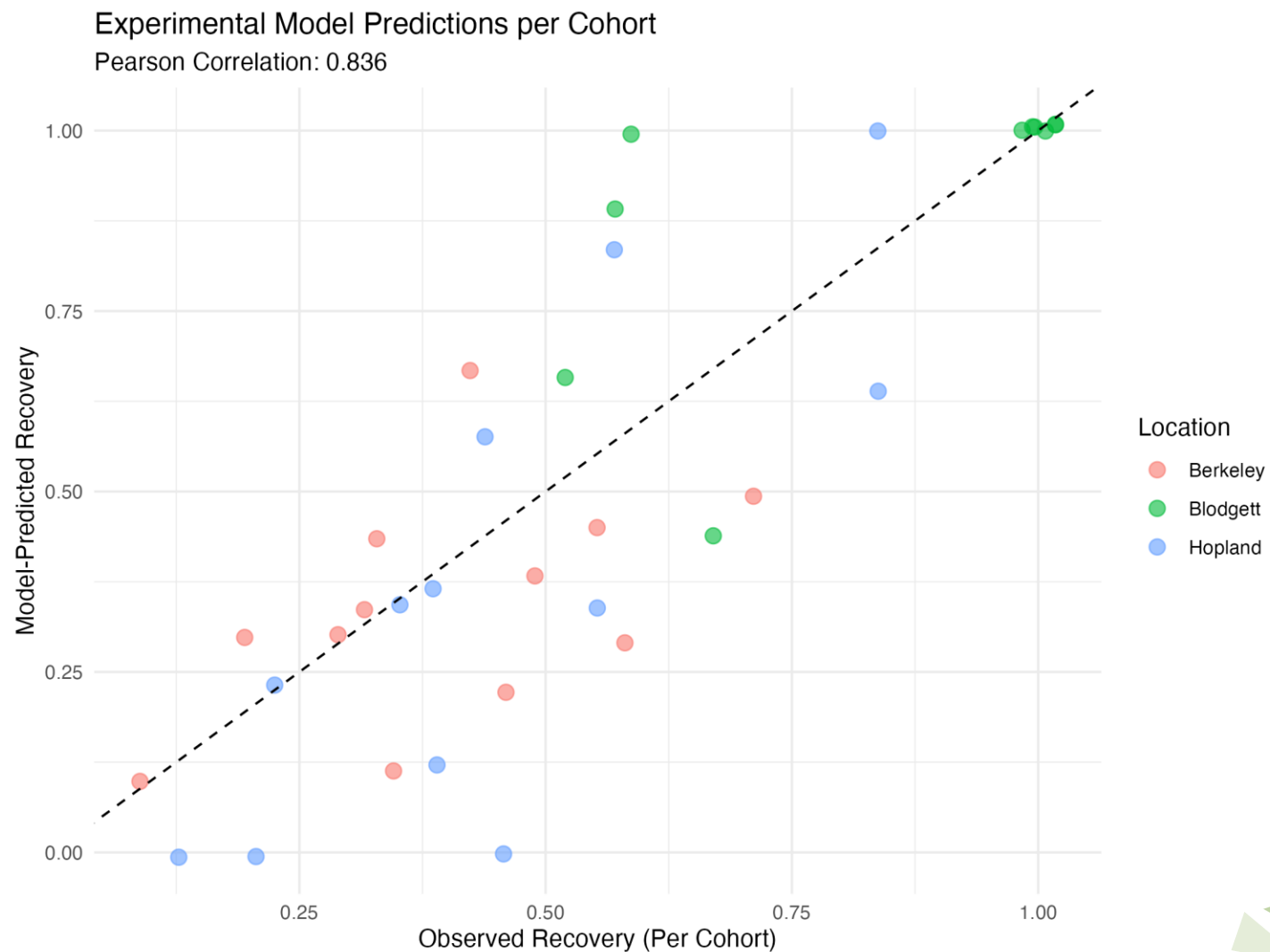
Percent of plants classified correctly by the model

Sensitivity: 79.4%, Specificity: 78.8%

Proportion of correctly classified recovered (sensitivity) and still infected (specificity) plants

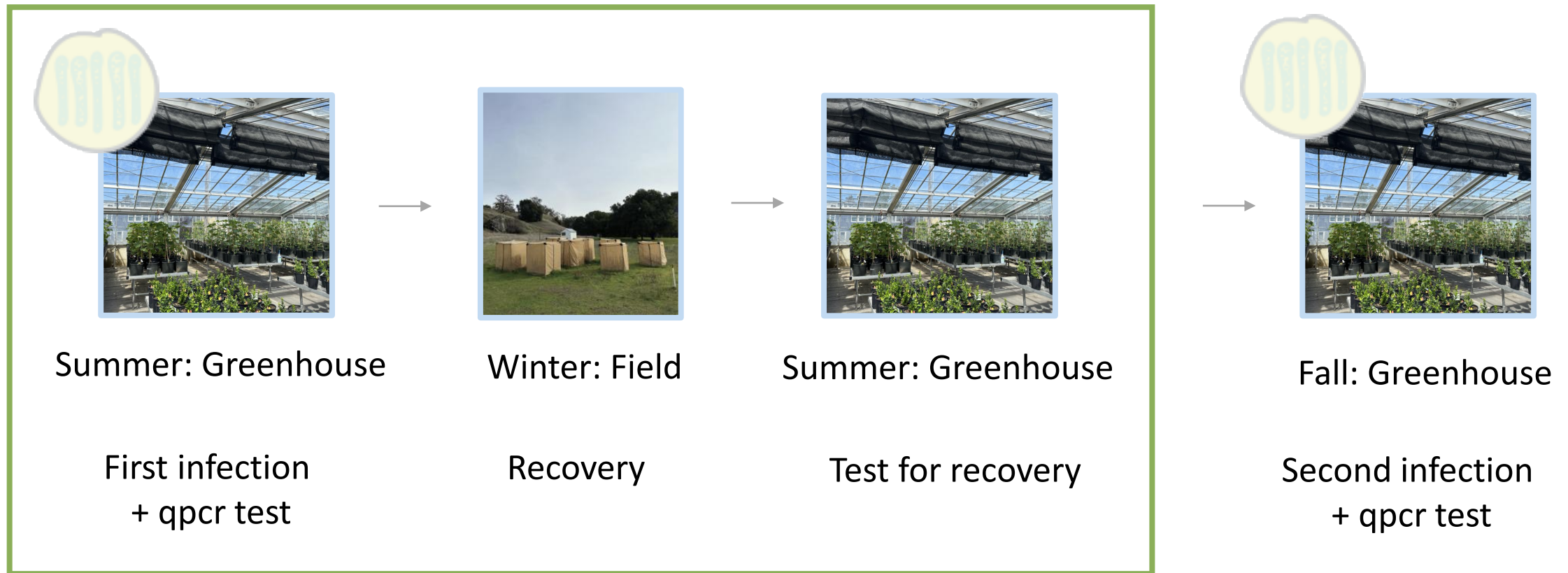
AUC-ROC: 0.87

How well the model distinguishes between the two outcomes



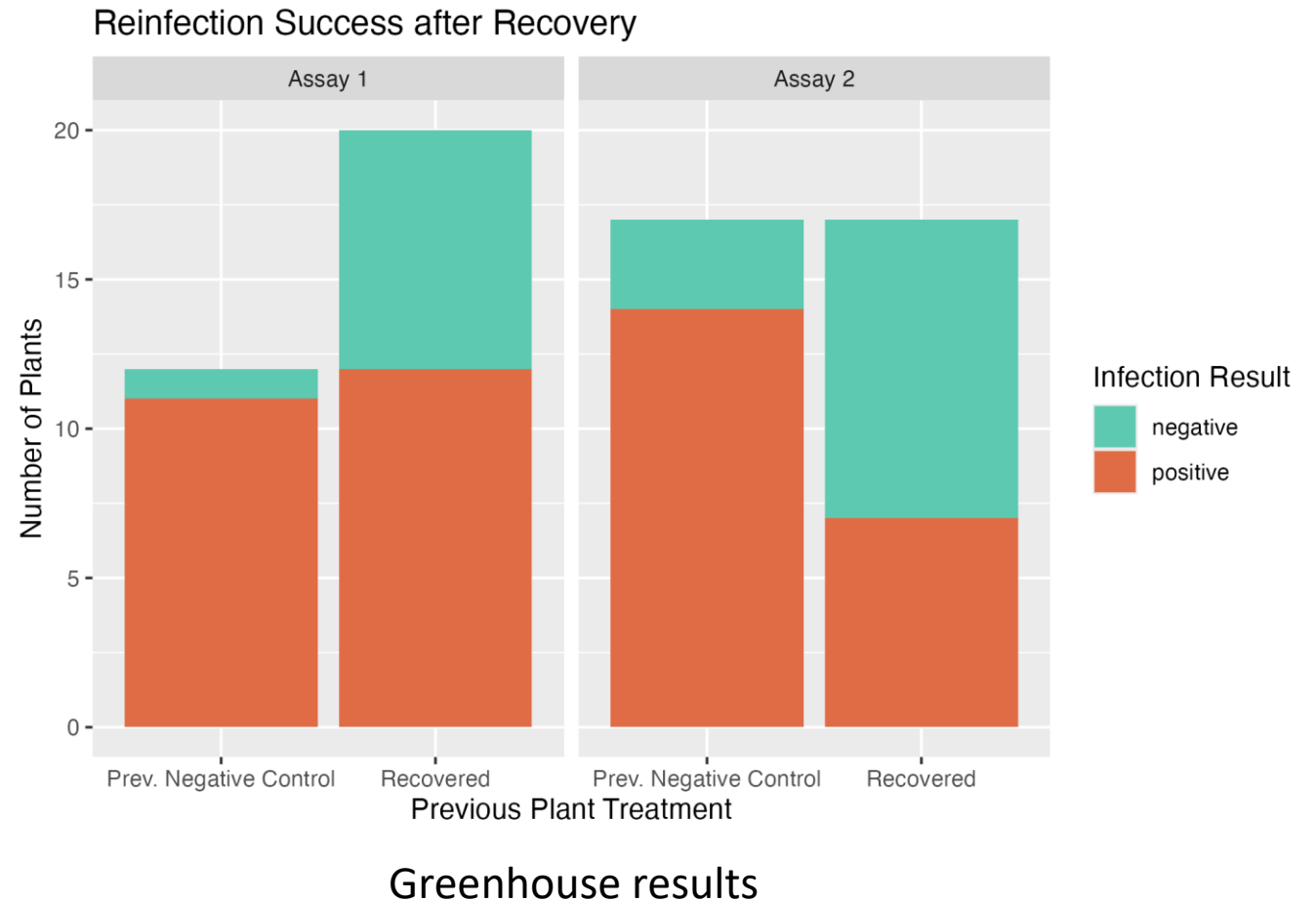
2. Reinfection after Recovery Experiment

Question: Does recovery impact a plant's likelihood of subsequent *Xf* reinfection?



2. Reinfection after Recovery Experiment

Across two **greenhouse** studies, recovered plants were **less likely to be reinfected** (one-way anova, $p = 0.0089$).



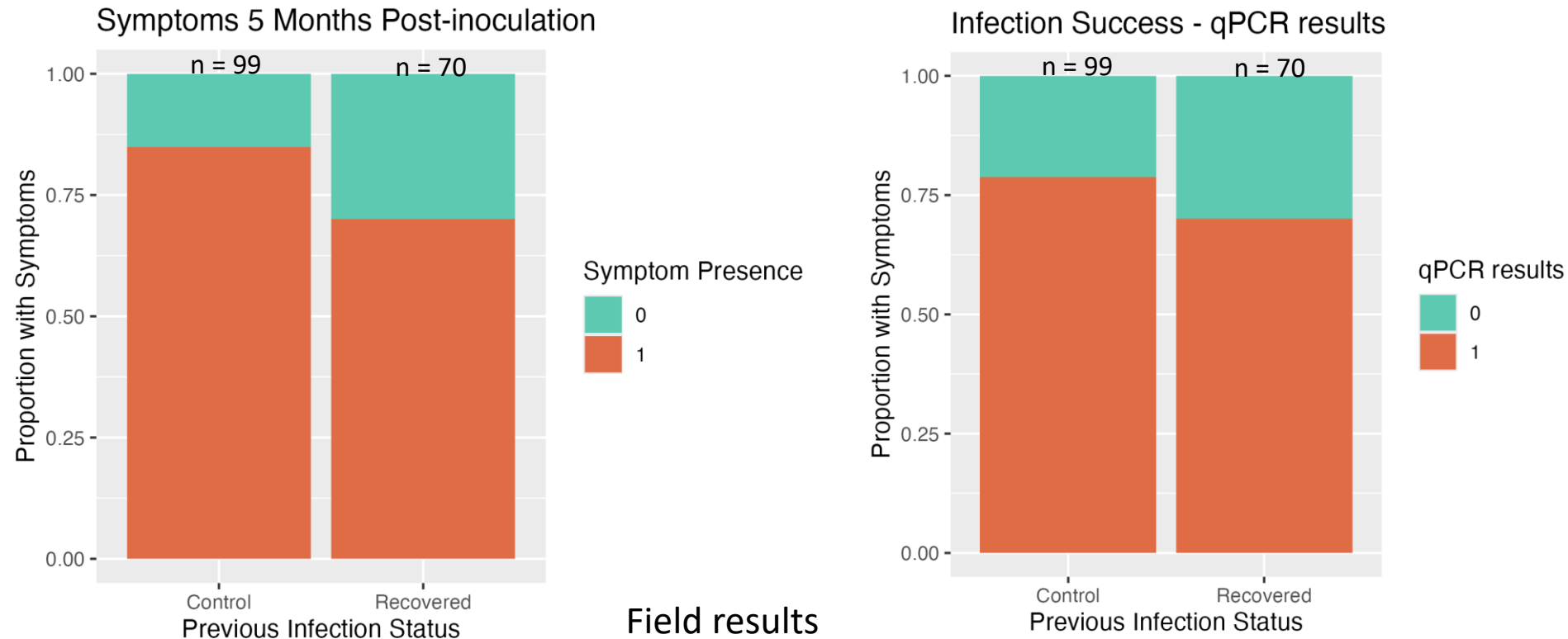
2. Reinfection after Recovery Experiment

Plants previously recovered (2021-22 and 2022-23 winters) from *Xf* infections were reinfected on 4/23/24 and sampled for qPCR in mid-September (9/13/24)

	Inoculated	Negative Control	Total
Previously recovered	72	15	87
Previous negative control	100	25	125
Total	172	40	212



2. Reinfection after Recovery Experiment



In the **field trial**, recovered plants had significantly fewer symptoms (type II anova, $p = .01$) but did not show a significant difference in inoculation success based on qPCR results (type II anova, $p = .06$).

2. Reinfection after Recovery Experiment

Takeaways

1. The effect of recovery on reinfection in the greenhouse experiment did not translate to the field
2. Recovery may have a **small impact** on plant's likelihood of reinfection
3. If reproducible, understanding the mechanisms behind these observations may be worth the effort



Conclusions

1. Cold exposure experiment

1. Plants with lower *Xf* populations were more likely to recover
2. Consistent mild cold and extreme cold events work in tandem to cause recovery in CA

2. Reinfection after recovery

Recovered plants may be slightly less likely to be reinfected, but the difference in the field is small

Ongoing work: Winter RNA-seq



Acknowledgements: M. Donegan, A. Kahn, P. Lee, K. Newman, E. Clark for assistance with field work, D. Christensen, T. Patel, M. Perez for assistance with qPCR testing, M. Daugherty for assistance with modelling

Funding: USDA NIFA Predoctoral Fellowship, UC Berkeley ESPM Continuing Fellowships, California Department of Agriculture PD/GWSS Board Award

Insights and prospects from the Apulian outbreak of *Xylella fastidiosa* subsp. *fastidiosa* in table grapes

Amoia S. S.⁽¹⁾, Boscia D.⁽¹⁾, Ragone G.⁽⁴⁾, Rossetti G.⁽²⁾, Rustioni L.⁽²⁾, Saldarelli P.⁽¹⁾, Ligorio A. M.⁽¹⁾, Dongiovanni C.⁽³⁾, Cavalieri V.⁽¹⁾, La Notte P.⁽¹⁾, Saponari M.⁽¹⁾

⁽¹⁾ Institute for Sustainable Plant Protection (IPSP)—National Research Council;

⁽²⁾ University of Salento, Centro Ecotekne;

⁽³⁾ Centro di Ricerca, Sperimentazione e Formazione in Agricoltura Basile Caramia;

⁽⁴⁾ Regional Plant Protection Service-Apulia Region.

Emergence of *Xylella fastidiosa* subsp. *fastidiosa* ST1 in Apulia



Xylella fastidiosa subsp. *fastidiosa* ST1 (Xff)
outbreak detected in February 2024



The etiological agent of **Pierce's disease**



Confirmed **hosts** in the Apulia region:

- *Vitis* spp.
- *Polygala myrtifolia*
- *Prunus dulcis*
- *Prunus avium*
- *Prunus armeniaca*



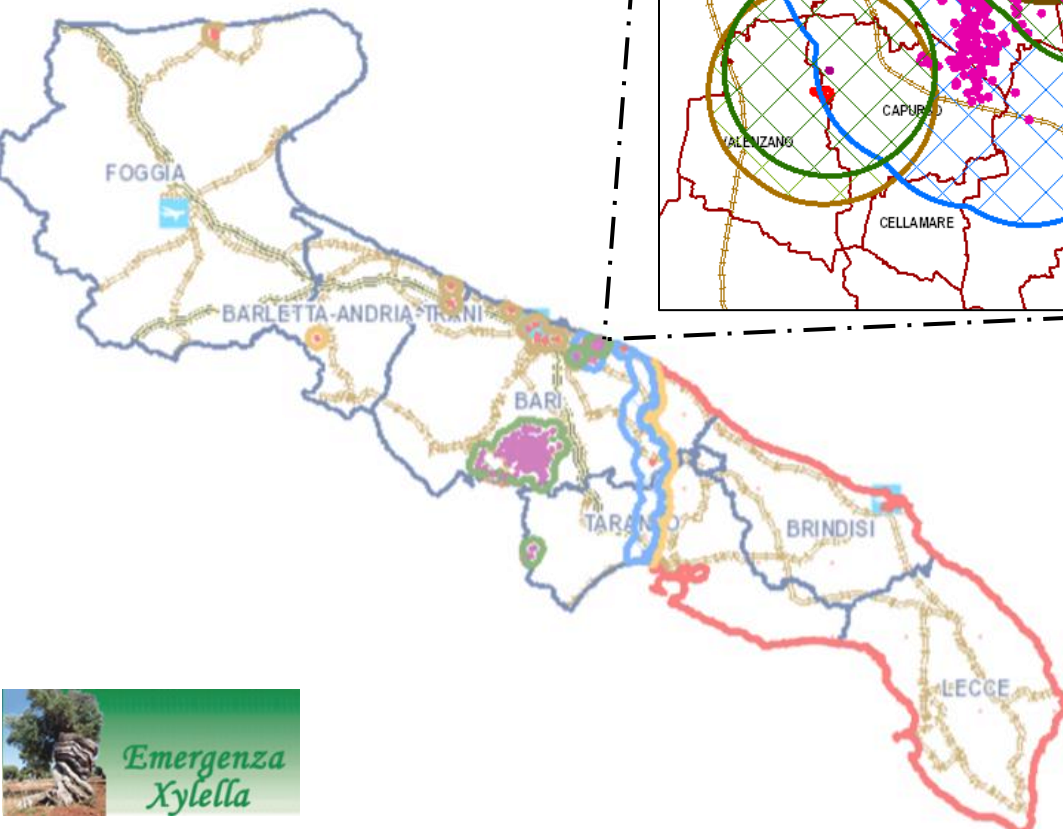
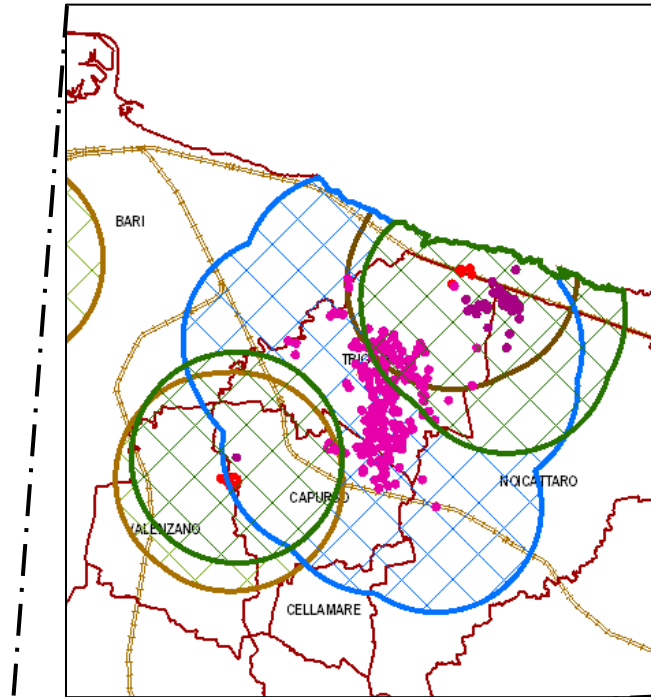
Identified in grape plants located in close proximity
to the main **table grape production district** in Apulia



Potential **threat** to the European **grapevine industry**



**Field surveys and experimental
investigations are necessary.**





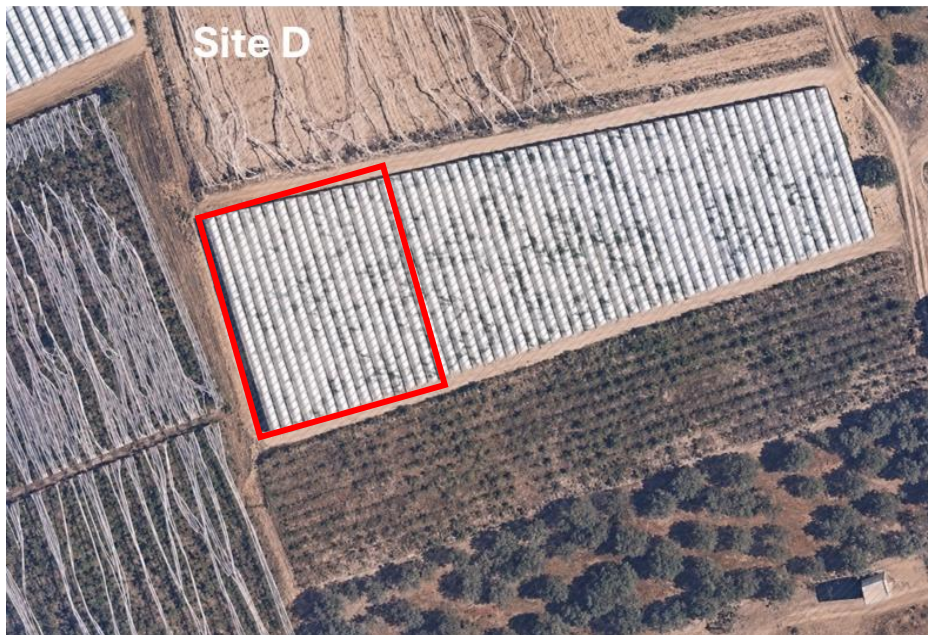
Objectives of the study

- ☐ To assess the impact of *Xff* ST1 in naturally infected vineyards in the Apulia region.
 - ☐ To evaluate the relationship between infection, symptom development and vine decline under field conditions.
 - ☐ To compare the response of different grapevine genotypes following artificial inoculation experiments.
 - ☐ To gather preliminary evidence on vector acquisition and transmission on grape plants.
- 

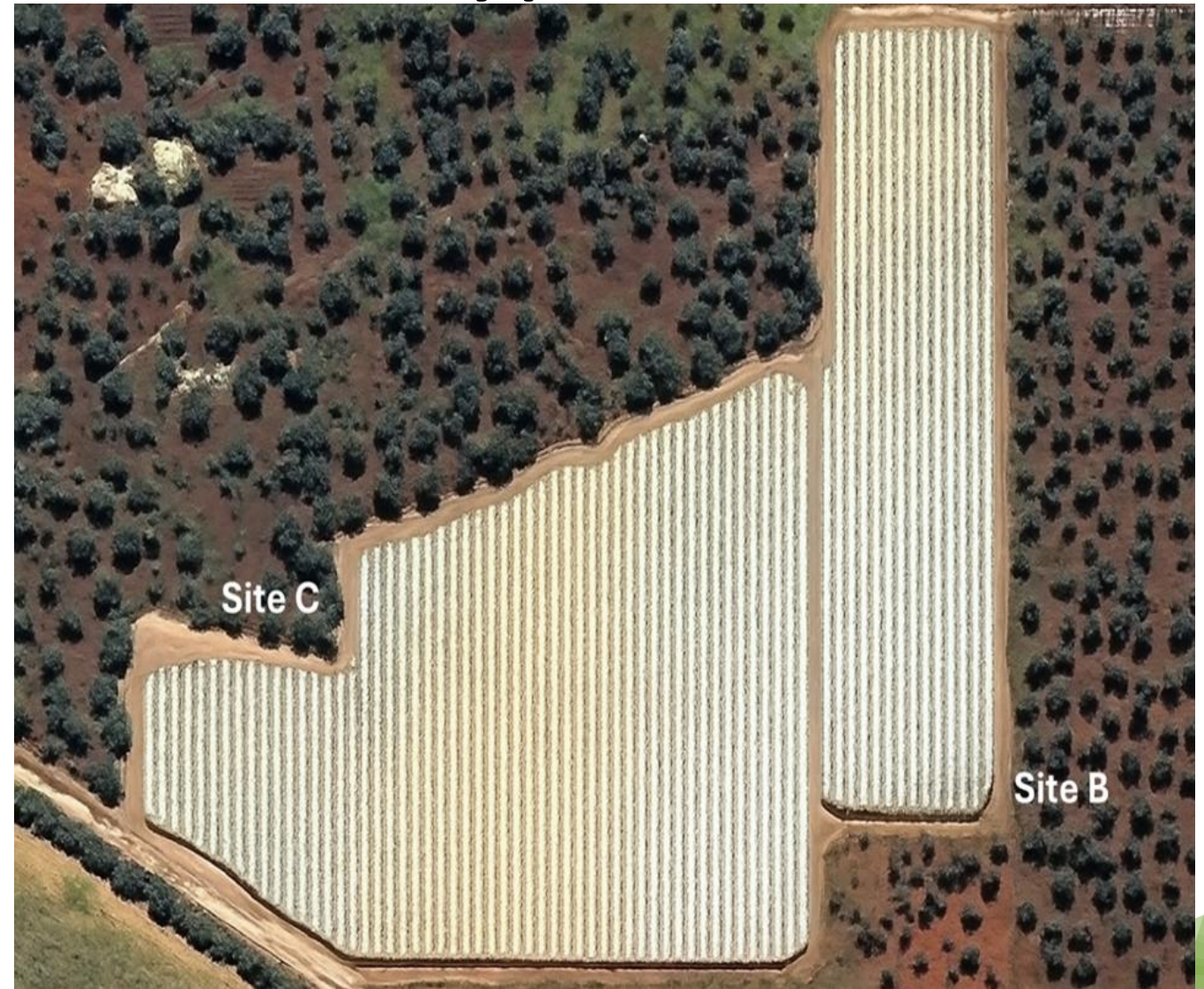
Overview of the field survey plots



**18-years-old;
Mixed Falanghina & Montepulciano**



**4-years-old;
Melanie™**



**4-years-old;
Site B: Superior Seedless® Sugraone
Site C: ARRA Sugar Drop™ (or ARRA 30)**

Representative symptoms observed during field surveys



Leaf scorch



Matchstick petioles



Shriveled berries



Green islands or uneven cane maturation



Shoot tip or branch desiccation

Distribution of disease severity classes across vineyards

Disease classes:

0 = Asymptomatic

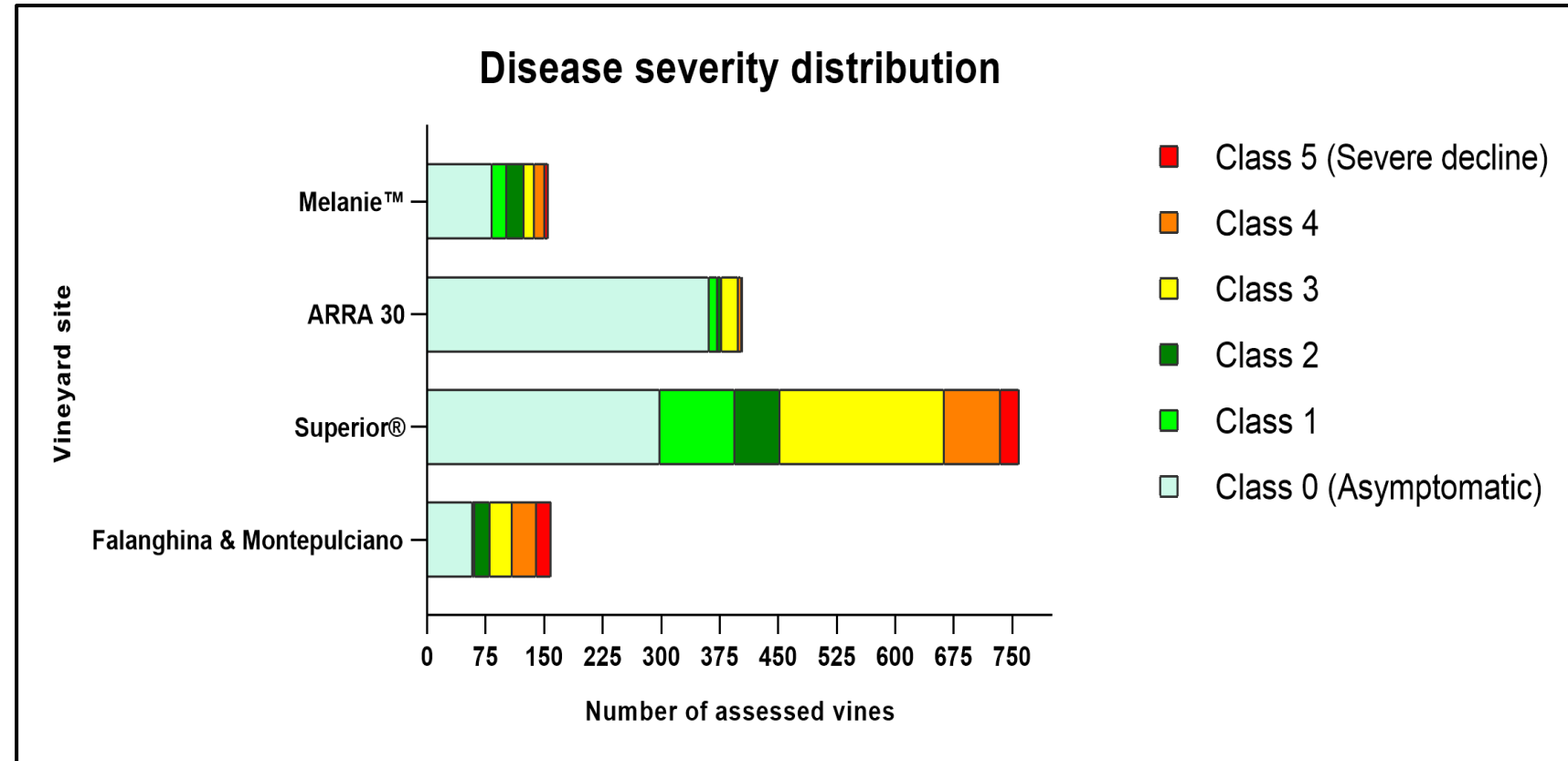
1 = Green islands and/or mild leaf scorching.

2 = Partial shoot tip desiccation.

3 = Complete desiccation of shoots scattered around the canopy.

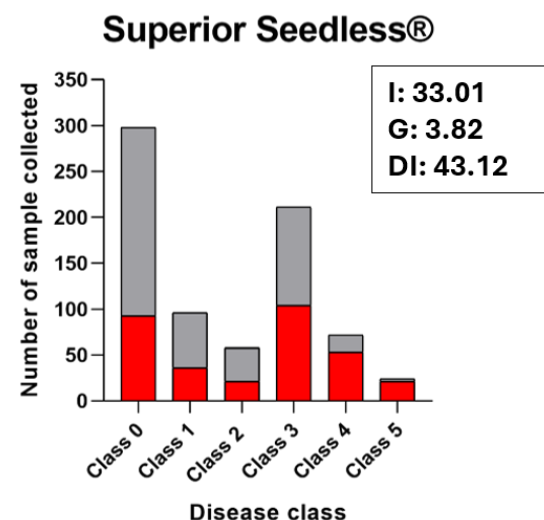
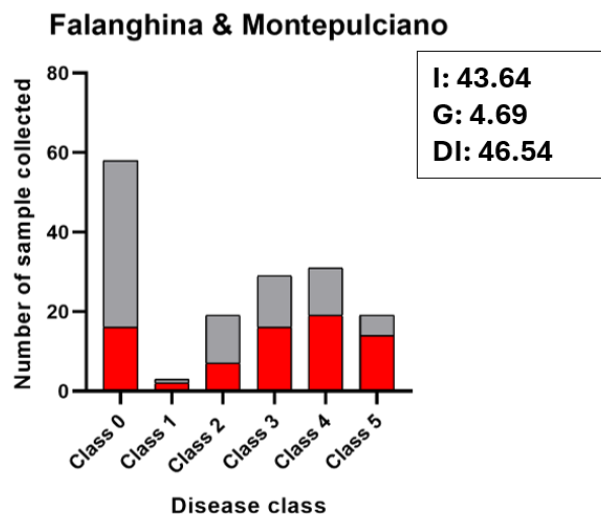
4 = Extensive branch dieback and/or shrivelled berries.

5 = Severe decline or plant fully collapsed.



Overall, **1477** grape plants were assessed

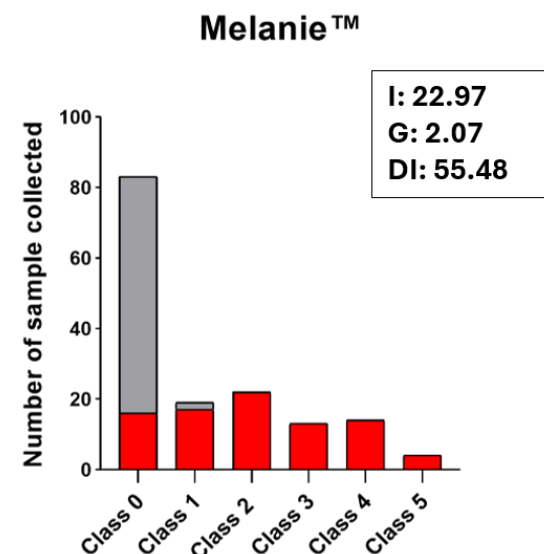
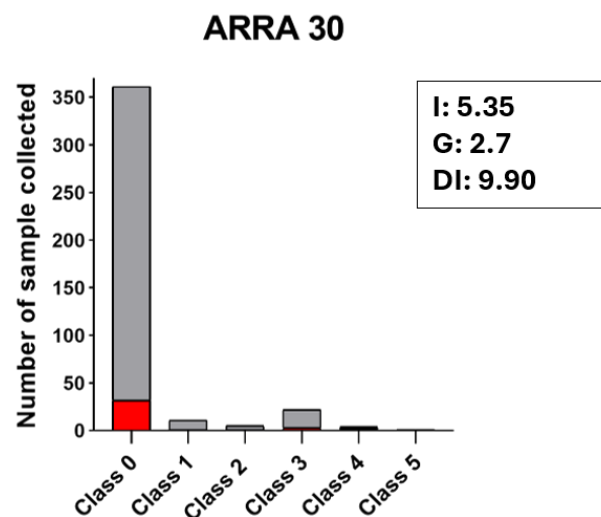
Relationship between disease severity classes and *Xff* detection



Legend:

- Xff-negative
- Xff-positive

I: McKinney Index
G: Severity Index
DI: Disease Index



- **Superior Seedless®** exhibited the highest number of positive plants across different severity classes;
- **Arra 30** showed a predominance of asymptomatic and *Xff*-negative vines;
- In **Melanie™** vineyard, there is the strongest association between symptomatic grapes and the presence of the bacterium.

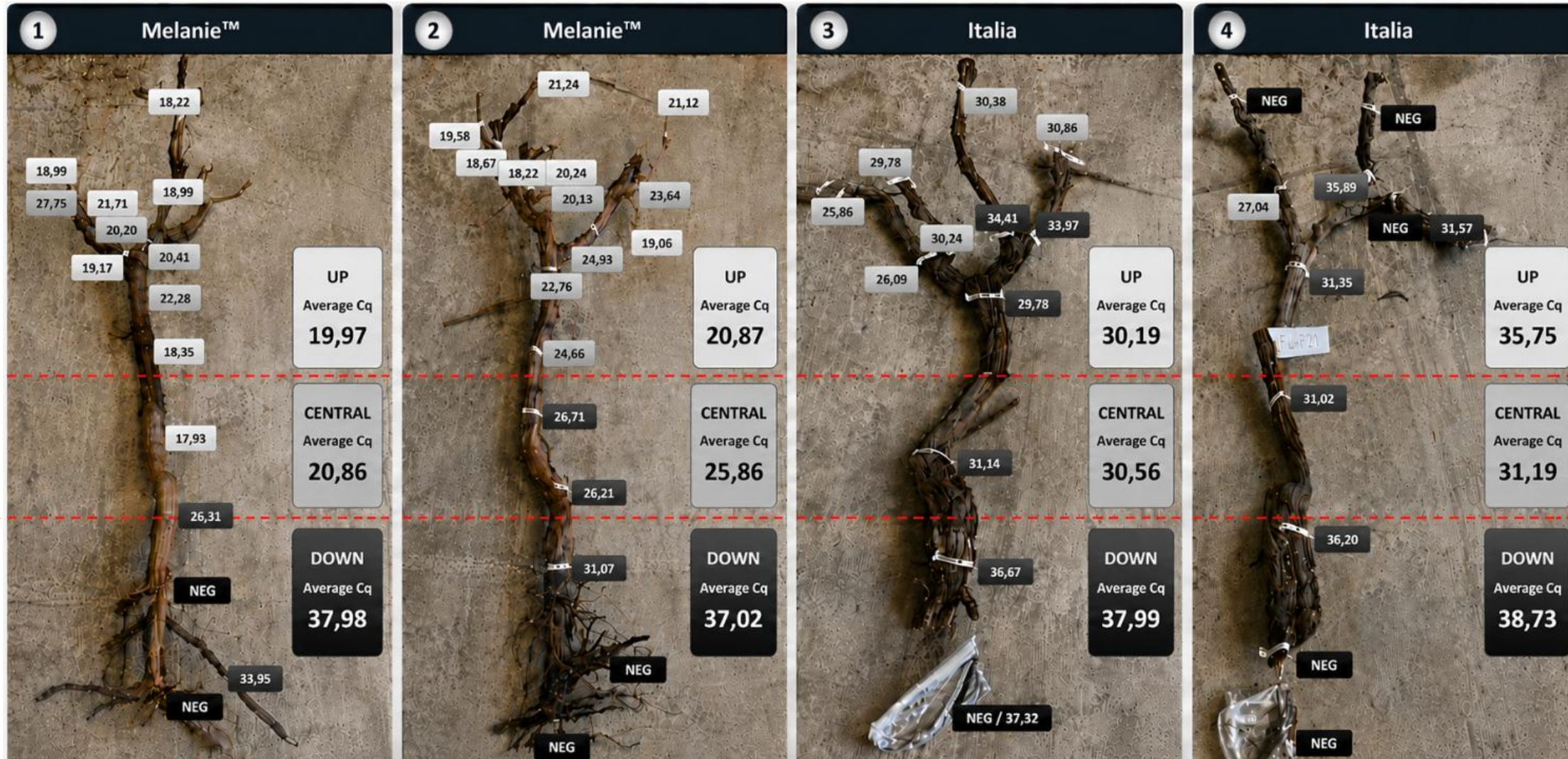
Systemic distribution of *Xff* in naturally infected grapevines

Legend:

Higher Cq values or negative:
Low bacterial load or absent

Lower Cq values:
High bacterial load

GRAFT UNION POINT ►



Key finding

All tissues below the graft union, including roots, tested negative for *Xff*

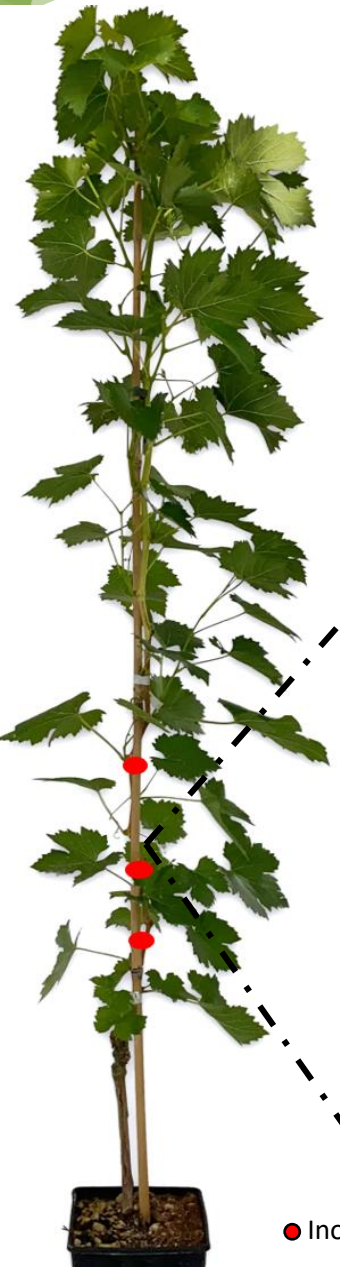
Experimental inoculation of grapevines under greenhouse conditions

Monitoring at 3 and 6 months post-inoculation

➤ qPCR:

- Leaves at 15 cm above the uppermost inoculation point (3 mpi);
- Tip shoot tissues (6 mpi);

➤ Symptom assessment: LS-LL (Leaf Scorch-Leaf Loss) index (Huerta-Acosta et al., 2023)



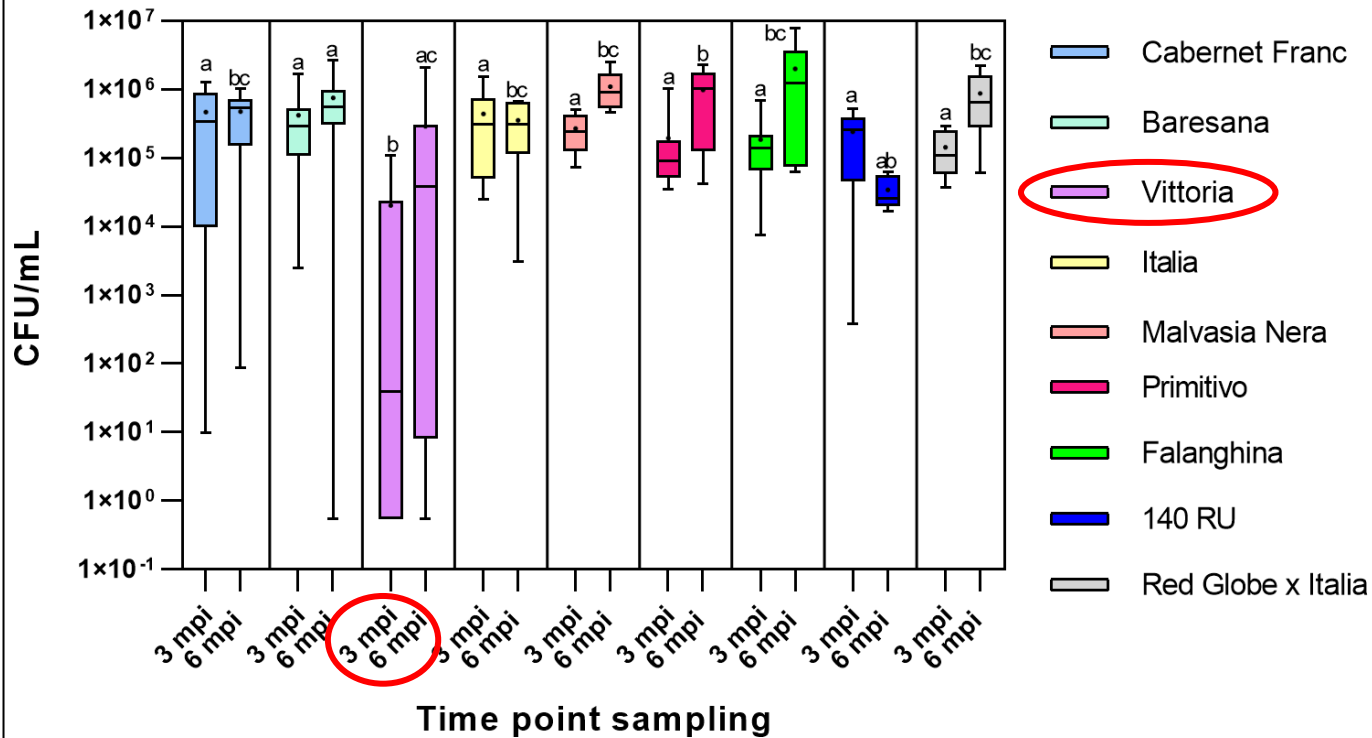
● Inoculation site

Grape species	Cultivar or genotype name	End use	Nr. of inoculated plants
<i>Vitis vinifera</i>	Baresana	Table grape	10 XFF + 3HC
<i>V. vinifera</i>	Italia	Table grape	10 XFF + 3HC
<i>V. vinifera</i>	Malvasia Nera	Wine grape	10 XFF+ 3HC
<i>V. vinifera</i>	Cabernet Franc	Wine grape	10 XFF + 3HC
<i>V. vinifera</i>	Vittoria	Table grape	10 XFF + 3HC
<i>V. vinifera</i>	Primitivo	Wine grape	10 XFF + 3HC
<i>V. vinifera</i>	Falanghina	Wine grape	10 XFF + 3HC
<i>V. vinifera</i>	Red Globe x Italia	Cross	10 XFF + 3HC
<i>V. vinifera</i>	140 RU	Rootstock	10 XFF + 3HC
<i>V. arizonica</i>	Genotype B	American wild grape	2 XFF + 1 HC
<i>V. arizonica</i>	Genotype C	American wild grape	2 XFF + 2 HC
<i>V. arizonica</i>	Genotype D	American wild grape	3 XFF + 2 HC
<i>V. arizonica</i>	Genotype E	American wild grape	3 XFF + 2 HC
<i>V. arizonica</i>	Genotype F	American wild grape	1 XFF + 1 HC

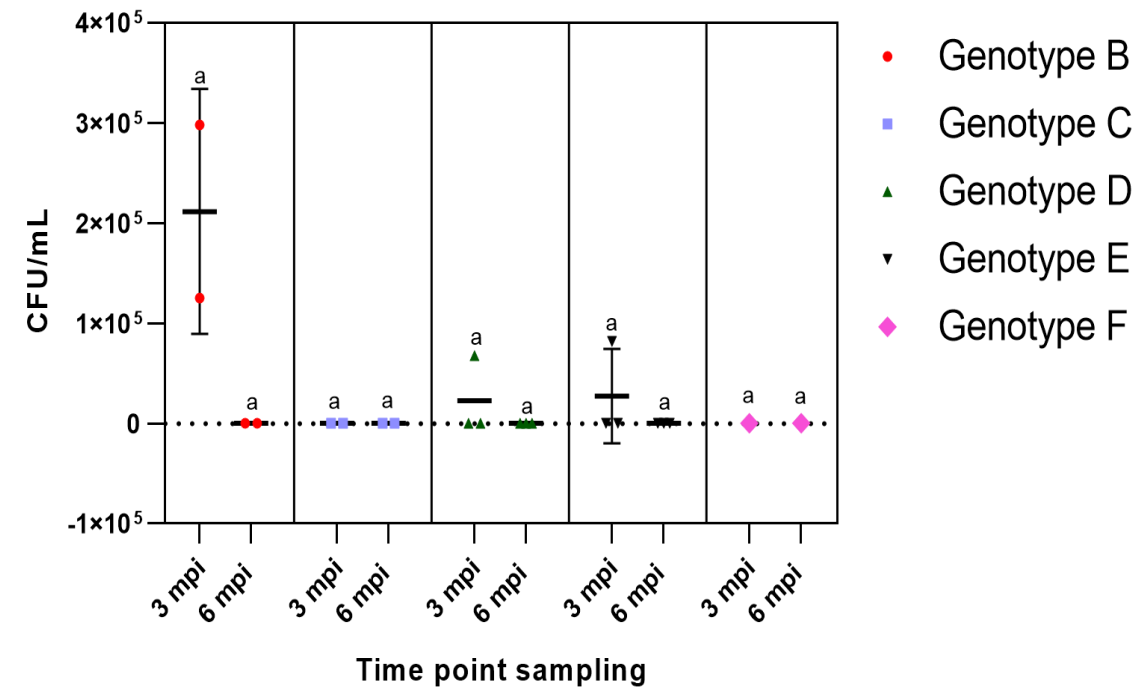
N. B. Genotypes B–F were clonally propagated from *V. arizonica* accessions maintained at the University of Milan and originating from **open-pollinated seed material** obtained through a historical germplasm exchange with a Californian ampelographic collection.

Differential *Xff* colonization among grape species

Bacterial quantification in *V. vinifera* stem



Bacterial quantification in *V. arizonica*-derived stem



Key finding

Among *V. vinifera* varieties, bacterial loads remained consistently high, generally ranging between 10^4 and 10^6 CFU mL⁻¹. In contrast, the *V. arizonica*-derived genotypes showed markedly lower bacterial populations, even if a considerable variability among them was observed.

Differential symptom expression among grape genotypes

Vitis vinifera varieties



PRIMITIVO



RED GLOBE X ITALIA



ITALIA



MALVASIA NERA



VITTORIA

Vitis arizonica geotypes



GENOTYPE B



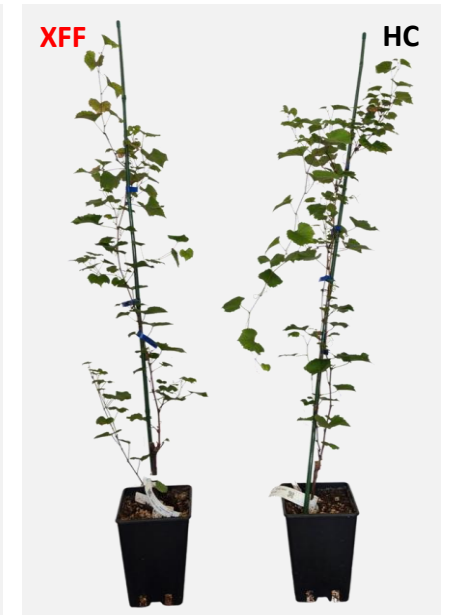
GENOTYPE C



GENOTYPE D

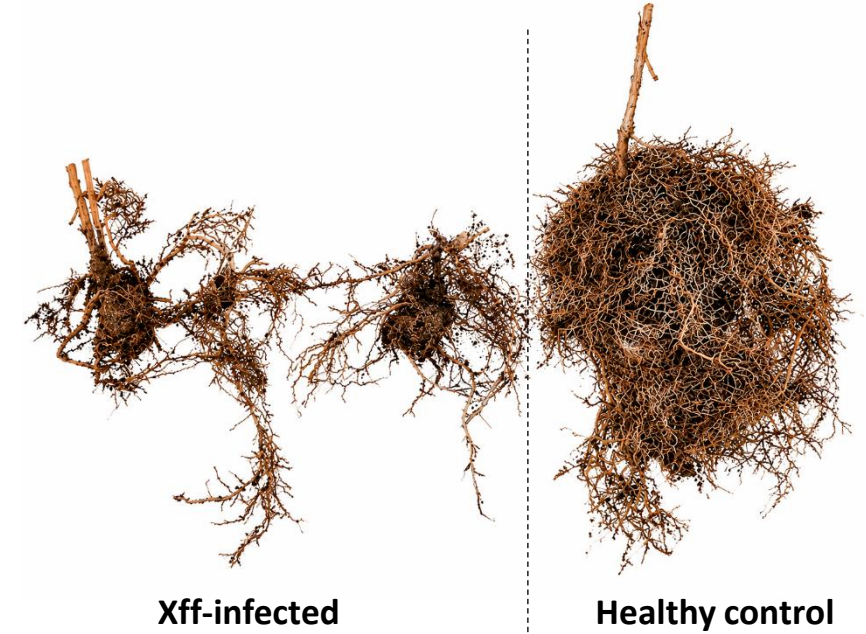
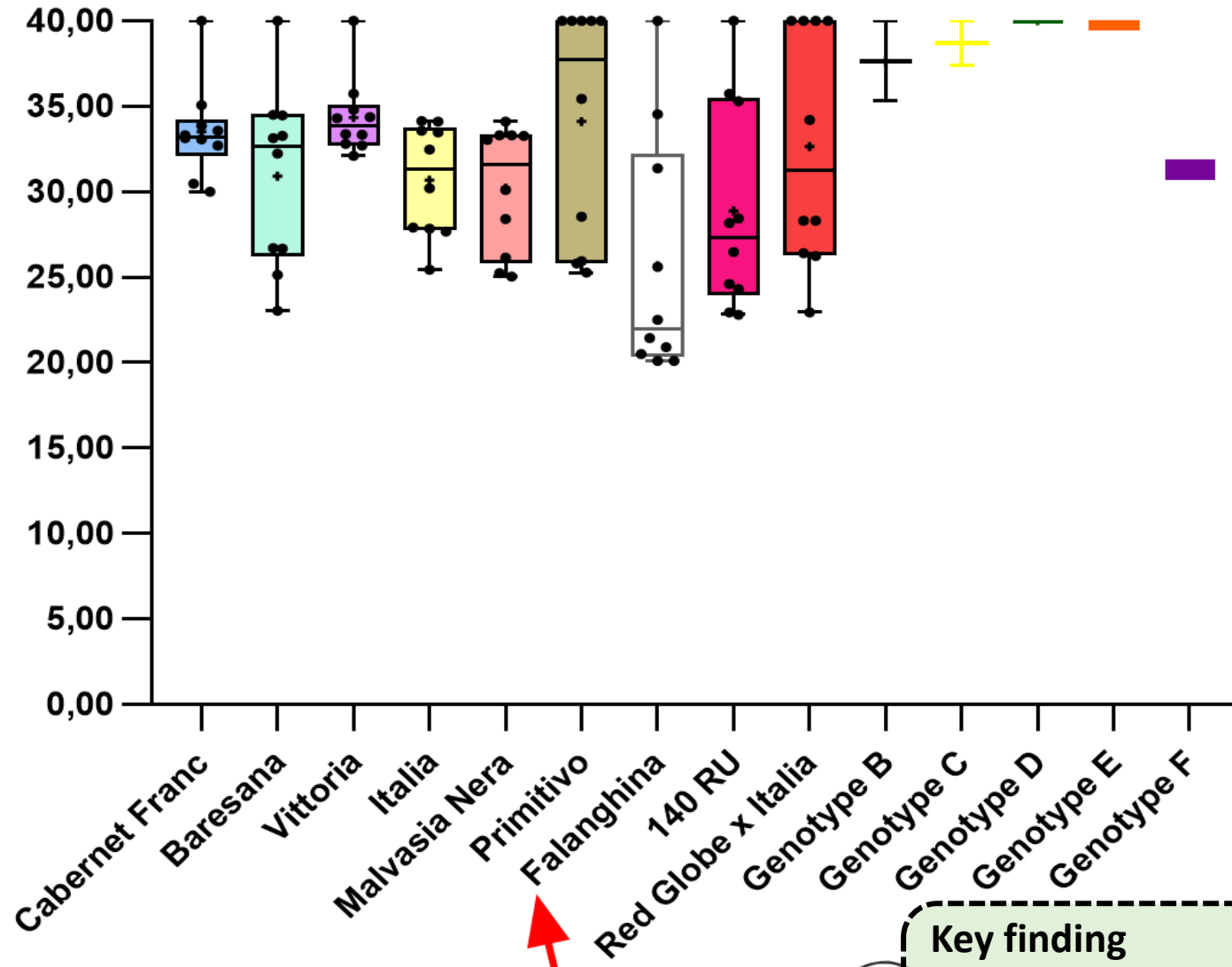


GENOTYPE E



GENOTYPE F

Xff detection in root system of cultivated and wild grapevines



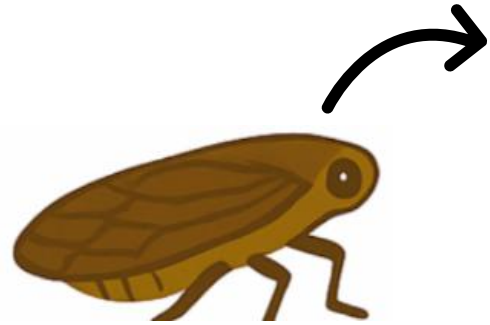
qPCR interpretation:

Low Cq = High bacterial presence
High Cq = Low bacterial presence

Key finding

V. arizonica genotypes showed markedly reduced root colonization compared with *V. vinifera* cultivars. In addition, *Xff* infection seems to be associated with a substantial reduction of root system size and biomass.

Preliminary vector acquisition and transmission experiments performed directly in the field in early autumn



Xf-free adults of
Philaenus spumarius

Acquisition access period (AAP)
96 hours
on naturally-infected
grape and almond shoots



Inoculation access period (IAP)
6 days on healthy
grape*

**Xylella fastidiosa
detection by qPCR**



% positive
specimens:
28.26



% positive
grapes:
24.25

Recipient plants were
tested 3 and 6 months
post IAP

* Survival percentage of *P. spumarius* after IAP close to 50%.



Concluding remarks on the ST1-outbreak in Apulia

- Environmental conditions in the outbreak area suggest that ***Xff* ST1 is able to induce typical Pierce's disease symptoms, including vine dieback and shriveling of the clusters.**
 - Most *V. vinifera* cultivars supported high bacterial populations, whereas, although with a certain degree of variability, *V. arizonica*-derived genotypes showed restricted stem and root colonization.
 - Systemic infections in *V. vinifera* cultivars developed pronounced leaf symptoms and stem desiccation, along with a great reduction of root biomass and development.
 - The successful transmission by *Philaenus spumarius* occurred under field conditions confirms its potential epidemiological role.
 - Testing wild grapevine germplasm confirmed that it represents a source of traits for Pierce's disease resistance breeding programs.
- 



Servizio Fitosanitario Regione Puglia



Consiglio Nazionale delle Ricerche
Istituto per la Protezione Sostenibile delle Piante



UNIVERSITÀ
DEL SALENTO



Centro di Ricerca
Sperimentazione e Formazione
in Agricoltura "BASILE CARAMIA"

***Thanks for your
attention***

serafinaserena.amoia@cnr.it





*Xylella
fastidiosa*

5th European conference

Bari, Italy | 22-26 June 2026

Prevalence and diversity of *Xylella fastidiosa* subsp. *multiplex* in the Eastern USA

Jingjing Yang, Dr. rer. nat.
June 25th 2026



REGIONE PUGLIA



Backgrounds

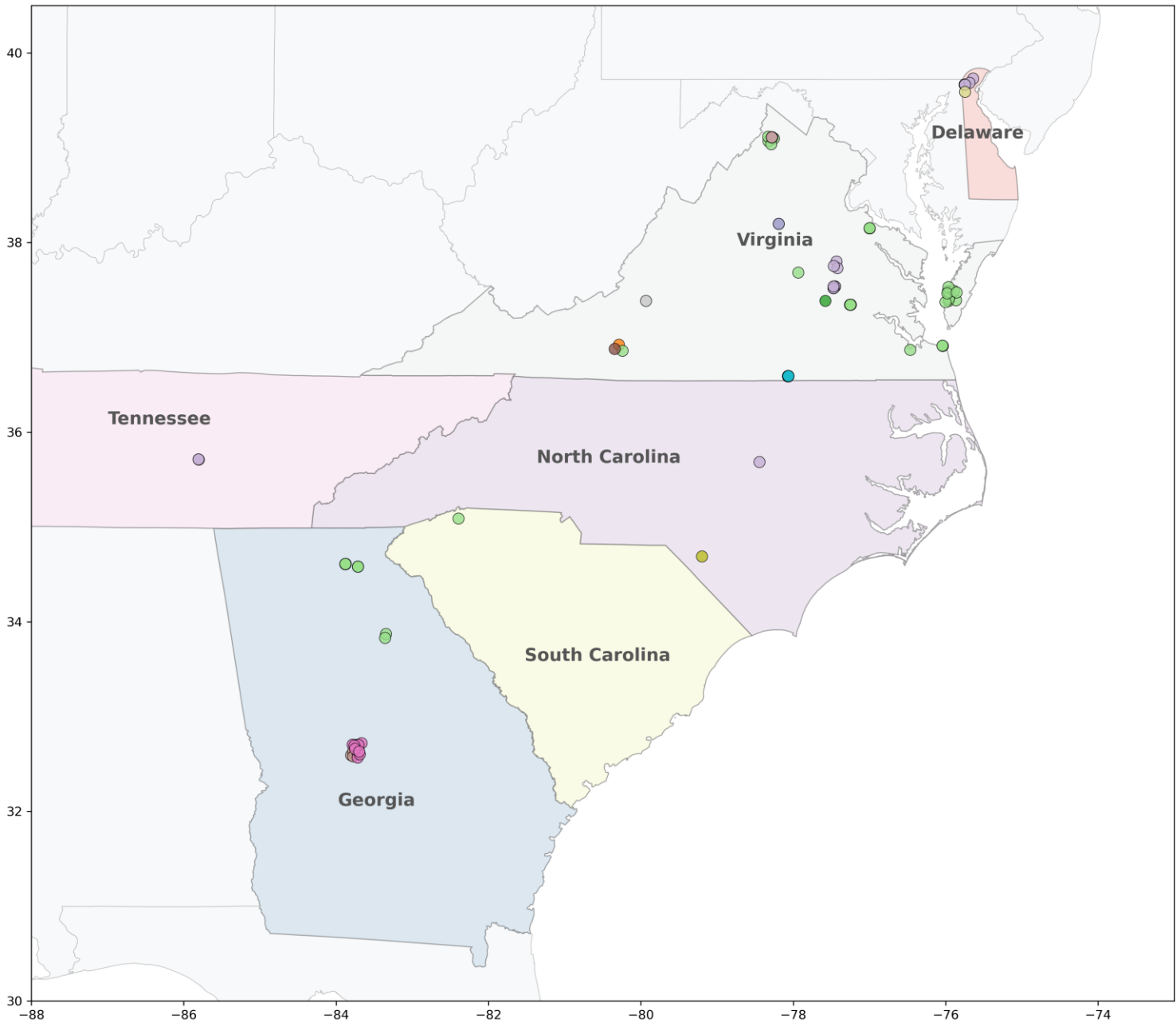
Xylella fastidiosa subsp. *multiplex* (Xfm)

- Considered native to the eastern U.S.
- Cold-tolerance and broad host range
- The prevalence and diversity of native population remains poorly characterized

Objectives:

- Survey plant species across the eastern U.S.
 - Characterize the genetic diversity and evolutionary patterns
 - Improve risk assessment
- 

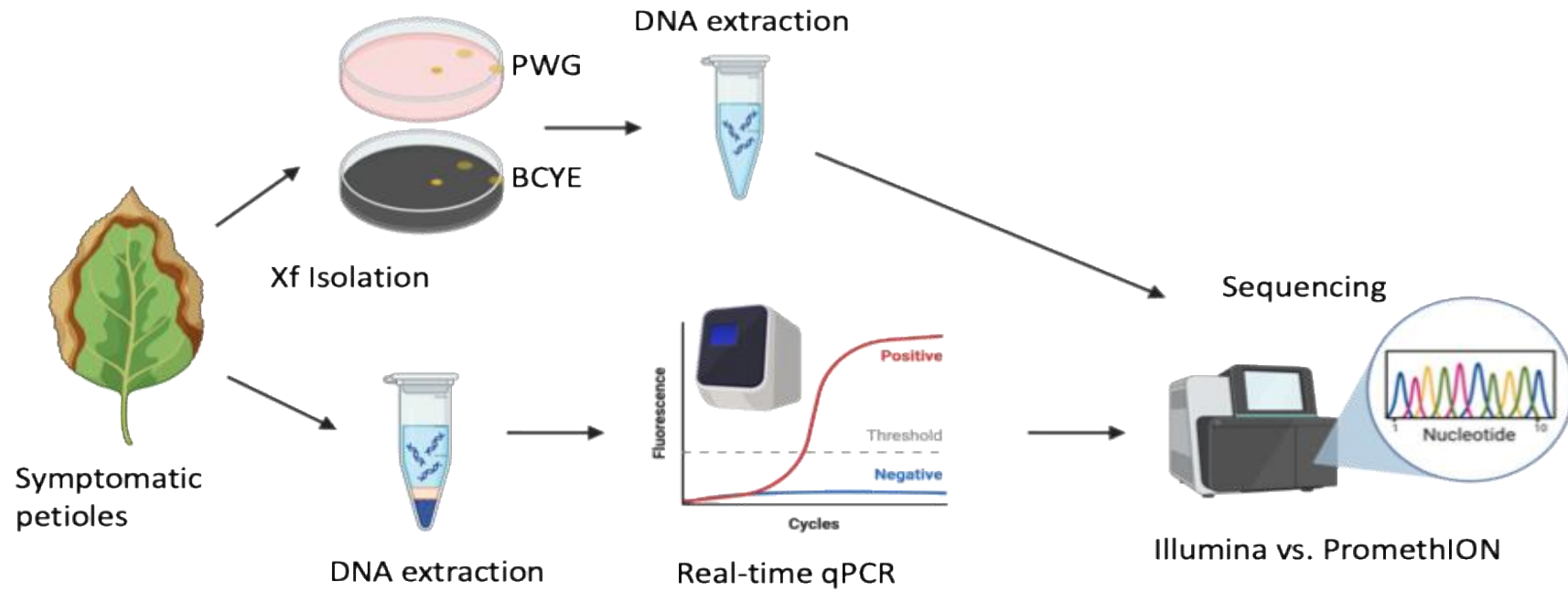
Sampling Locations in Eastern US (2025)



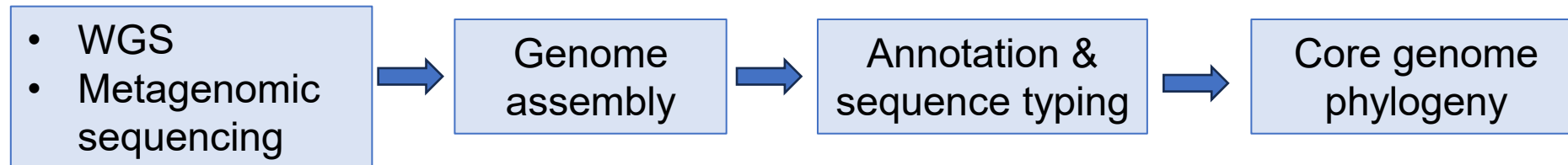
Sampling in 2025

- 6 states
- 122 samples in total
 - 81 in Virginia
 - 41 from others
 - ~17 host species
- ~12 wild plant

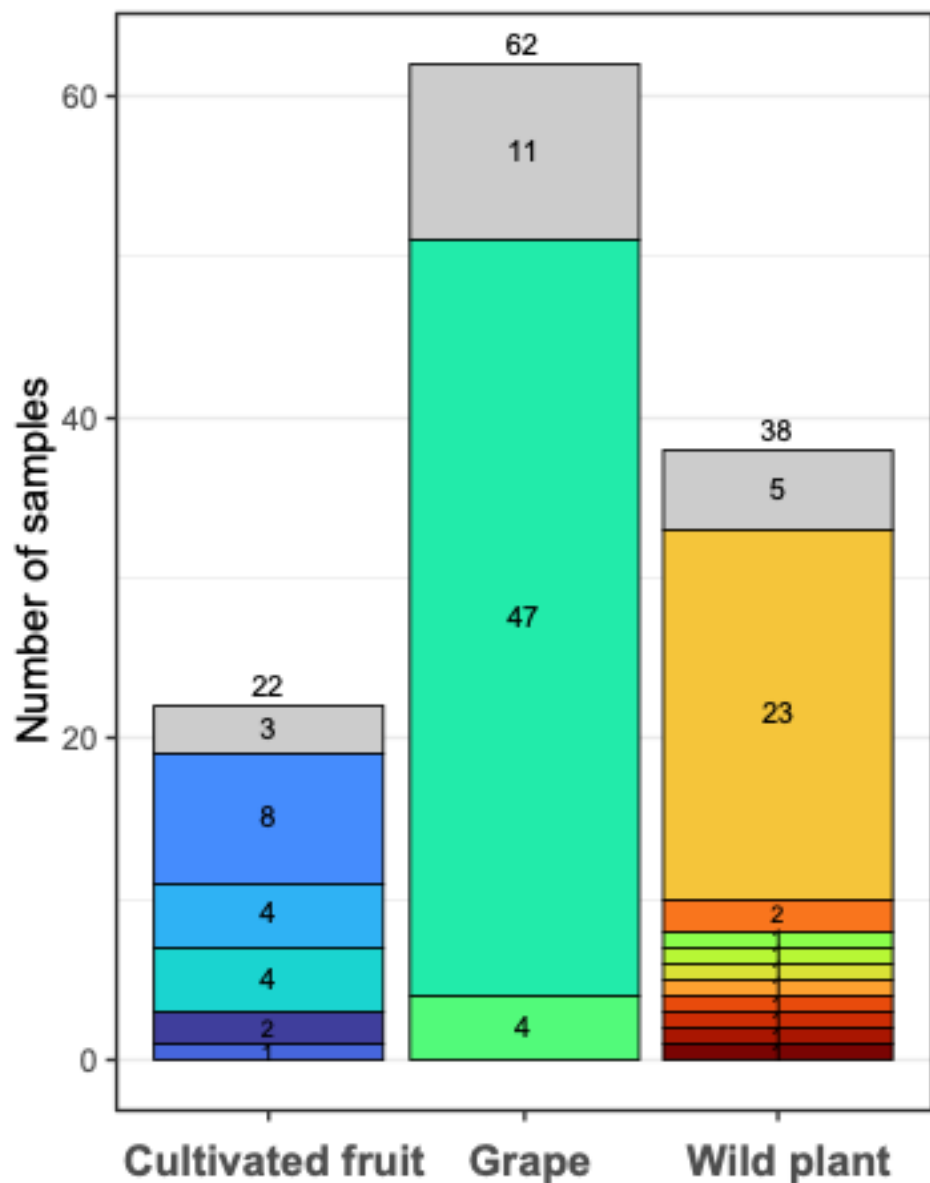
Methods



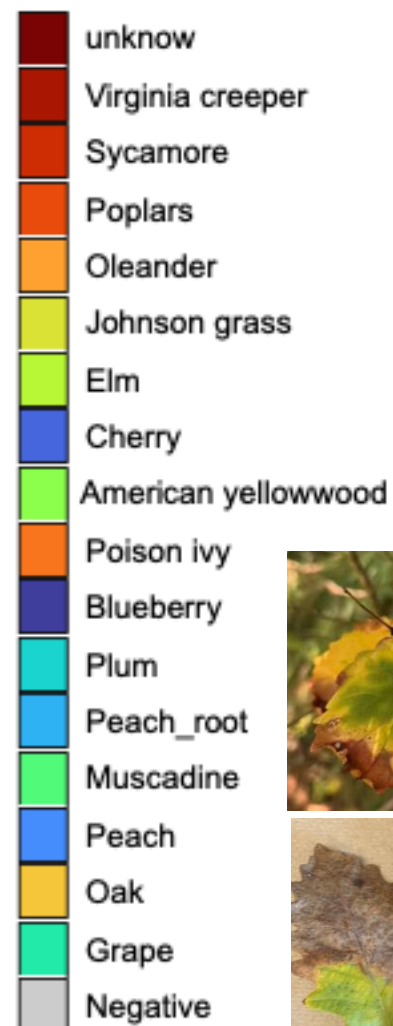
Bioinformatic workflow



High prevalence of *X. fastidiosa* across surveyed hosts



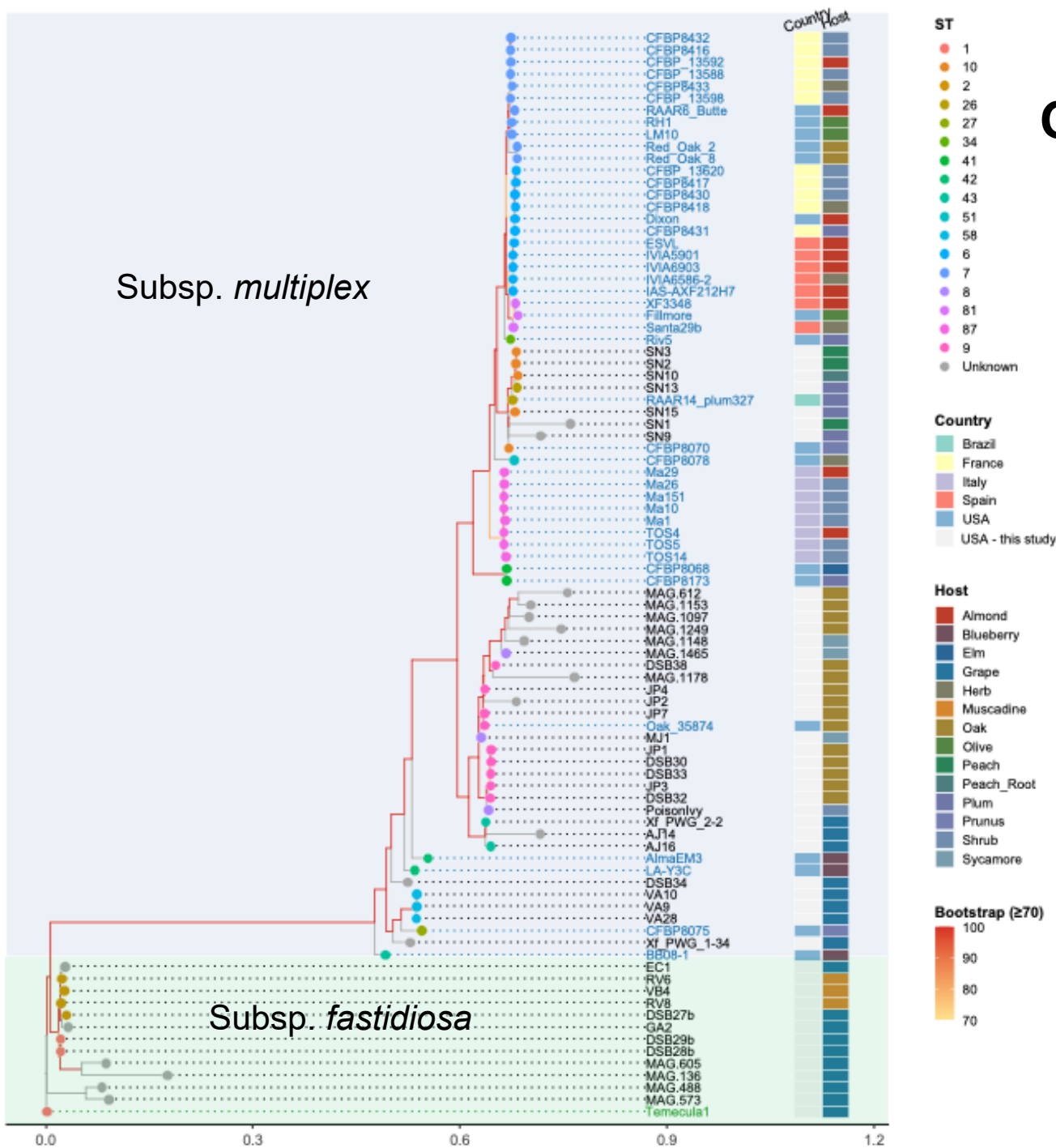
Plant



84% - positive (Cq < 35; n = 103)

- 86% - cultivated fruits (n=19; peach, plum, blueberry and cherry)
- 75.8% grapevines (n=47), 6.5% wild grape/muscadine (n=4)
- **87% - wild plants** (n=33; woody and shrubs, 10 species)





Overall core genome phylogeny (n=90)

- 45 new genomes (40 MAGs, 5 isolates)

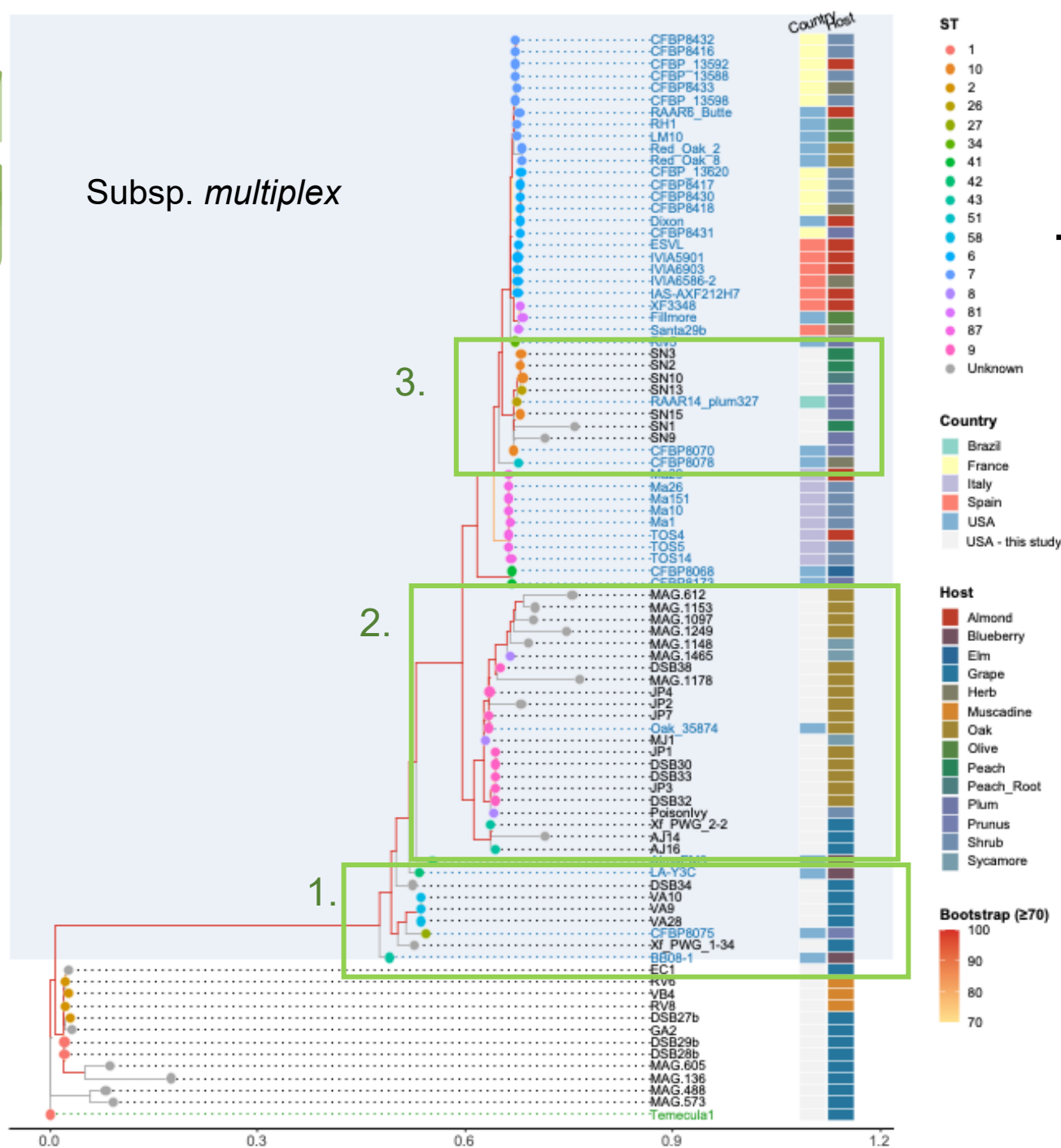
Xf subsp. *fastidiosa* (n=12)

- All grape-associated hosts
- 9 grapevines (ST1)
- 3 wild muscadines (ST2)

Xf subsp. *multiplex* (n=33)

- greater phylogenetic diversity
- broader host associations

Subsp. *multiplex*

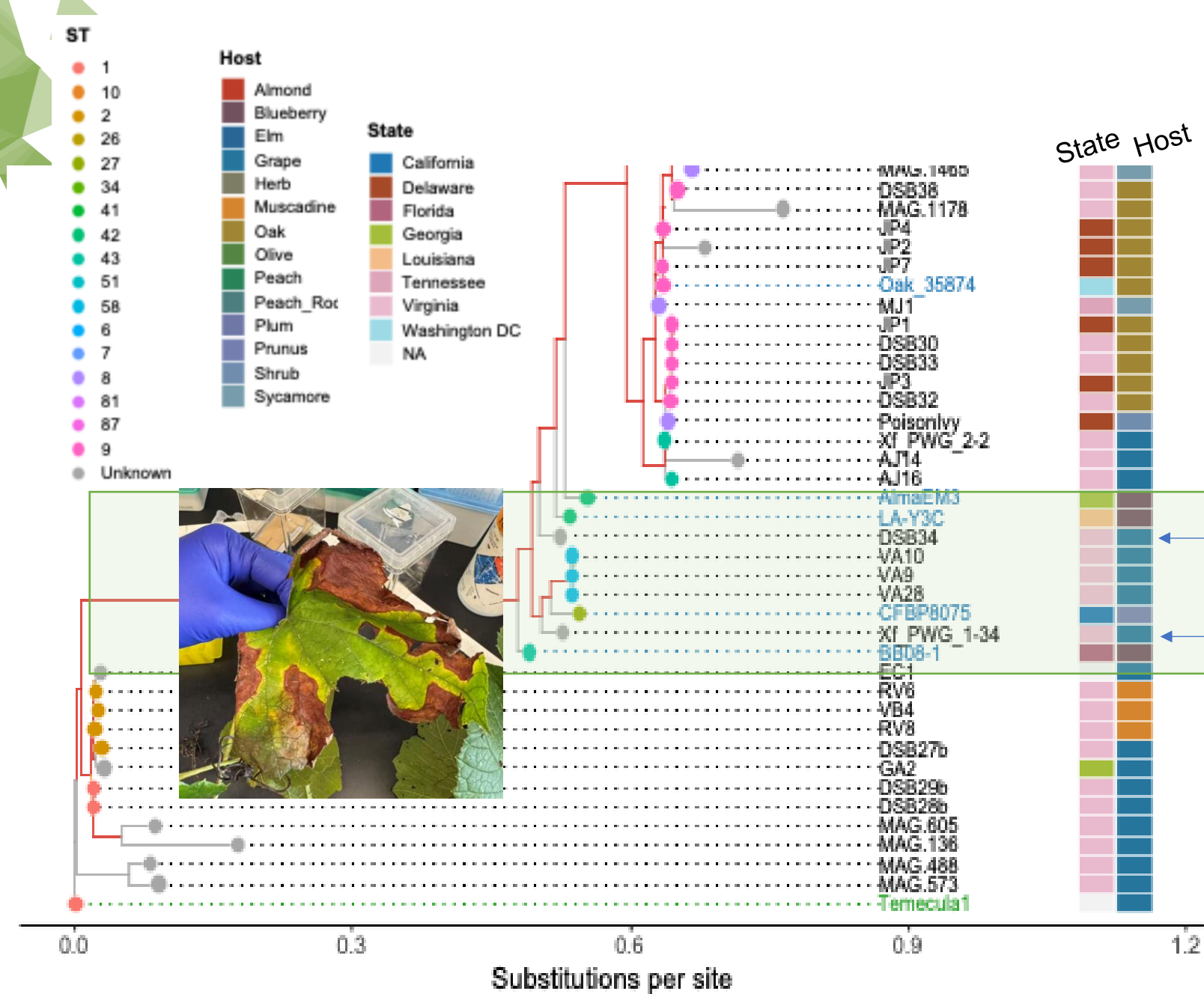


Three major host-associated lineages of Xfm

1. Blueberry lineages (n=5)

2. Oak lineage (n=21)

3. Peach/plum lineage (n=7)



1. Blueberry lineages

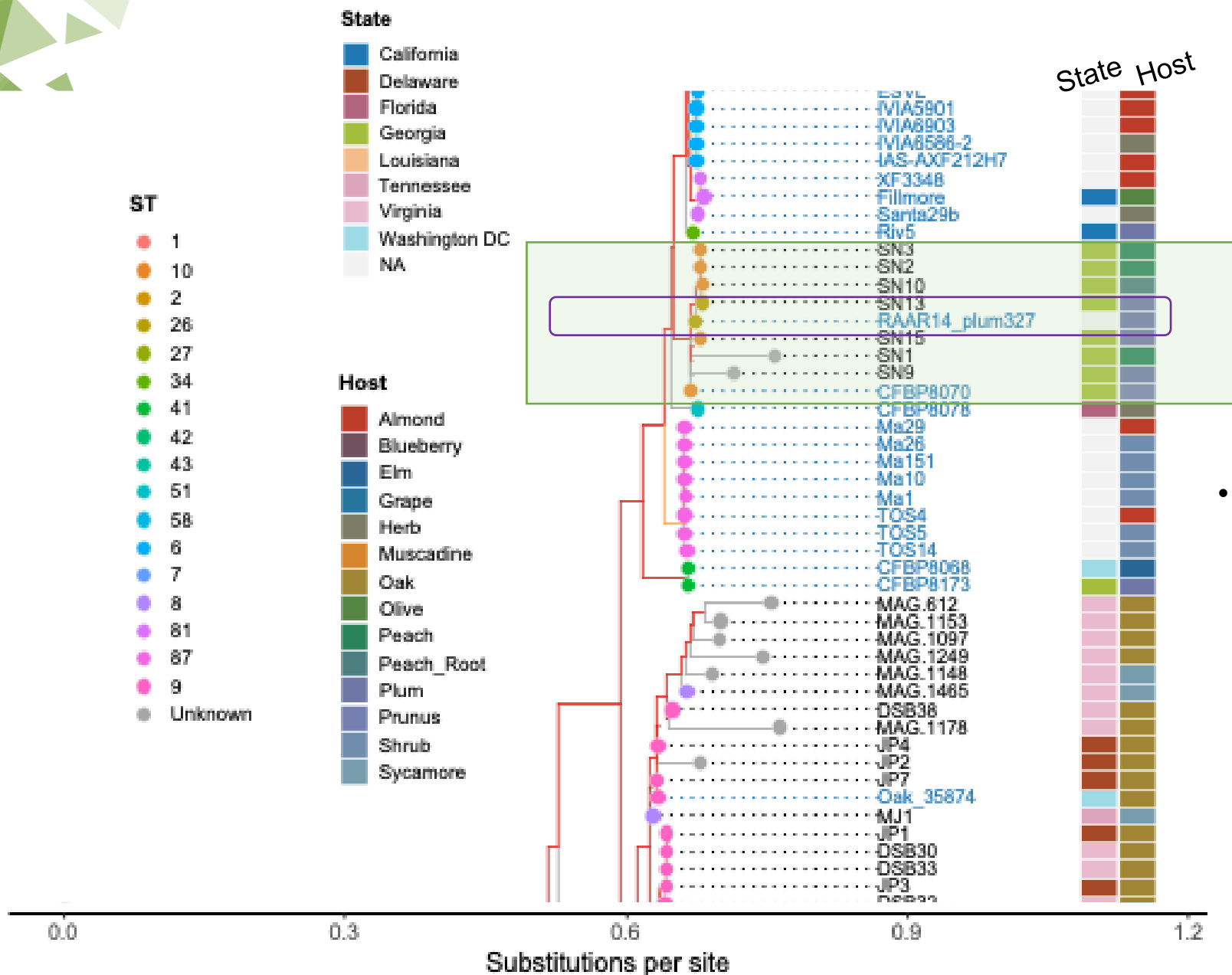
- 4 published genomes (ST42, ST43 & ST27)
- Phylogenetically dispersed
- 5 new genomes (ST58; 4 isolates) from grapes further expanded the diversity

1 wild grape (DSB34)

1 pure culture
(Xf_PWG_1_34)

Unassigned
ST

Undersampled diversity



3. Peach/plum lineage

- 7 new genomes from plum and peach, southern Georgia (Byron)
- 2 published genomes from VA (*Prunus sp.*, ST10) and Brazil (Plum, ST26)
- 2 sequence types
 - Six ST10 (plum and peach)
 - One ST26 (SN13: plum grafted on peach root)



Host specificity



Take-home messages

- Undersampled diversity within native *Xfm* populations
- Host-associated lineages exhibit distinct evolutionary patterns
- Wild woody hosts as reservoirs facilitating pathogen spillover

*Understanding native *Xfm* populations is essential for predicting future disease emergence*

Next step:

- Linking genomic diversity with geography and climate
- 

Acknowledgements

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Dr. Sarah Lower (GA)

Dr. Chunxian Chen (GA)

Dr. Fulya Baysal-Gurel (TN)

Mark McClanahan (NC)

Jill Pollok (DE)

Mack Johnson (GA)

Eric Case (SN)

Thank you for your attention!



Xylella fastidiosa

5th European conference

Bari, Italy | 22-26 June 2026



Effective Cover Crop Management in Vineyards Reduces the Abundance of *Philaenus spumarius*, the Main European Vector of *Xylella fastidiosa*



Lago, C. Hernández-Lao, T., Plaza, M., Moreno, A., Fereres, A.



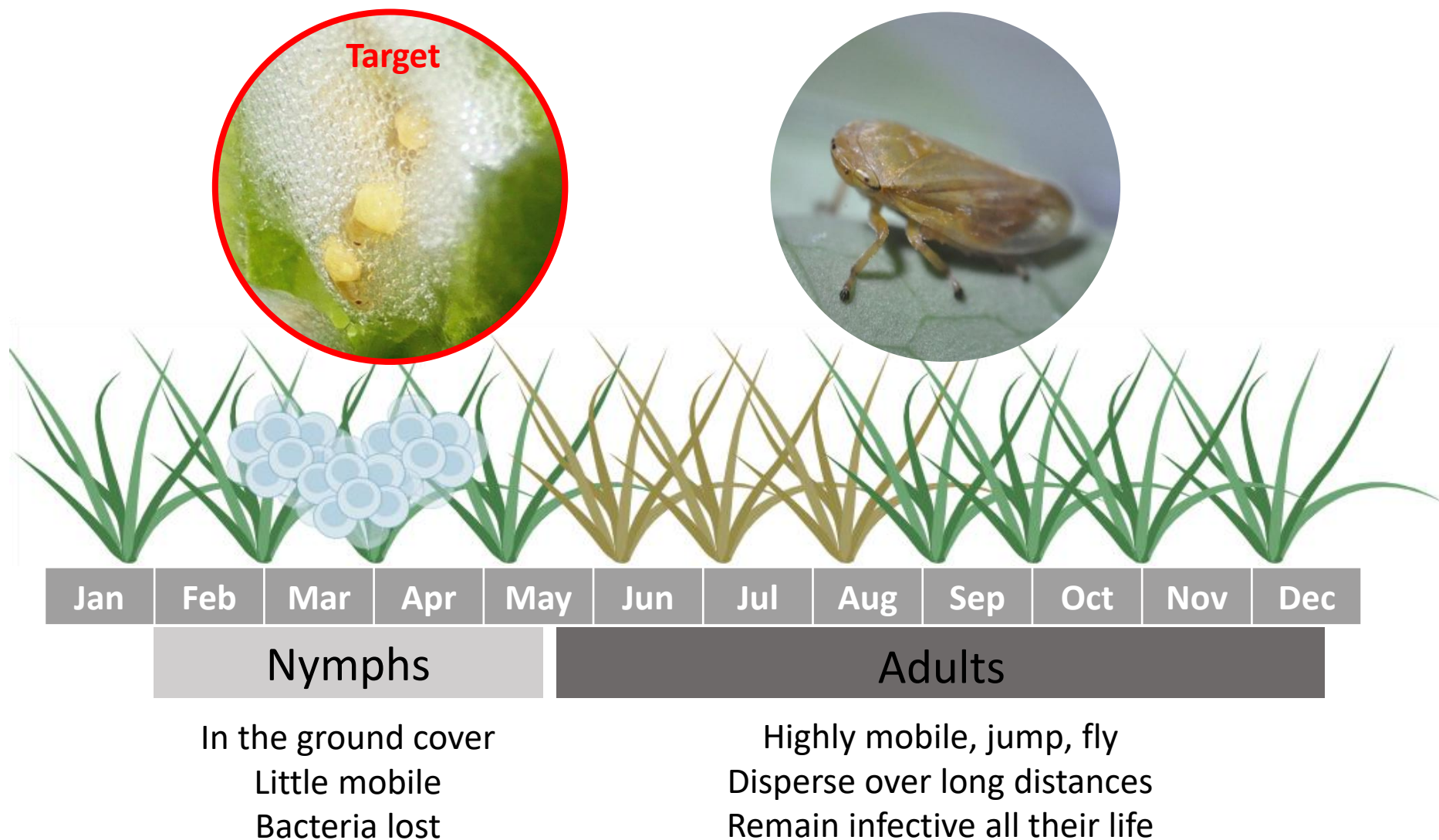
Cofinanciado por
la Unión Europea
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la Unió Europea



Fondos Europeos
Fons Europeus



Life cycle of *P. spumarius*



Suppressing vector populations

Pesticides



Soil tillage



Ground cover management



Selection of plant species to be used as cover crops

From the greenhouse



To the field



Extremely polyphagous
Over 1000 host plants!!!



Anthriscus cerefolium

Trap



Sinapis alba

Repellent



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la Unión Europea
Cofinanciat per
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DE TRABAJO
Y ECONOMÍA SOCIAL



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Fons Europeus



Govern de les
Illes Balears
Conselleria d'Educació
i Universitats

Goal

To evaluate the effectiveness of specific cover crops in reducing the density of *P. spumarius* nymphs under field conditions





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la Unión Europea
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la Unió Europea



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Field experiments in Spanish vineyards



**Areeiro
Pontevedra**
Galicia

2024-2025-2026



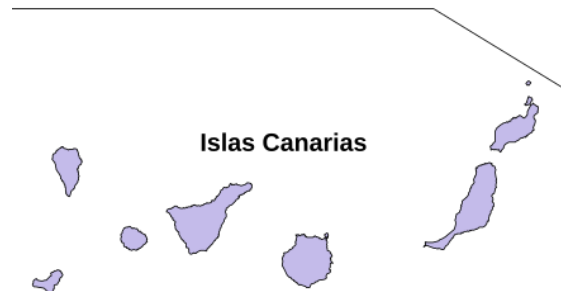
**Cenicientos
Madrid**
Comunidad de Madrid

2025-2026



**Felanitx
Mallorca**

2025-2026
Islas Baleares



Experimental design

Cover crop treatments sown in autumn



A. cerefolium



S. alba

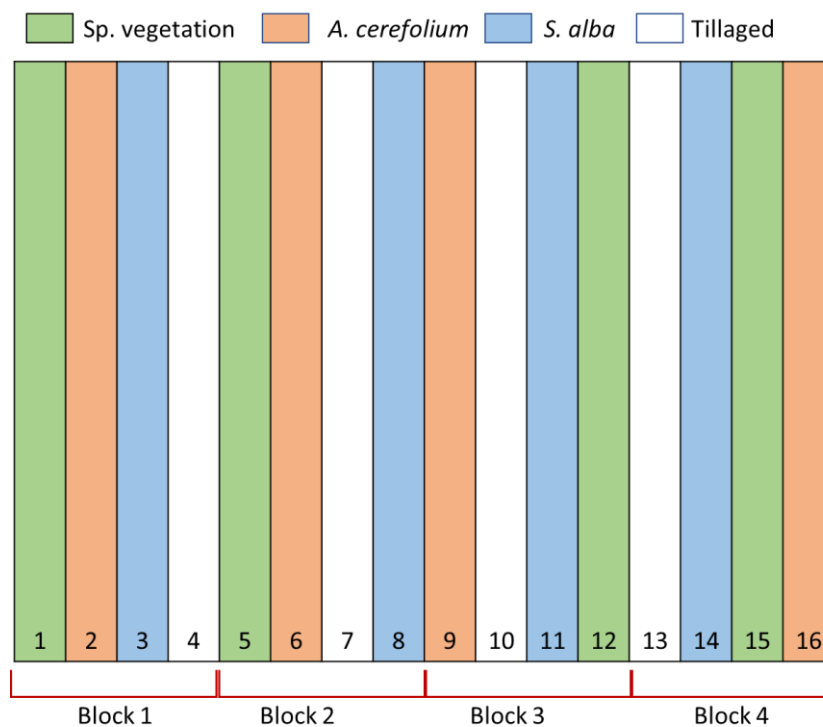


Spontaneous
vegetation



Tillage
(2026)

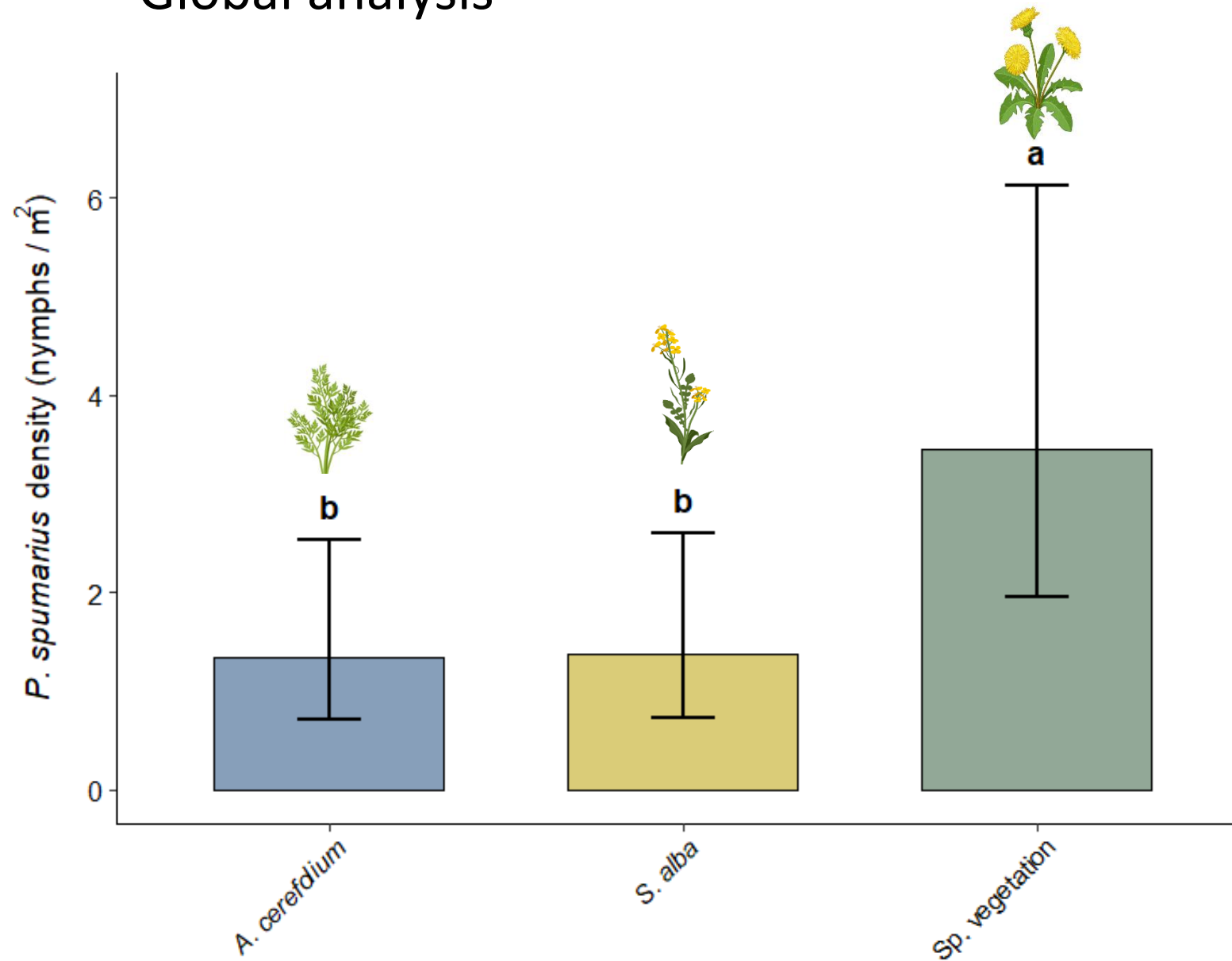
Block design



Total nymphs per row were counted every 15 days



Global analysis



*Cenicientos was excluded because *S. alba* did not grow,

*Tillage treatment was excluded because this treatment only appears in 2026



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la Unión Europea
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MINISTERIO
DE TRABAJO
Y ECONOMÍA SOCIAL



Fondos Europeos
Fons Europeus



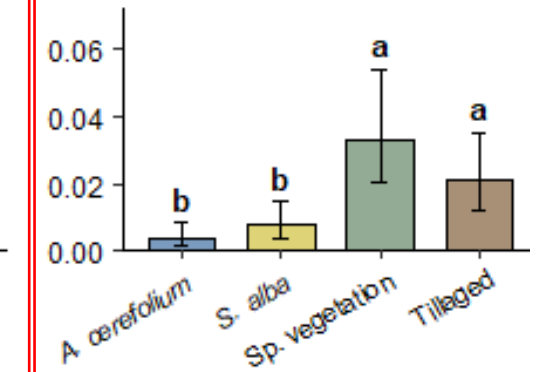
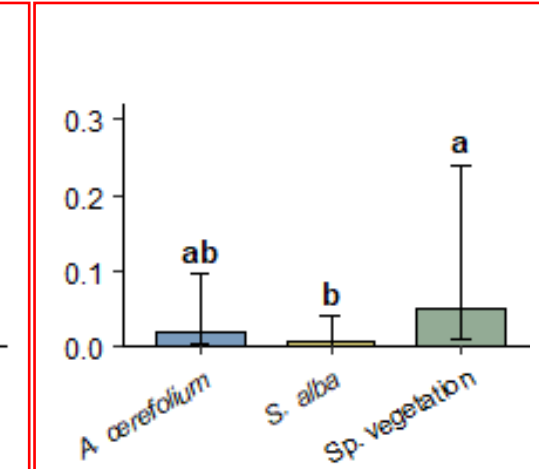
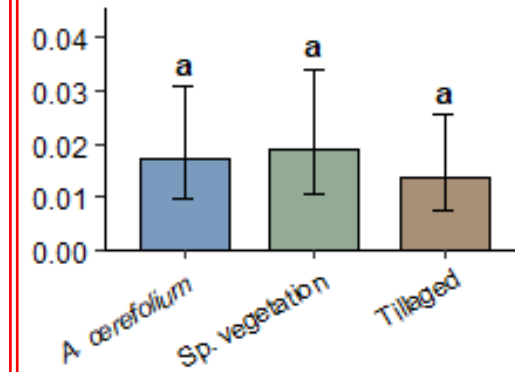
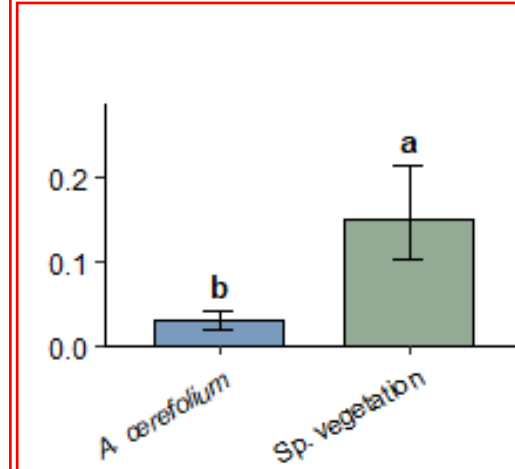
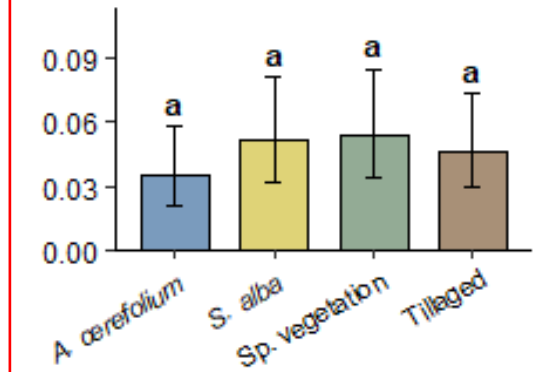
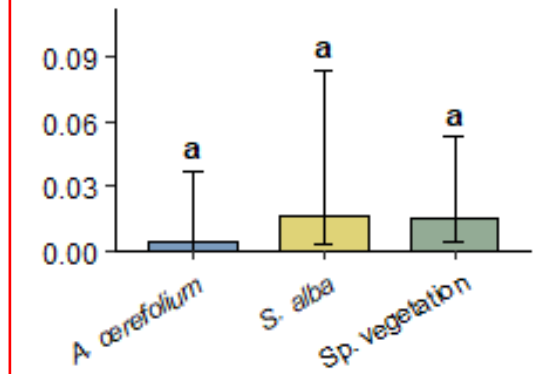
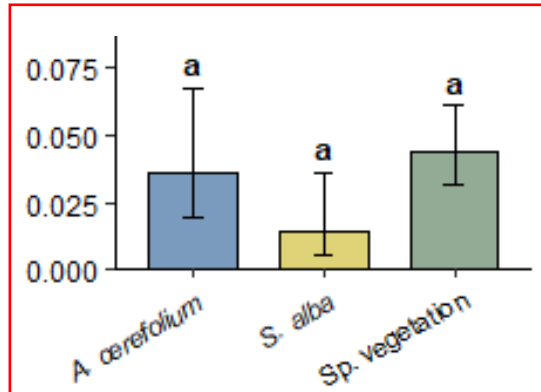
Govern de les
Illes Balears
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i Universitats

Areiro

Cenicientos

Felanix

P. spumarius density (nymphs / m²)



2024

2025

2026

Take-home message



Selected cover crops reduced *Philaenus spumarius* abundance compared with spontaneous vegetation.



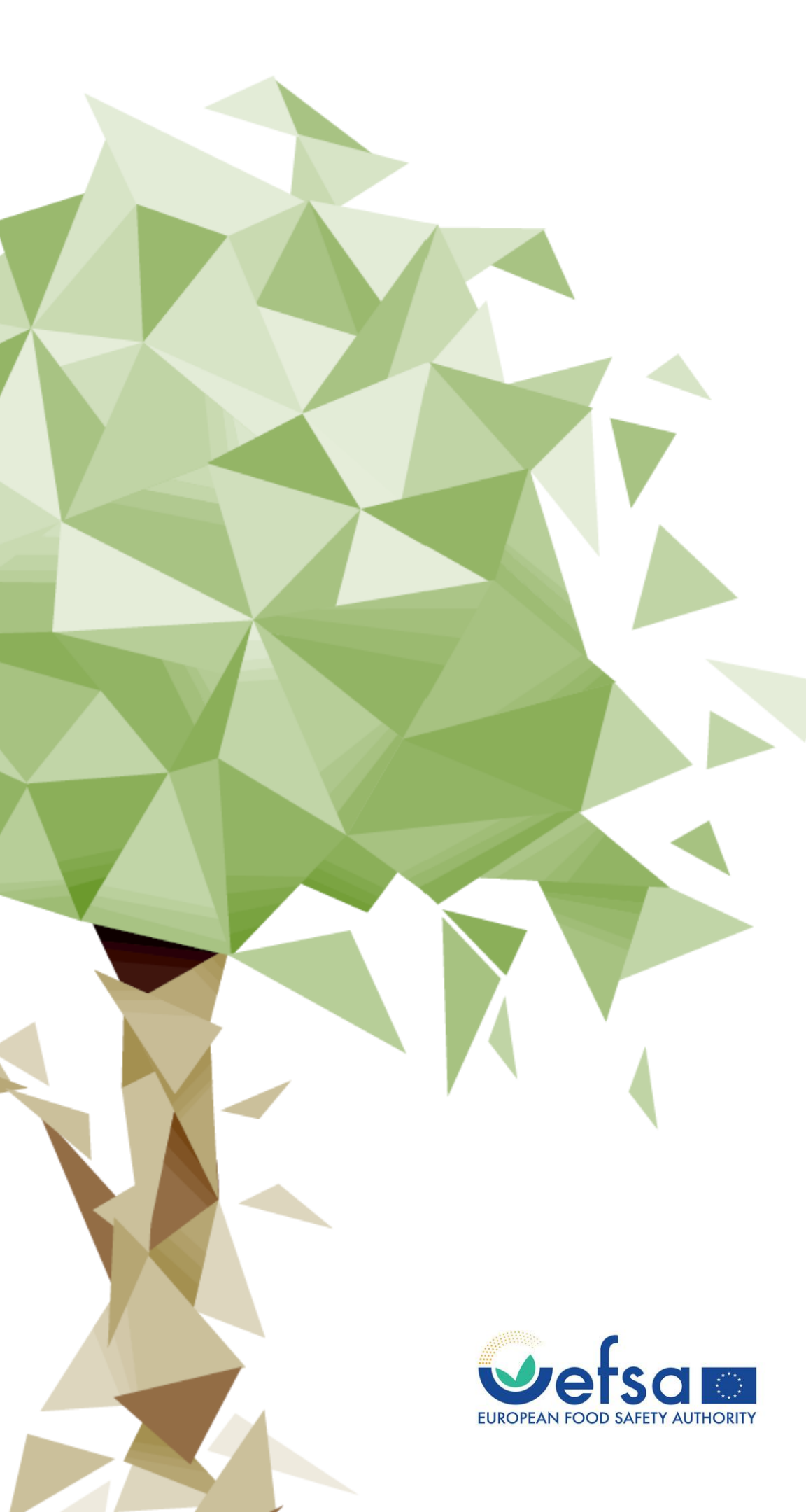
Treatment efficacy depended on local conditions, highlighting the importance of site-specific implementation.



Cover crop management can contribute to sustainable vector suppression while preserving ecosystem services.



Thank you!



Xylella fastidiosa

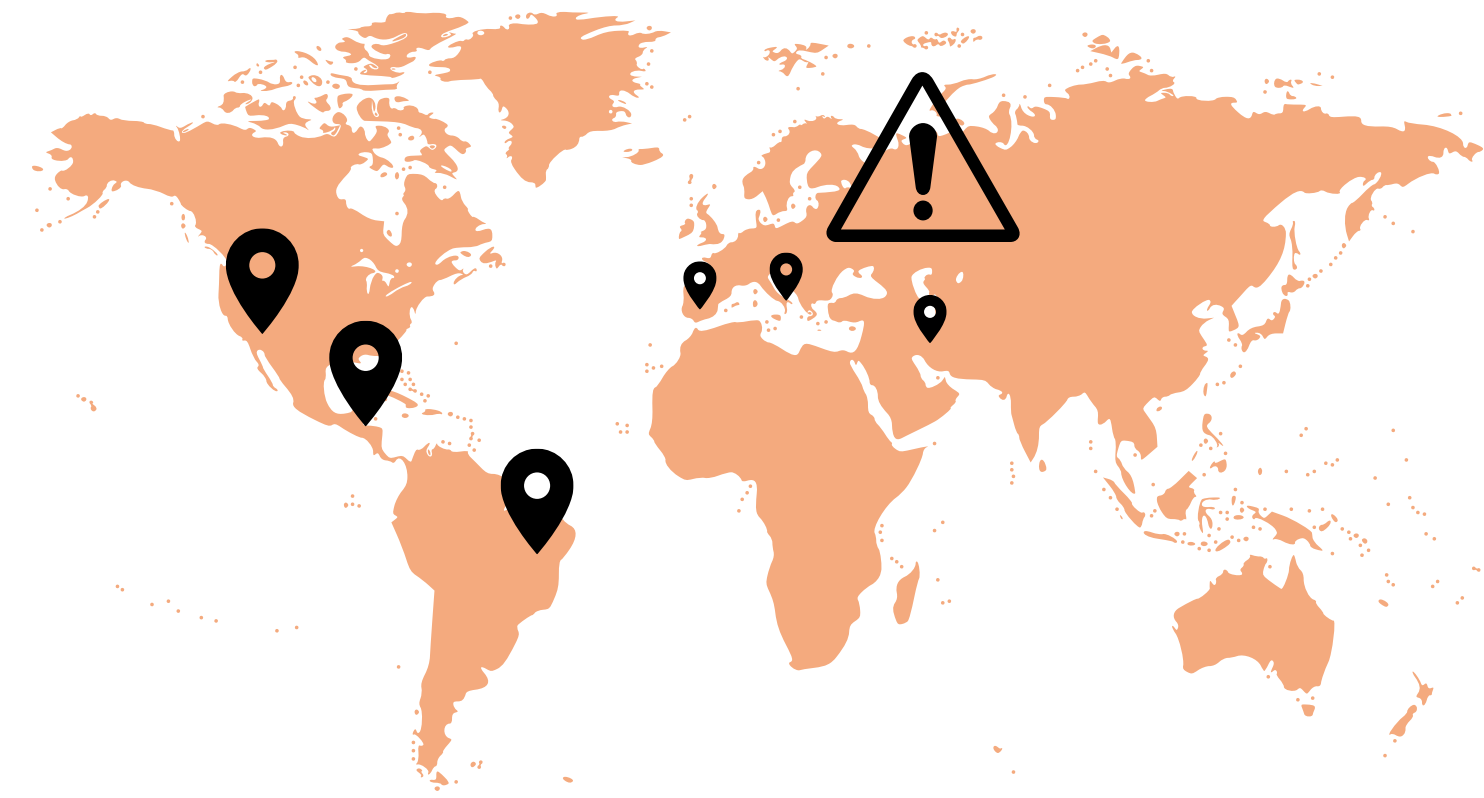
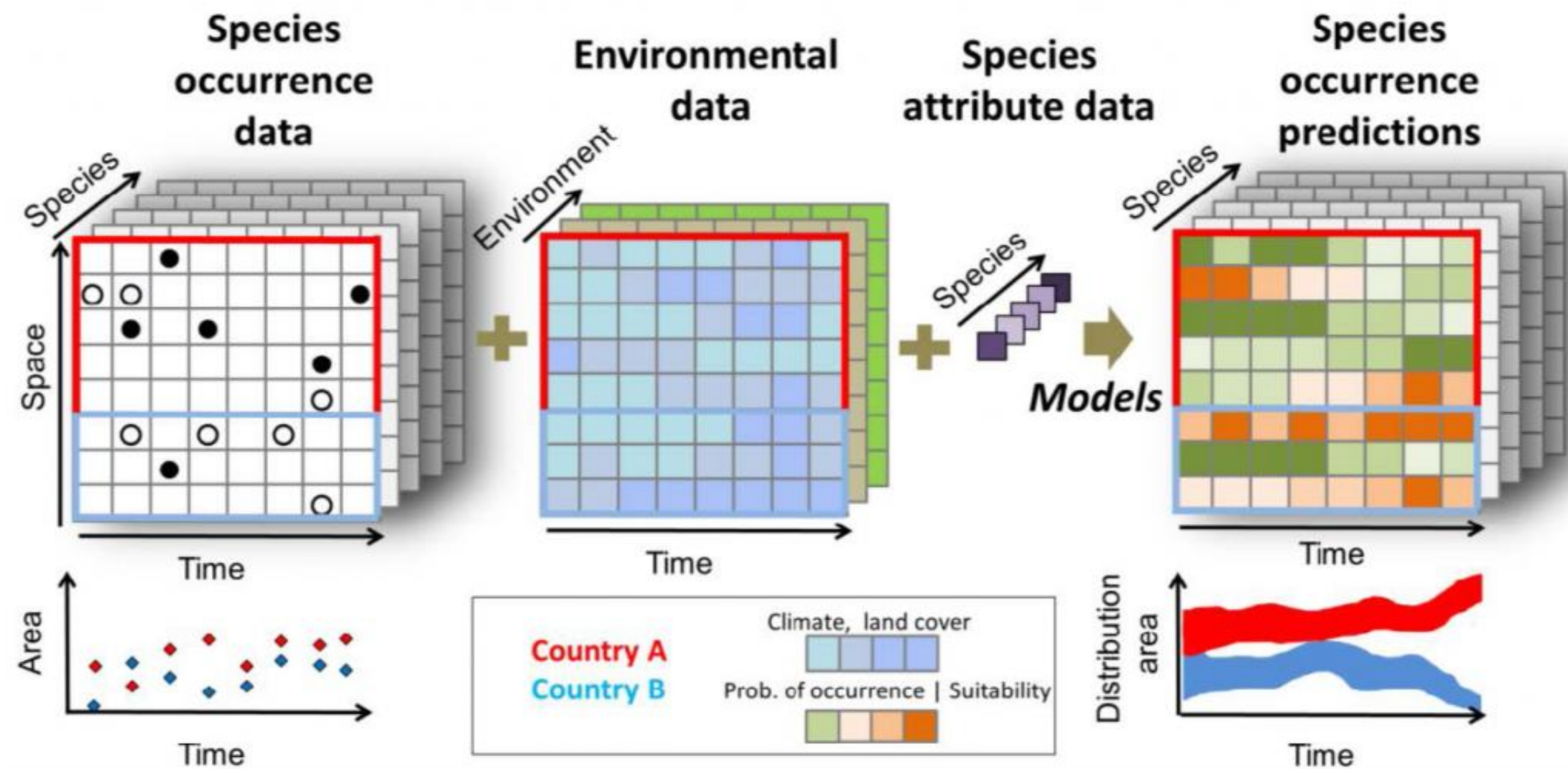
5th European conference

Bari, Italy | 22-26 June 2026



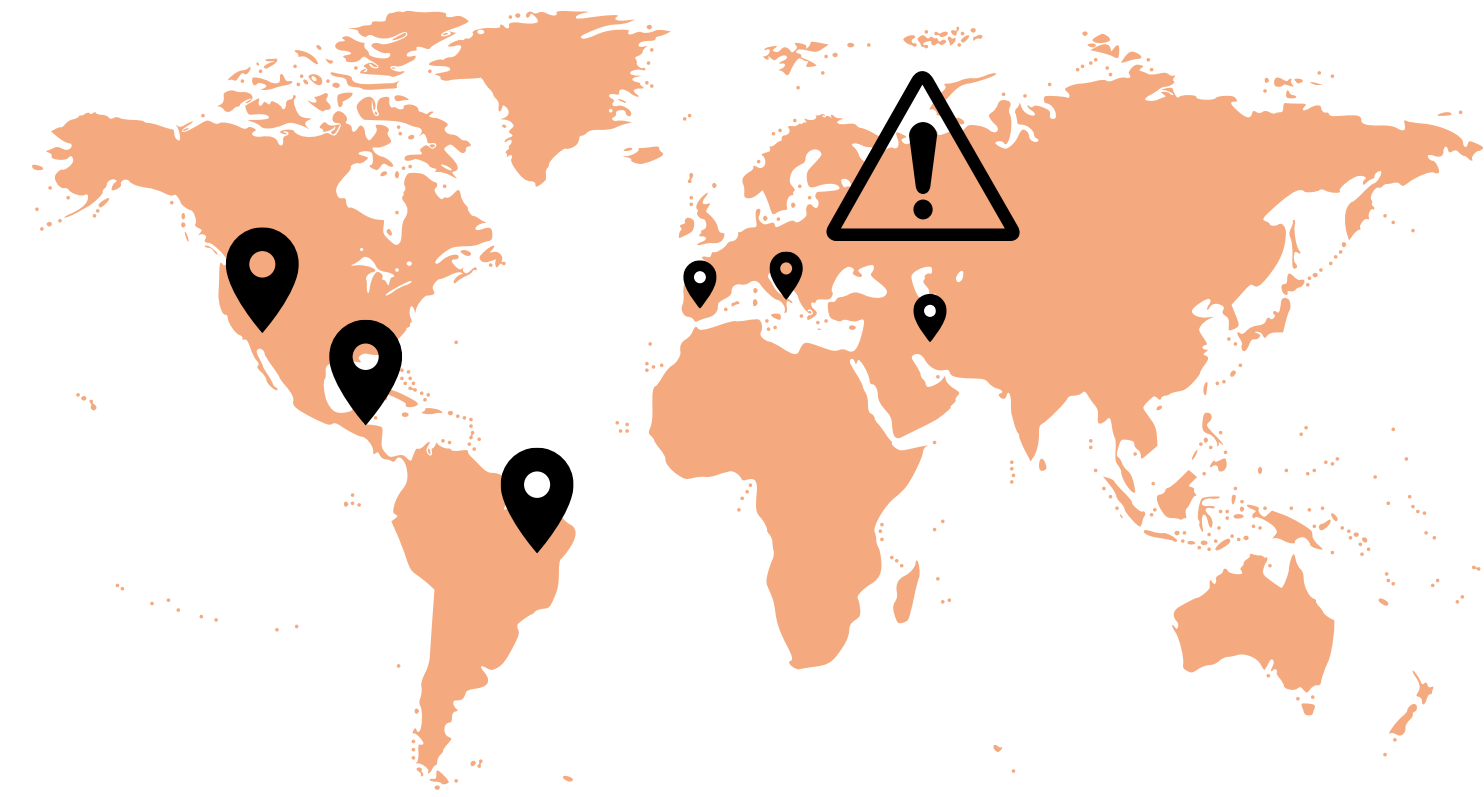
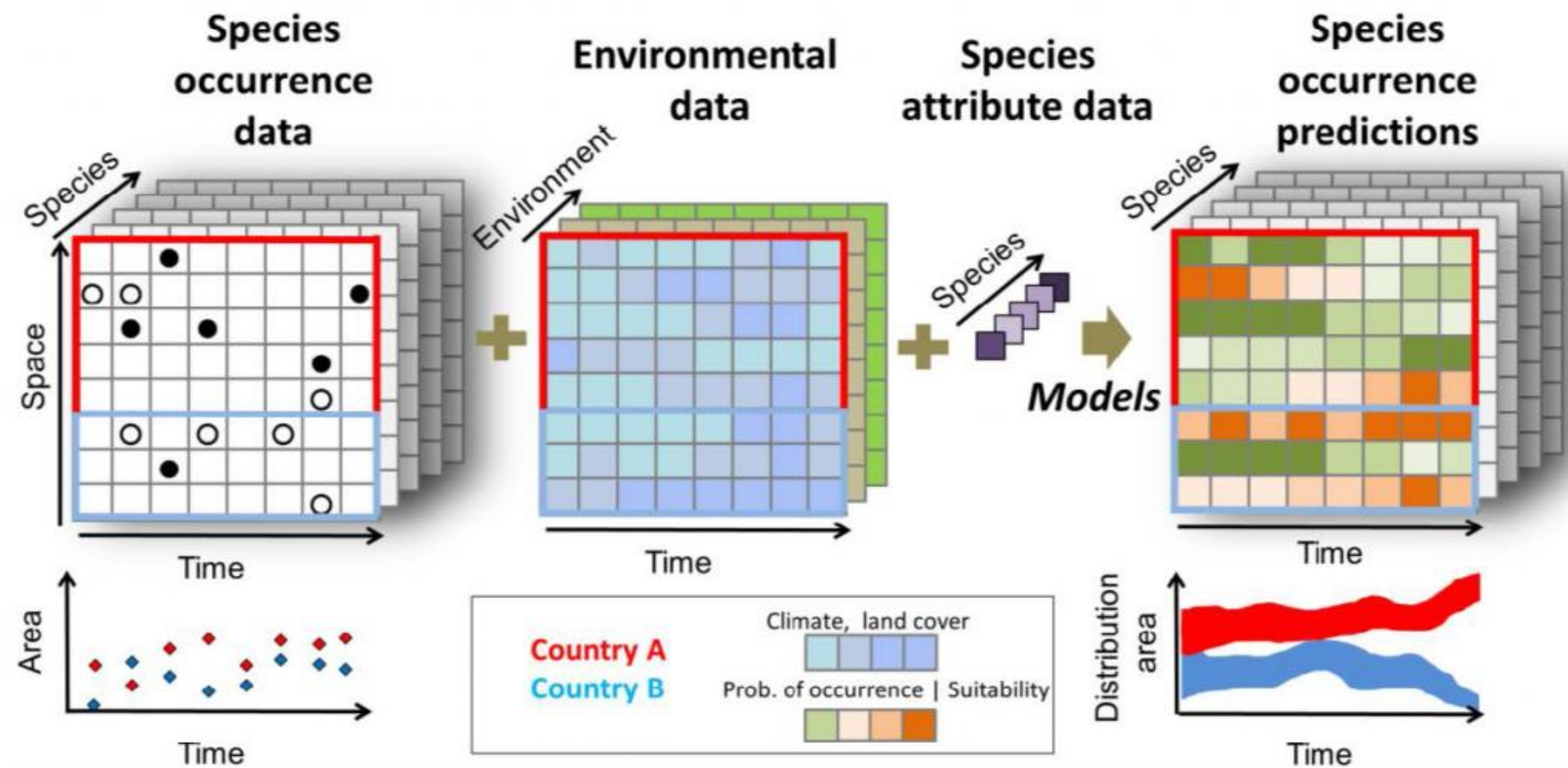
Modeling the risk of vector-borne plant diseases

“Which is the risk of Xf diseases establishing and spreading through Europe?”



Modeling the risk of vector-borne plant diseases

“Which is the risk of Xf diseases establishing and spreading through Europe?”



A. Townsend Peterson

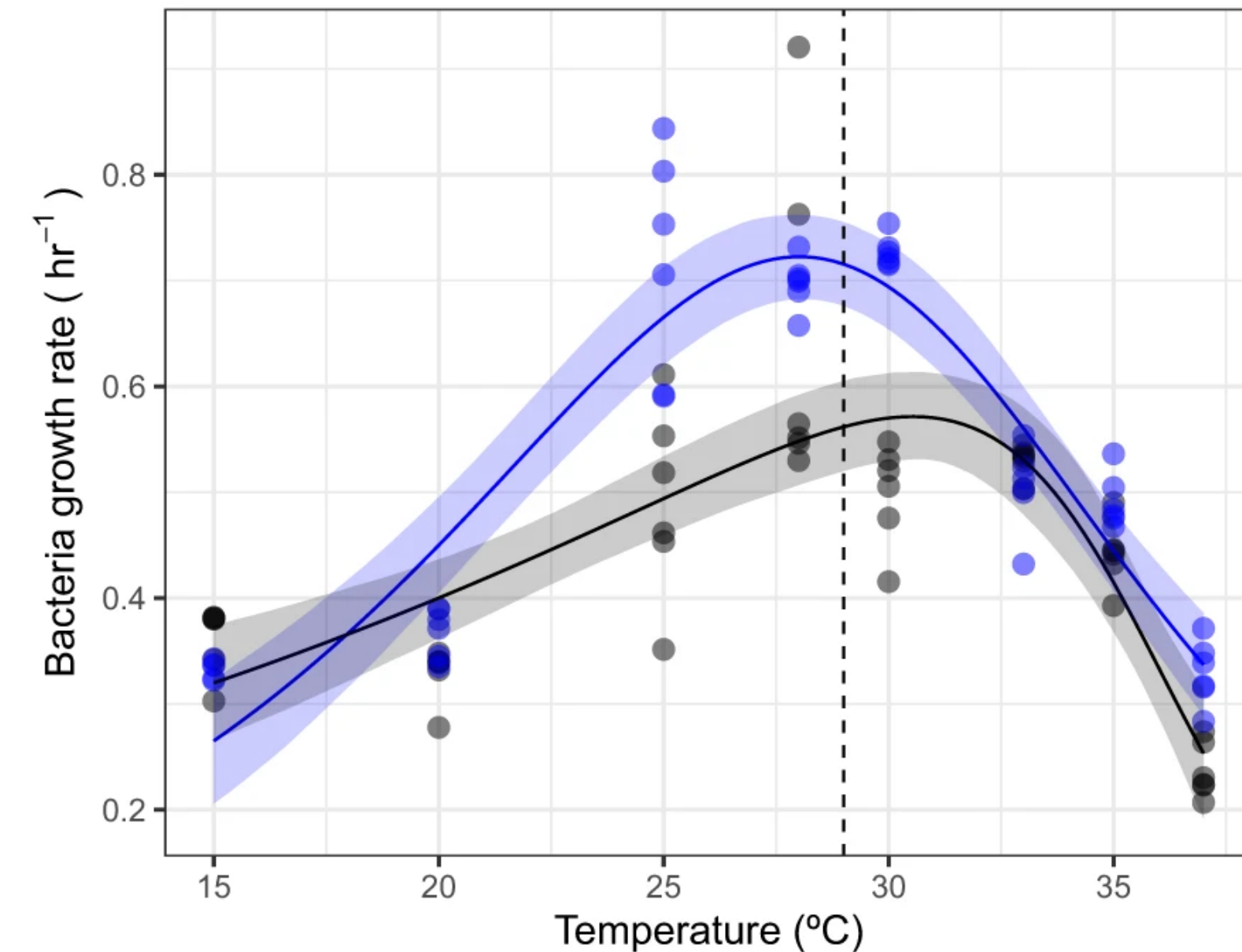
*Because disease processes are **dynamic**, taking place on extremely diverse scales of space (microscopic to continental) and time (minutes to centuries), and are the products of **interactions** among species (pathogens, reservoirs, vectors, etc.), their ecological and distributional dynamics may differ from those of more normal species.*

Within-host pathogen dynamics depend on temperature, and can be modelled

temperature-dependent growth rate

$$\frac{dP}{dt} = \sigma(T(t))P$$

(b) Thermal performance of bacterial growth rate



Within-host pathogen dynamics depend on temperature, and can be modelled

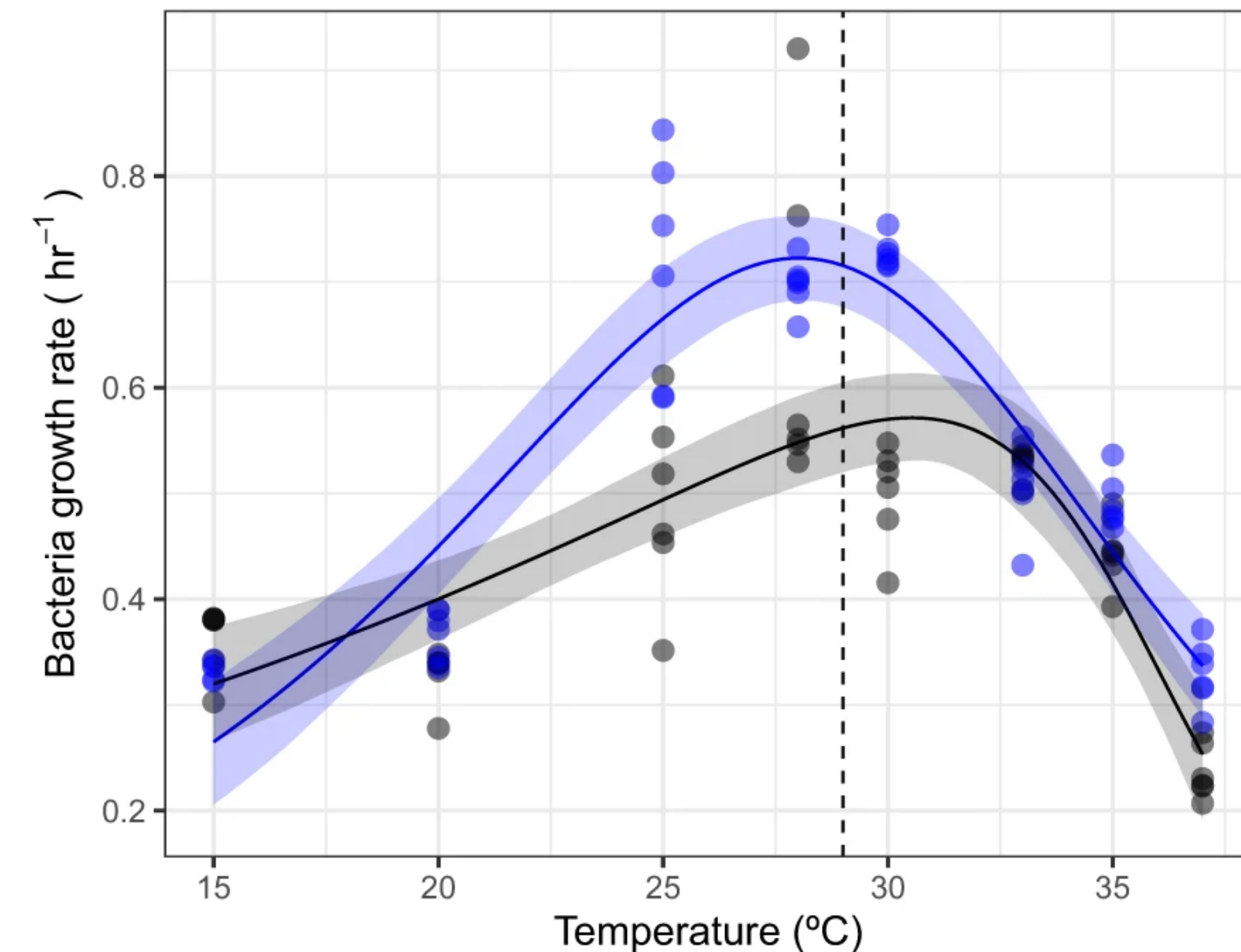
temperature-dependent growth rate

Giménez-Romero et al., *Communications Biology* (2022)

J.C. Rodríguez-Cabanillas, M.A. Matías and À. Giménez-Romero, *In prep* (2026)

$$\frac{dP}{dt} = \sigma(T(t))P \implies P(t) = P_0 \exp \left(\int_{t_0}^t \sigma(T(t')) dt' \right) = P_0 \exp (\mathcal{T}(t))$$

(b) Thermal performance of bacterial growth rate



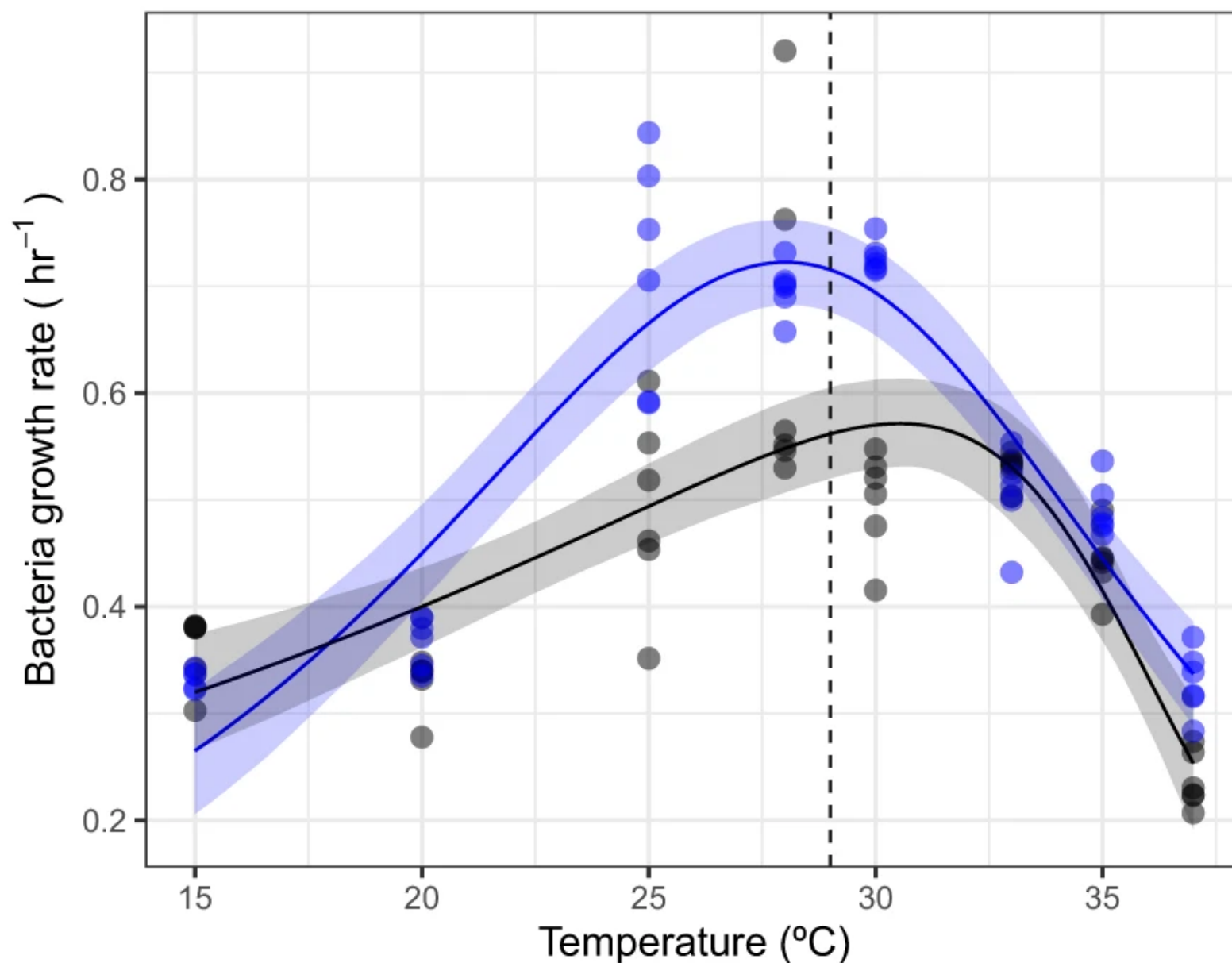
Within-host pathogen dynamics depend on temperature, and can be modelled

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(b) Thermal performance of bacterial growth rate



We can compute the thermal part from
temperature time-series

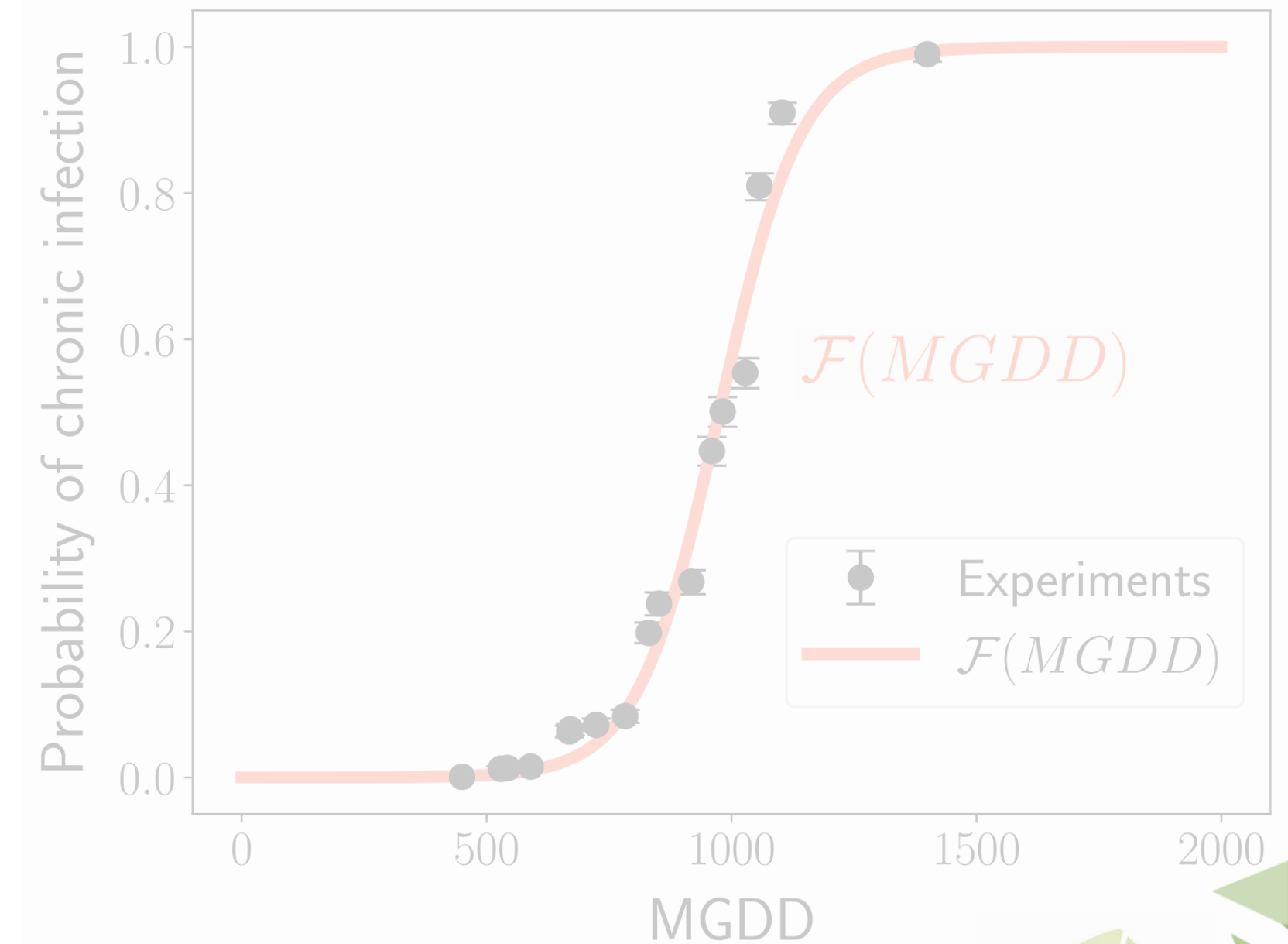
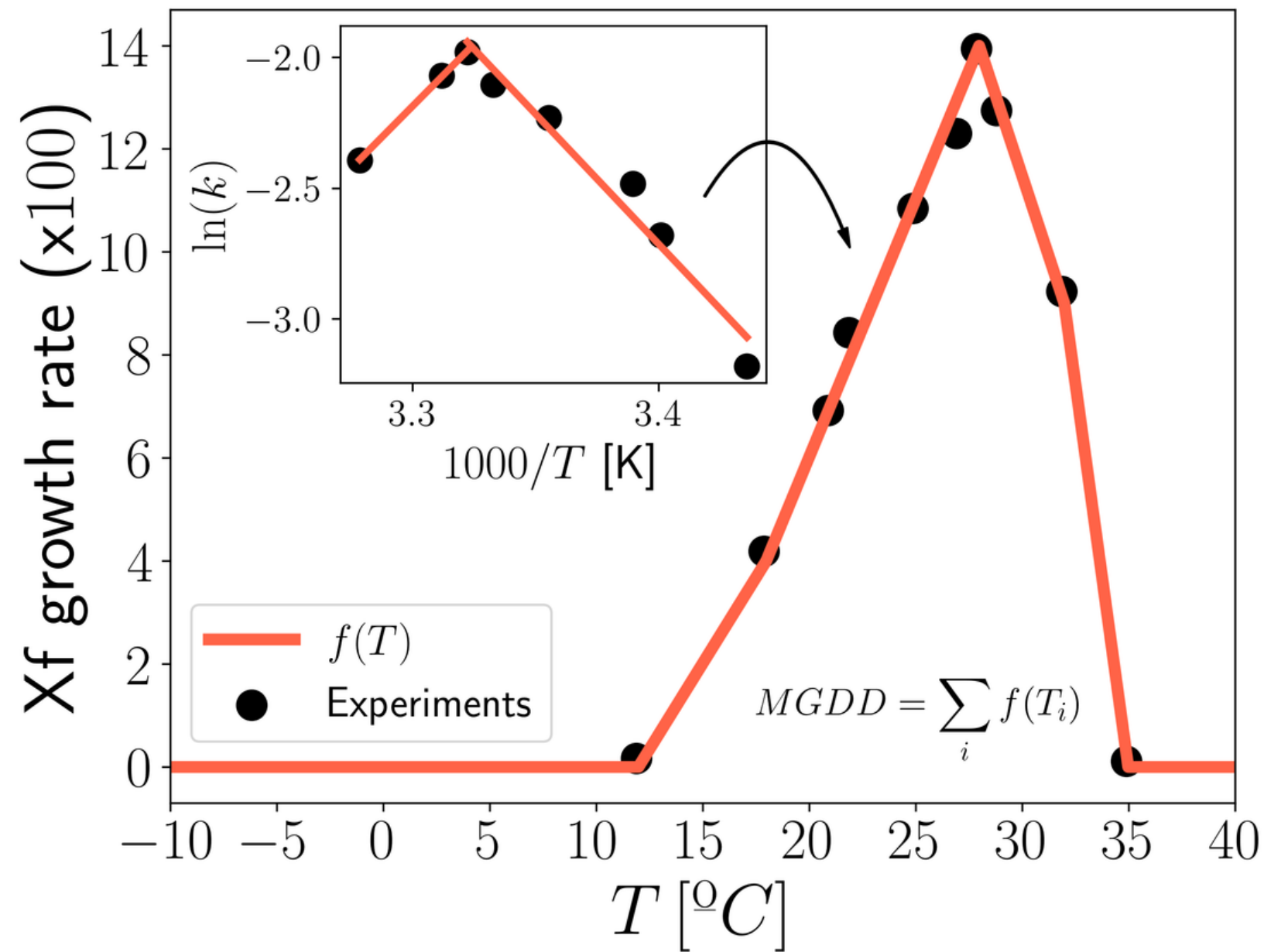
$$\mathcal{T}(t) \approx \sum_{t=t_0}^t \sigma(T(t_i))$$

In essence, this is the same idea that **degree-days**,
much used in biology

Symptom development can be linked to temperature-dependent pathogen load

Giménez-Romero et al., *Communications Biology* (2022)

Infection process (after inoculation) depends on temperature



$$\frac{dN}{dt} = \sigma(T(t))N(1 - N/K) \implies N(t) = \frac{K}{1 + C \exp(-\underbrace{\int_{t_0}^t \sigma(T(t'))dt'}_{MGDD})}$$

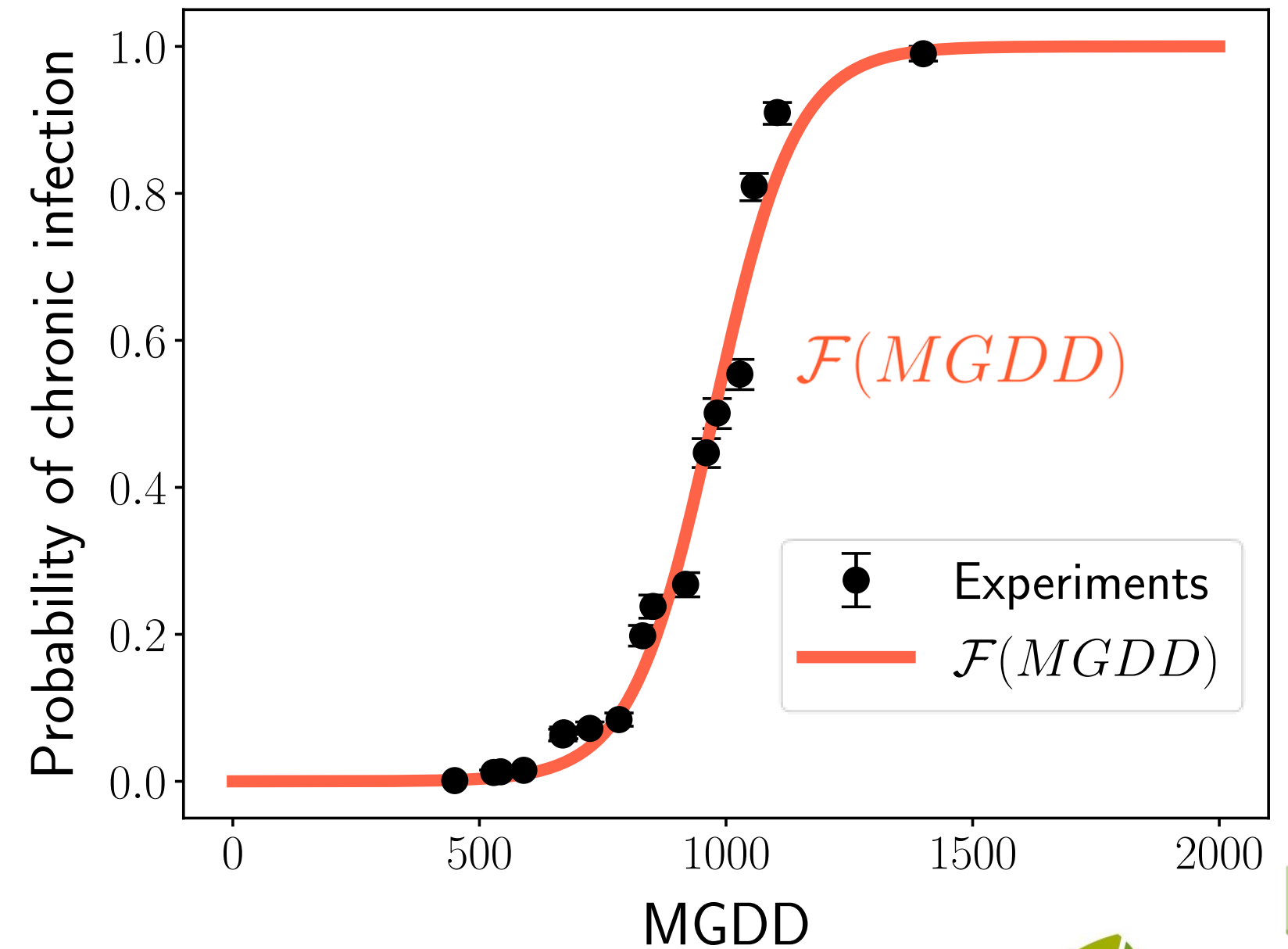
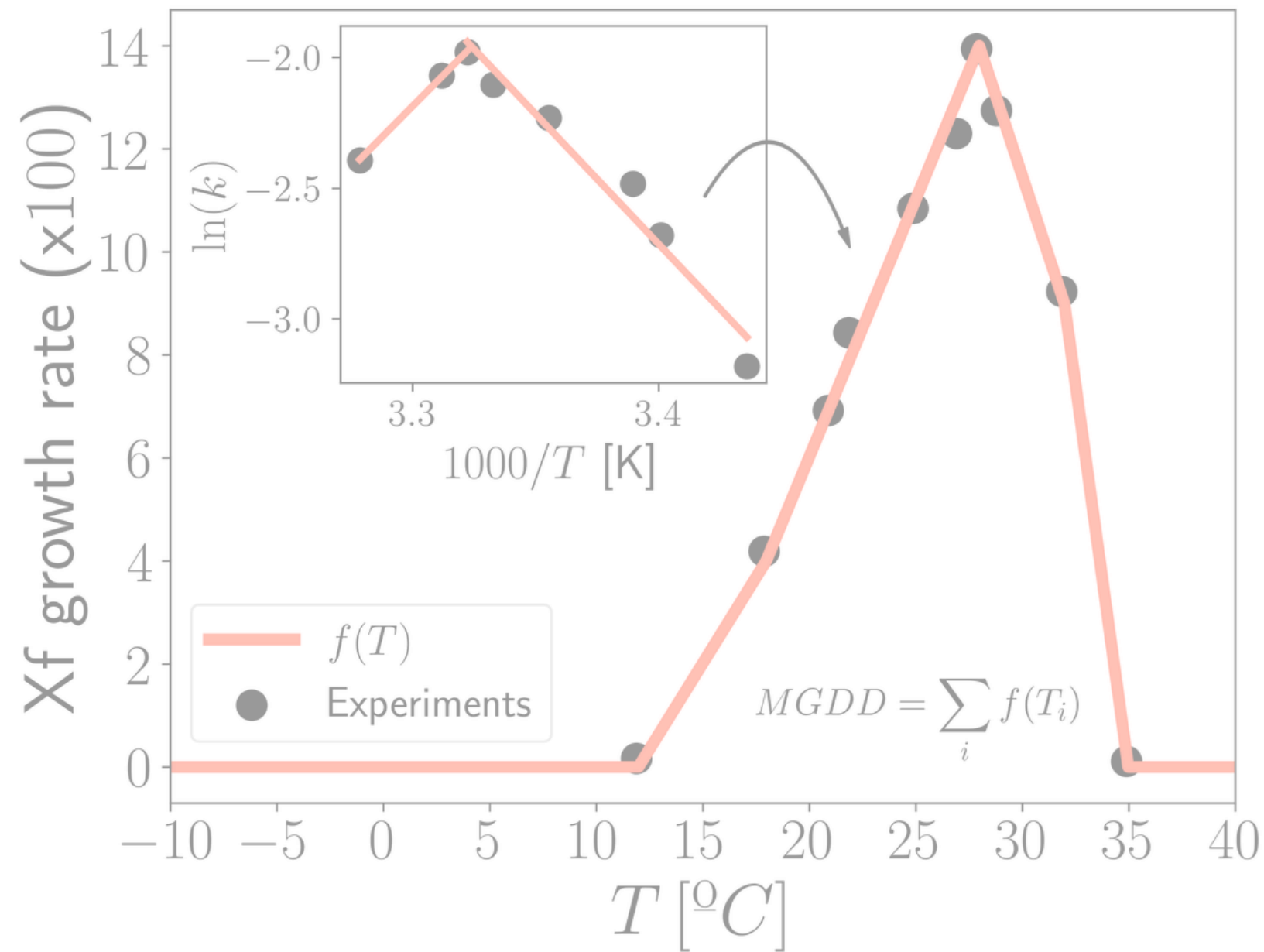
Eduardo Moralejo
Marina Montesinos



Symptom development can be linked to temperature-dependent pathogen load

Giménez-Romero et al., *Communications Biology* (2022)

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Eduardo Moralejo
Marina Montesinos



A climate-based epidemiological model

Dynamics of the infected population

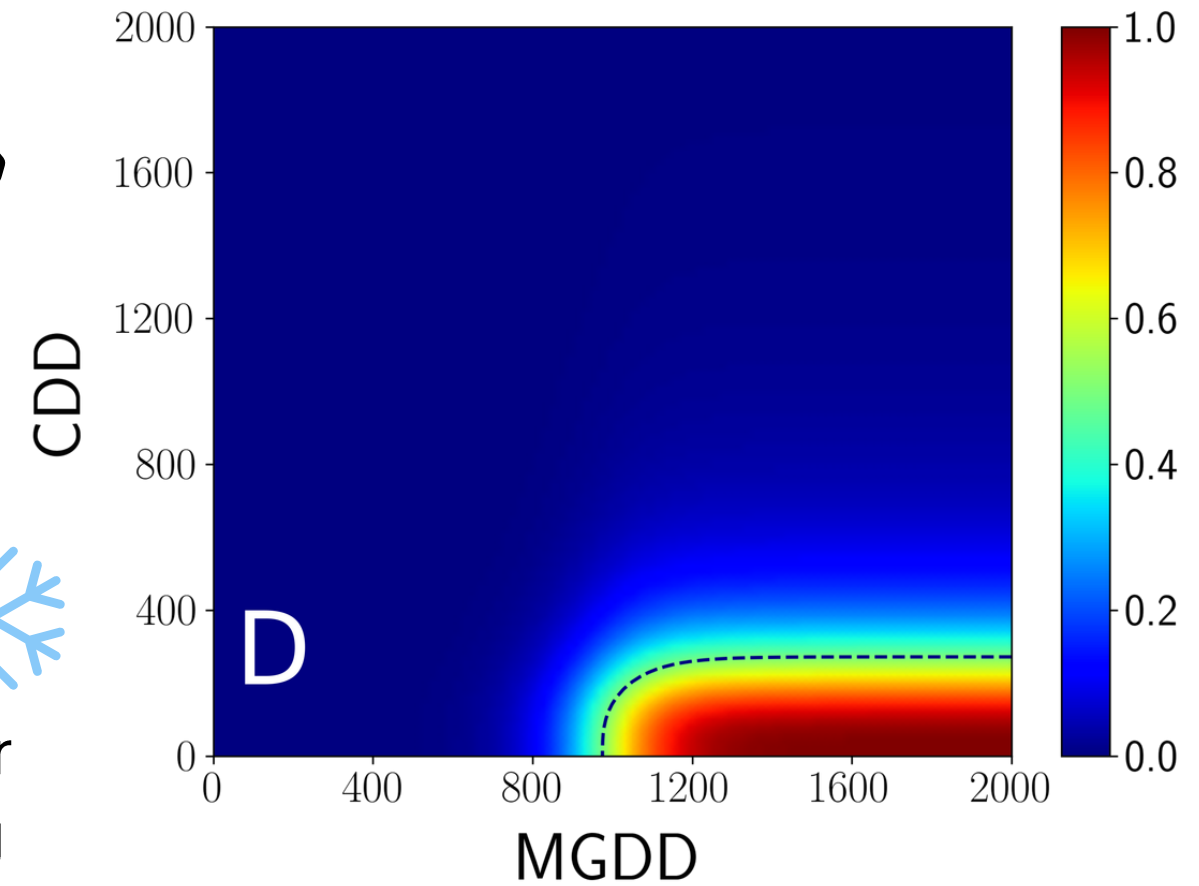
Prob. infection

$$I(t) = I(t-1) \exp(\gamma(R_0 - 1)t) \cdot \mathcal{F}(MGDD(t)) \cdot \mathcal{G}(CDD(t))$$

Transmission

modulated by the vector

Winter curing

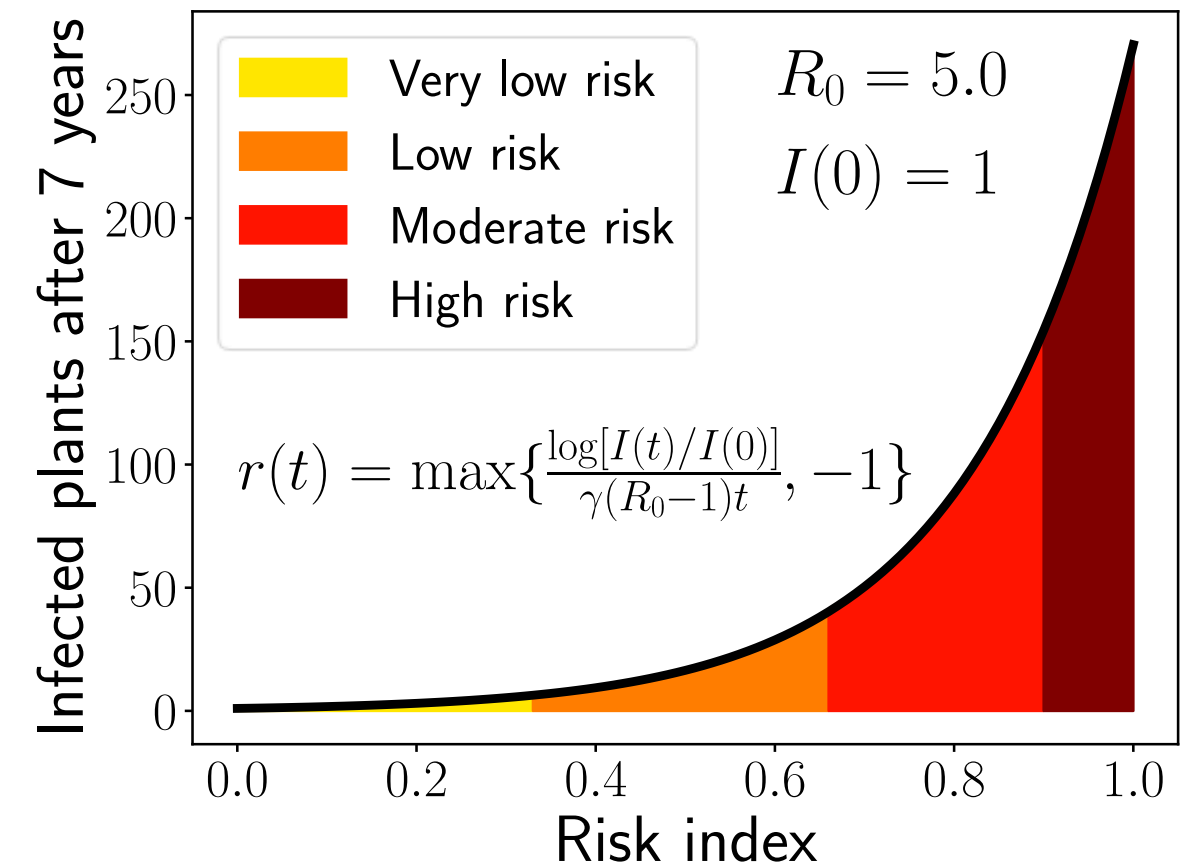


Risk index as effective relative growth

$$r = \max \left\{ -1, \frac{\ln [I(\tau)/I(0)]}{\gamma (R_0 - 1) \tau} \right\}$$

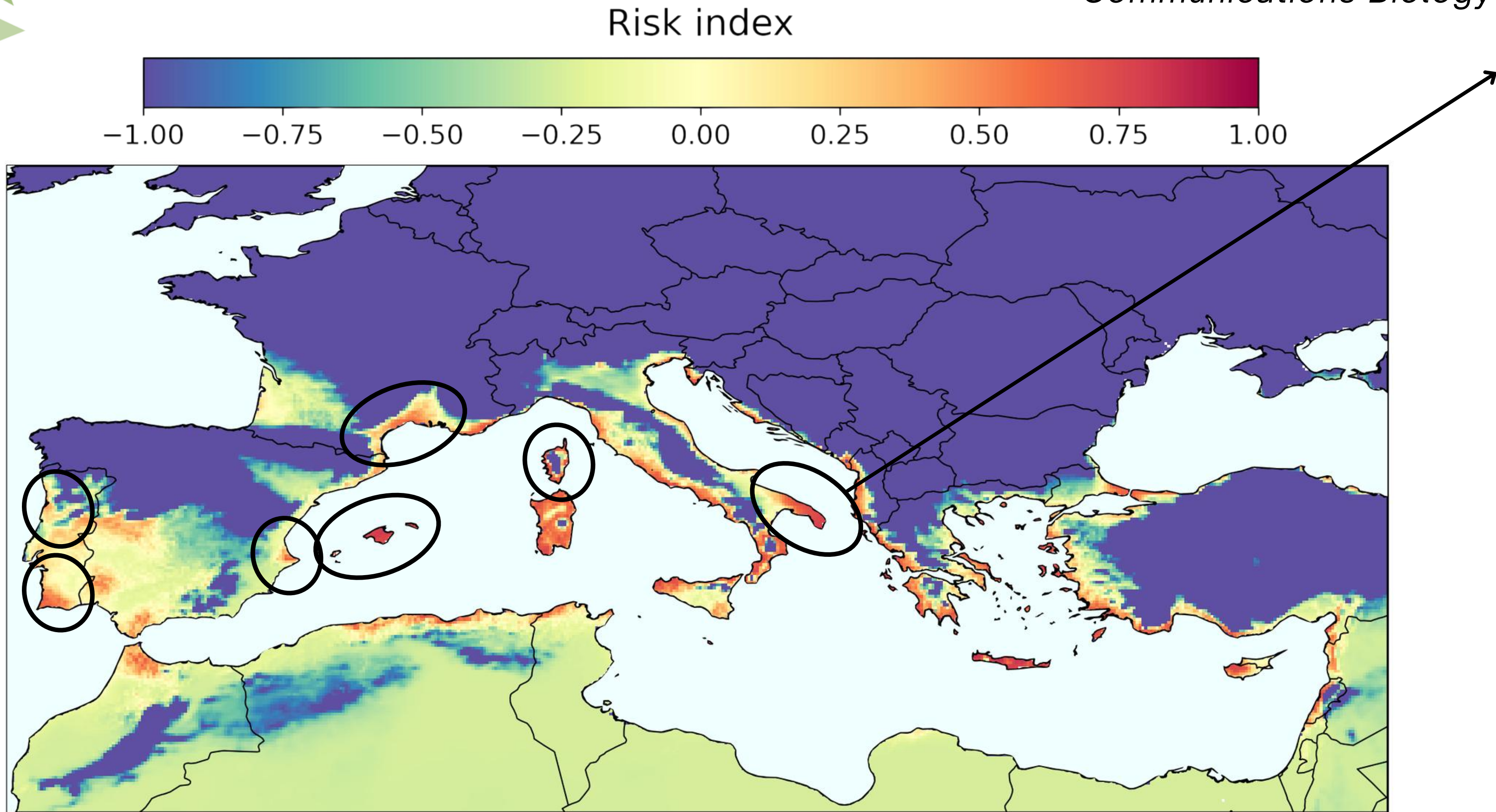
realized growth

maximum possible growth



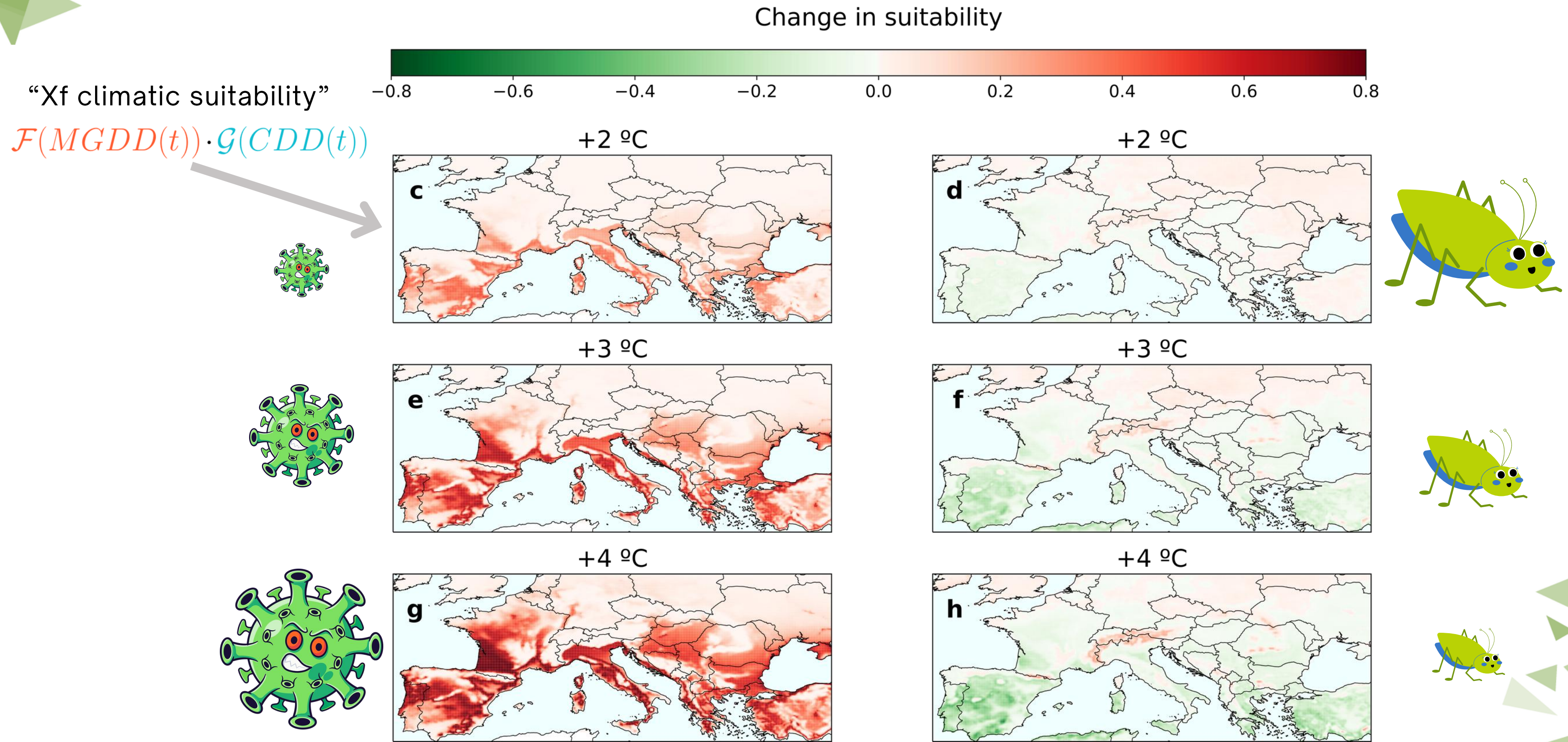
The risk of Pierce's disease in Europe

Giménez-Romero et al.,
Communications Biology (2022)



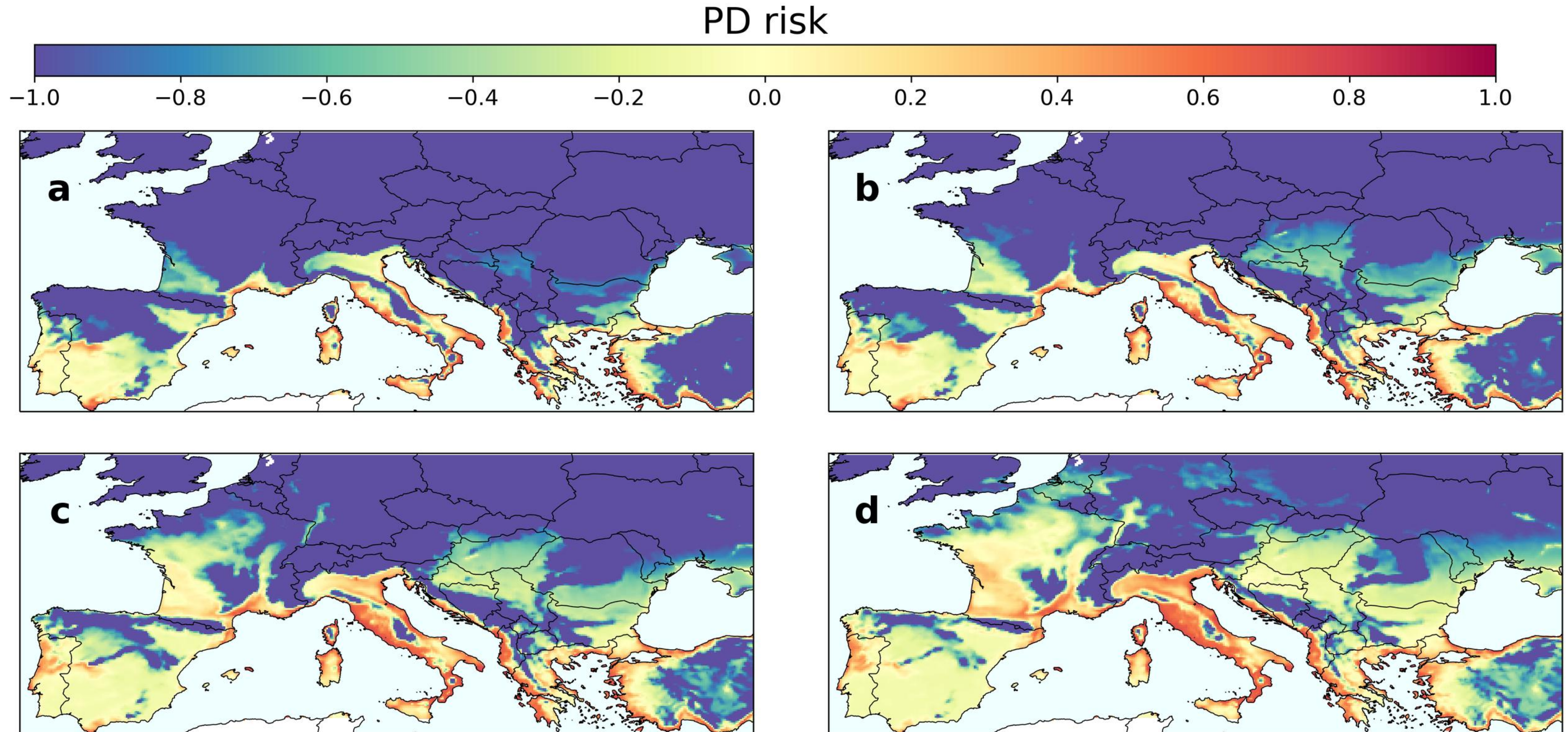
The future risk of Pierce's disease in Europe

Giménez-Romero et al., *Scientific Reports* (2024)



The future risk of Pierce's disease in Europe

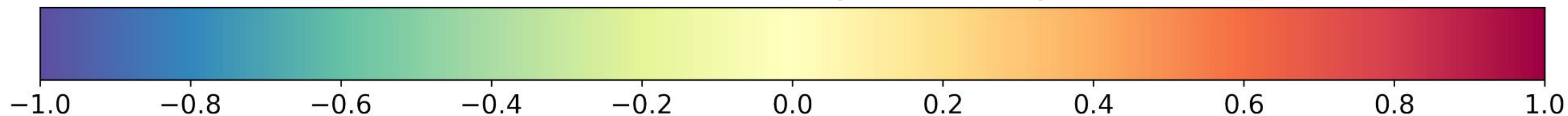
Giménez-Romero et al., *Scientific Reports* (2024)



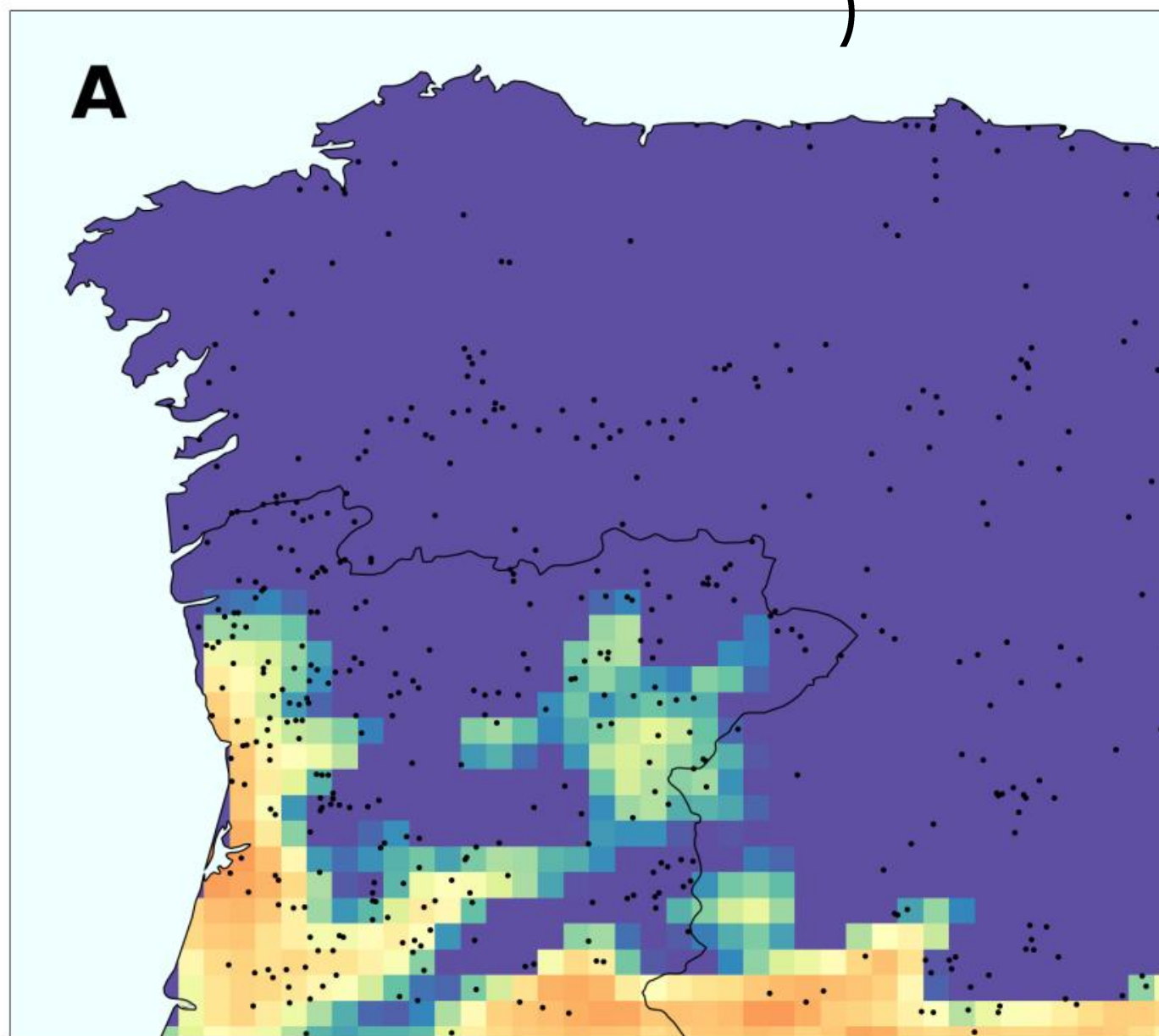
The importance of the spatial resolution of climate data

Giménez-Romero et al, *Scientific Reports* (2025)

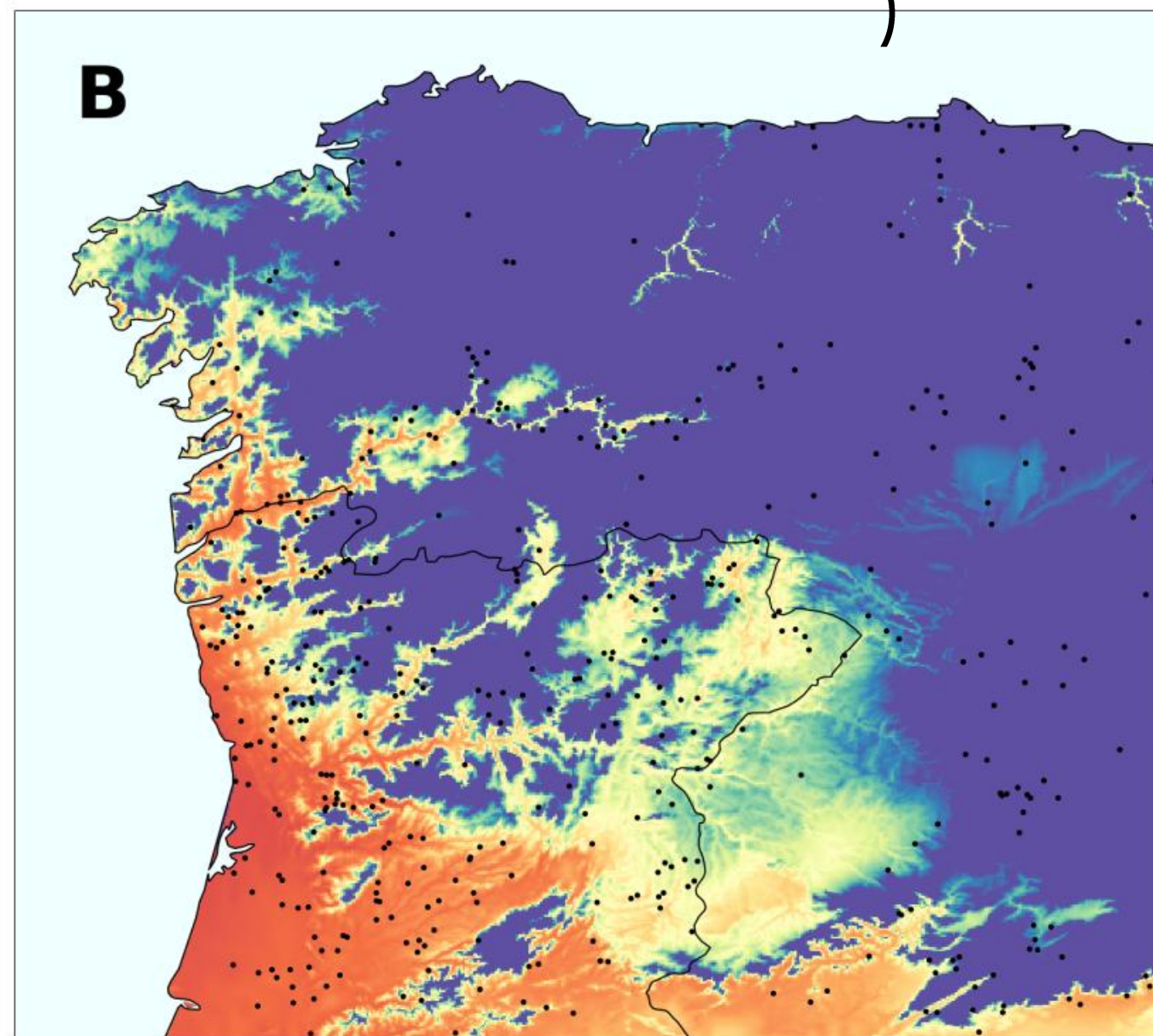
r (risk index)



ERA5 (~10km
)

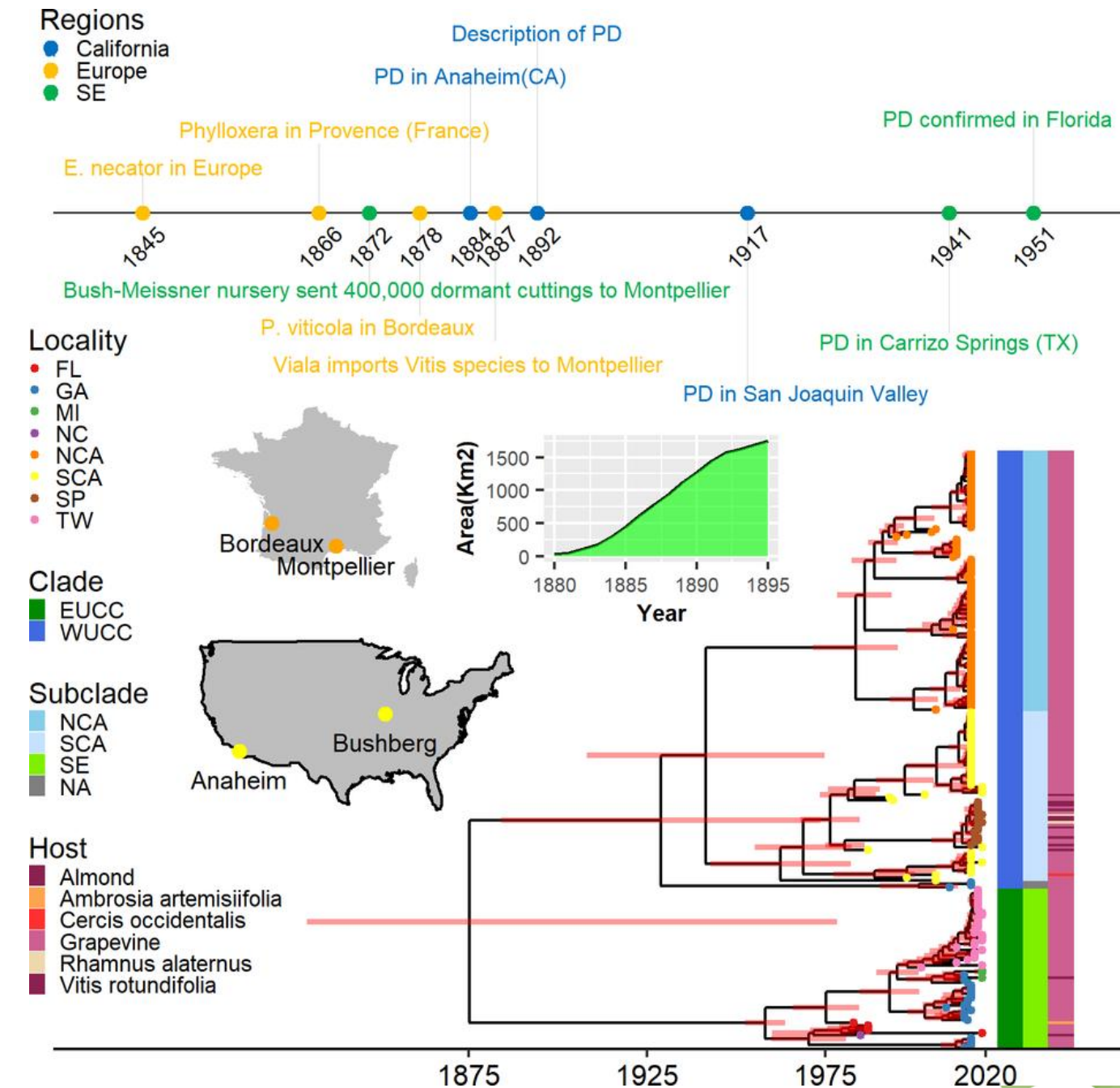
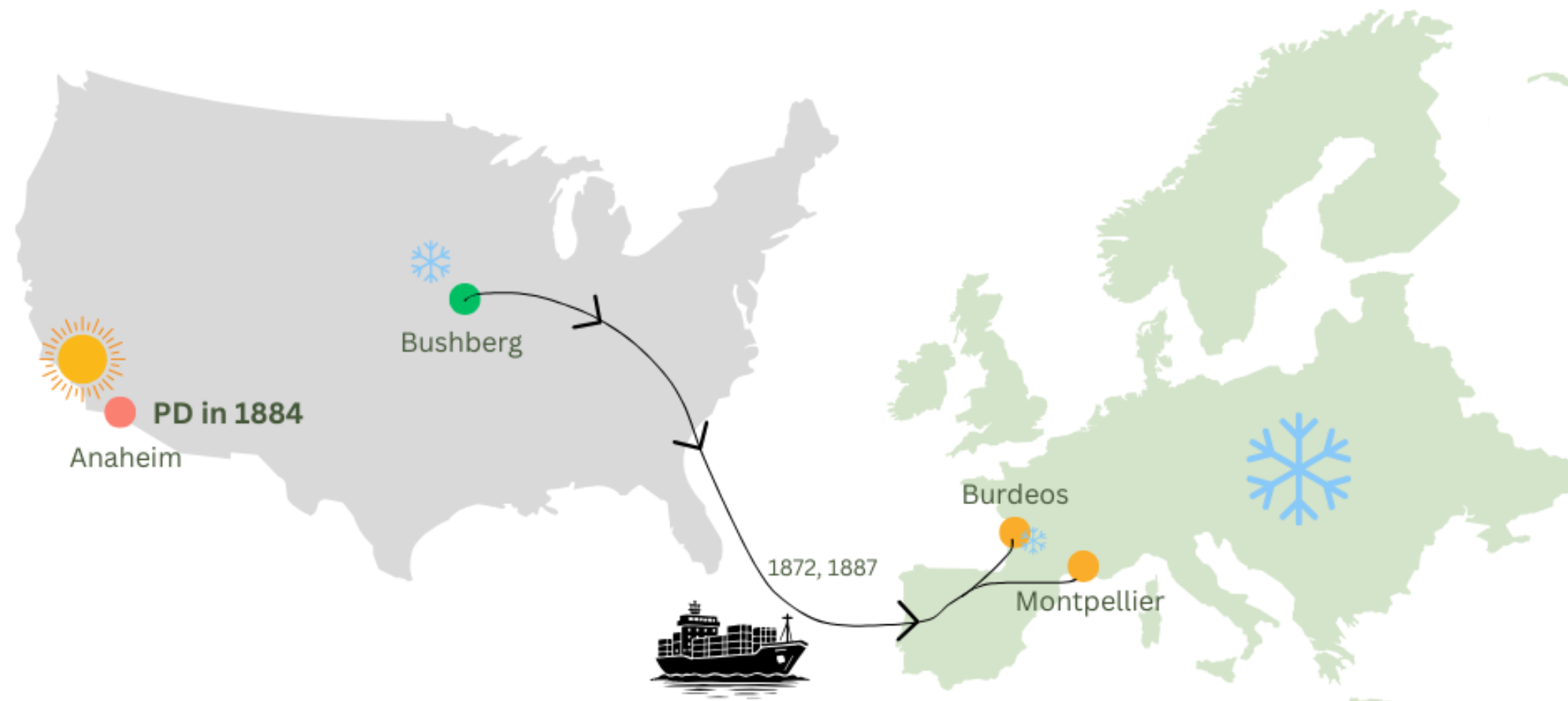
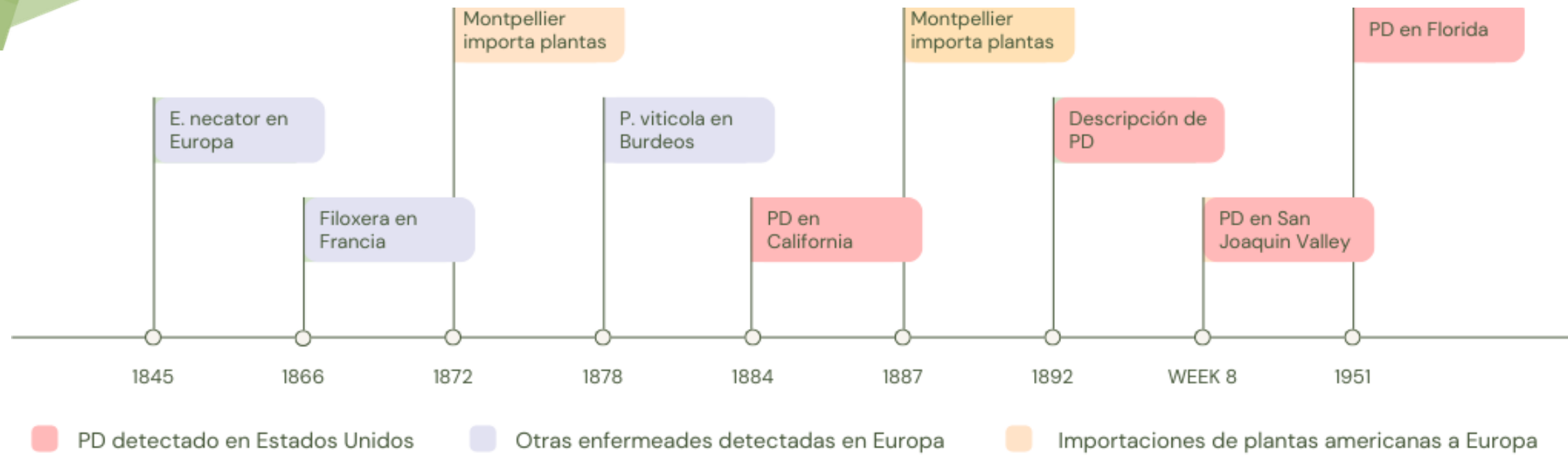


CHELSA (~1km
)



Why PD didn't establish in Europe until now?

E. Moralejo et al, *Proceedings B* (2025)



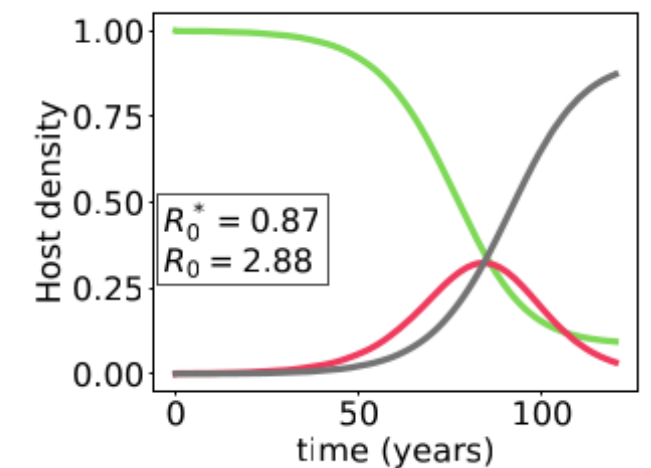
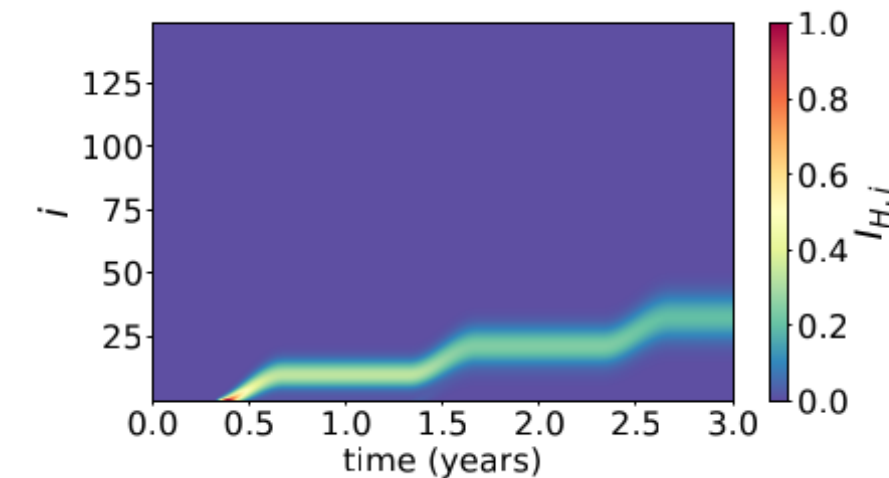
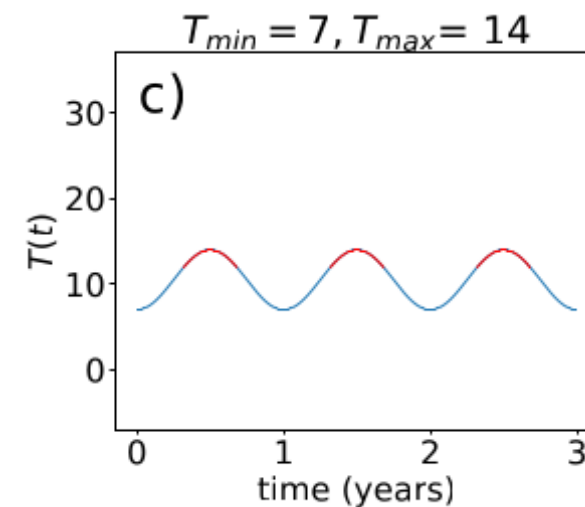
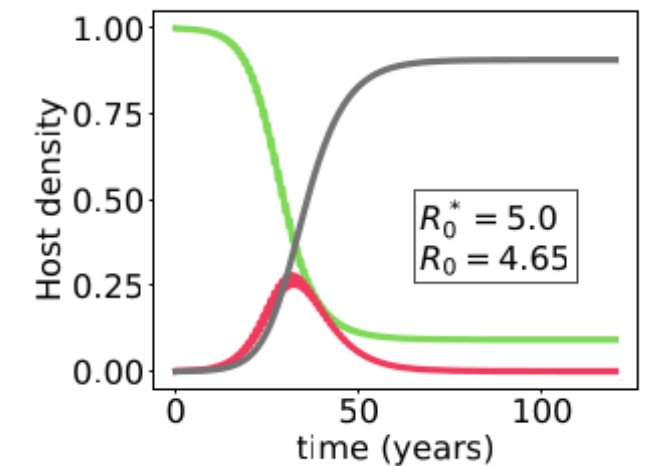
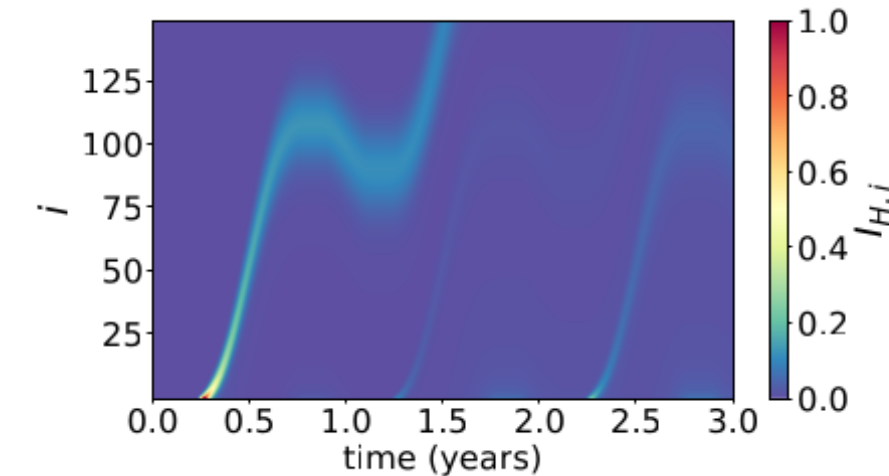
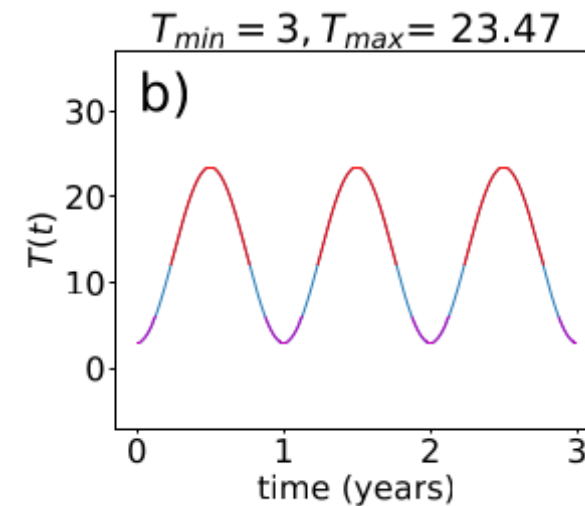
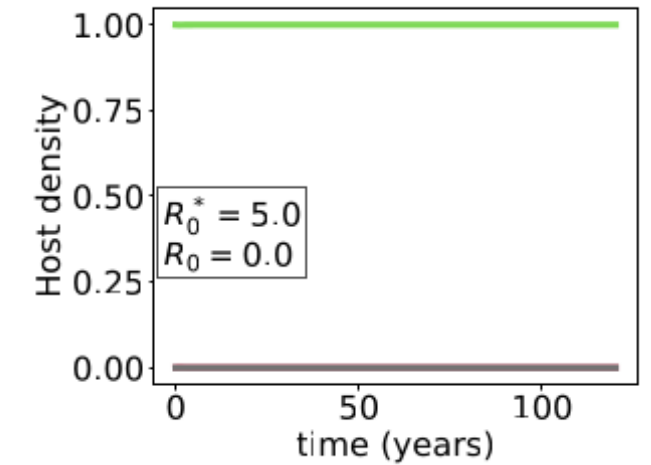
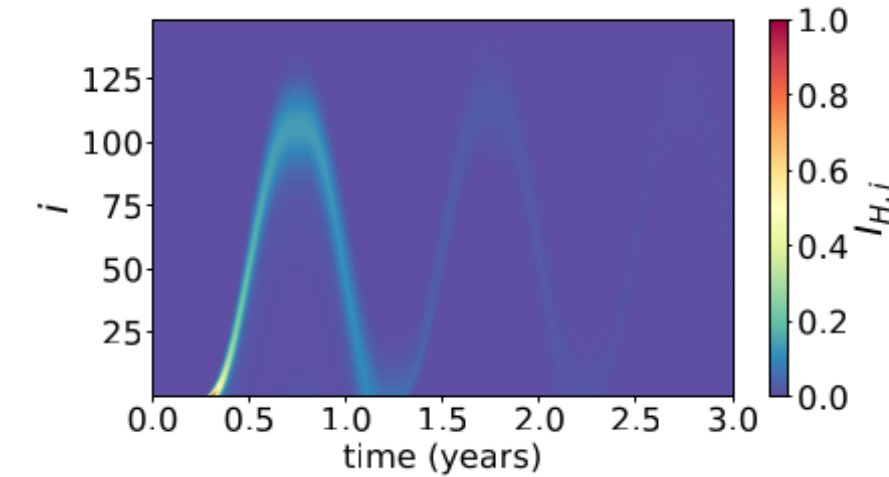
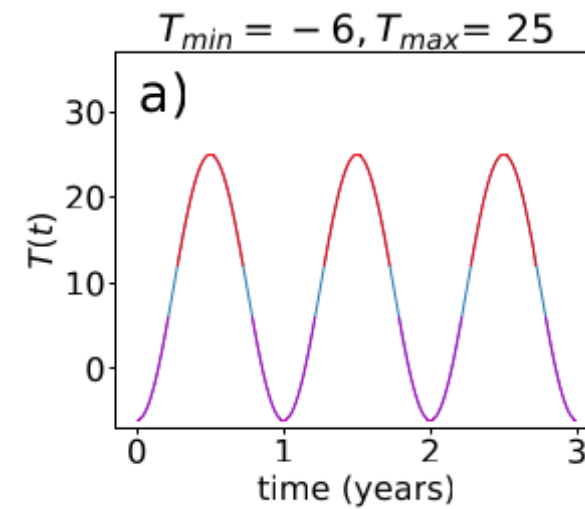
What about potential epidemic dynamics?

J.C. Rodríguez-Cabanillas, M.A. Matías
and À. Giménez-Romero, *In prep* (2026)

$$\begin{aligned}
 \dot{S}_H &= -\beta S_H I_v + \chi(t) I_{H,1}, \\
 \dot{I}_{H,1} &= \beta S_H I_v - \gamma(t) I_{H,1} + \chi(t) (I_{H,2} - I_{H,1}), \\
 \dot{I}_{H,i} &= \gamma(T(t)) (I_{H,i-1} - I_{H,i}) + \chi(T(t)) (I_{H,i+1} - I_{H,i}) \\
 \dot{I}_{H,n-1} &= \gamma(T(t)) (I_{H,n-2} - I_{H,n-1}) - \chi(T(t)) I_{H,n-1}, \\
 \dot{I}_{H,n} &= \gamma(T(t)) I_{H,n-1} - \Gamma I_{H,n}, \\
 \dot{R}_H &= \Gamma I_{H,n}, \\
 \dot{S}_v &= \delta - S_v \sum_{i=1}^n \alpha_i I_{H,i} - \mu S_v, \\
 \dot{I}_v &= S_v \sum_{i=1}^n \alpha_i I_{H,i} - \mu I_v.
 \end{aligned}$$



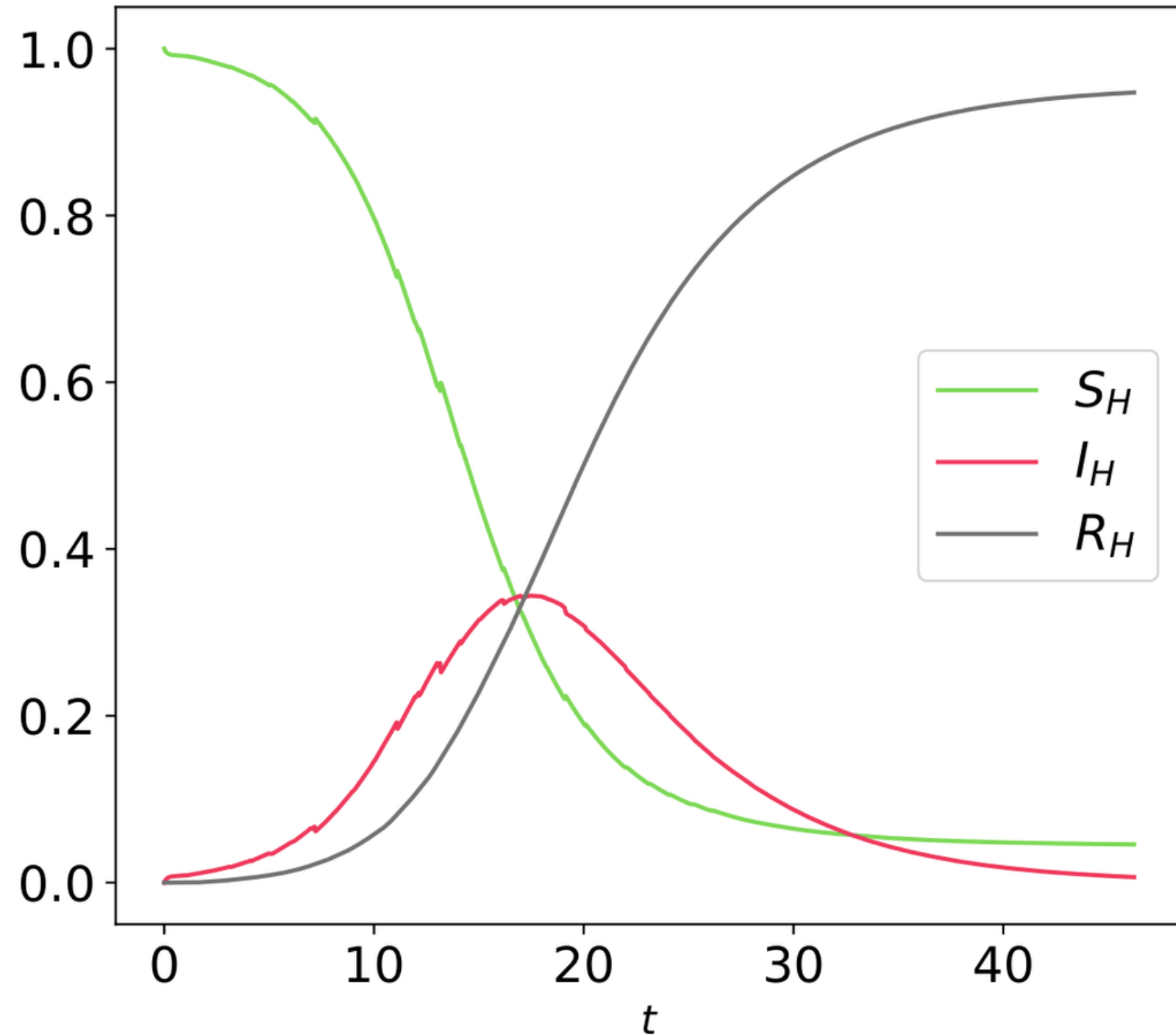
$$R_0 = R_0^* \left[1 + \frac{\Gamma}{f(T)} \int_0^{\mathcal{T}^*} \mathcal{F}(\mathcal{T}) d\mathcal{T} \right]$$



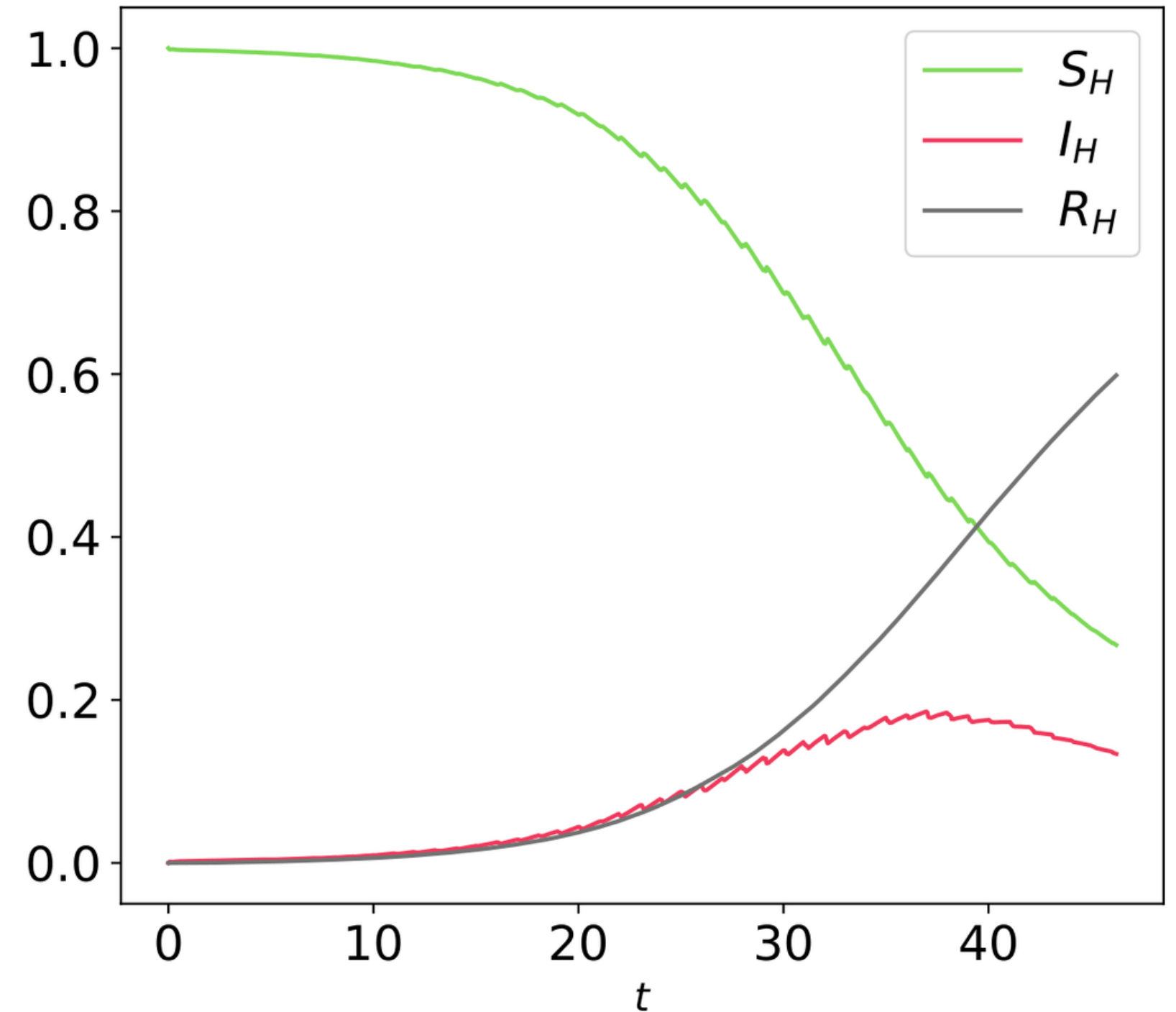
What about potential epidemic dynamics?

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and À. Giménez-Romero, *In prep* (2026)

Mola di Bari, risk=0.65



Mottola, risk=0.39



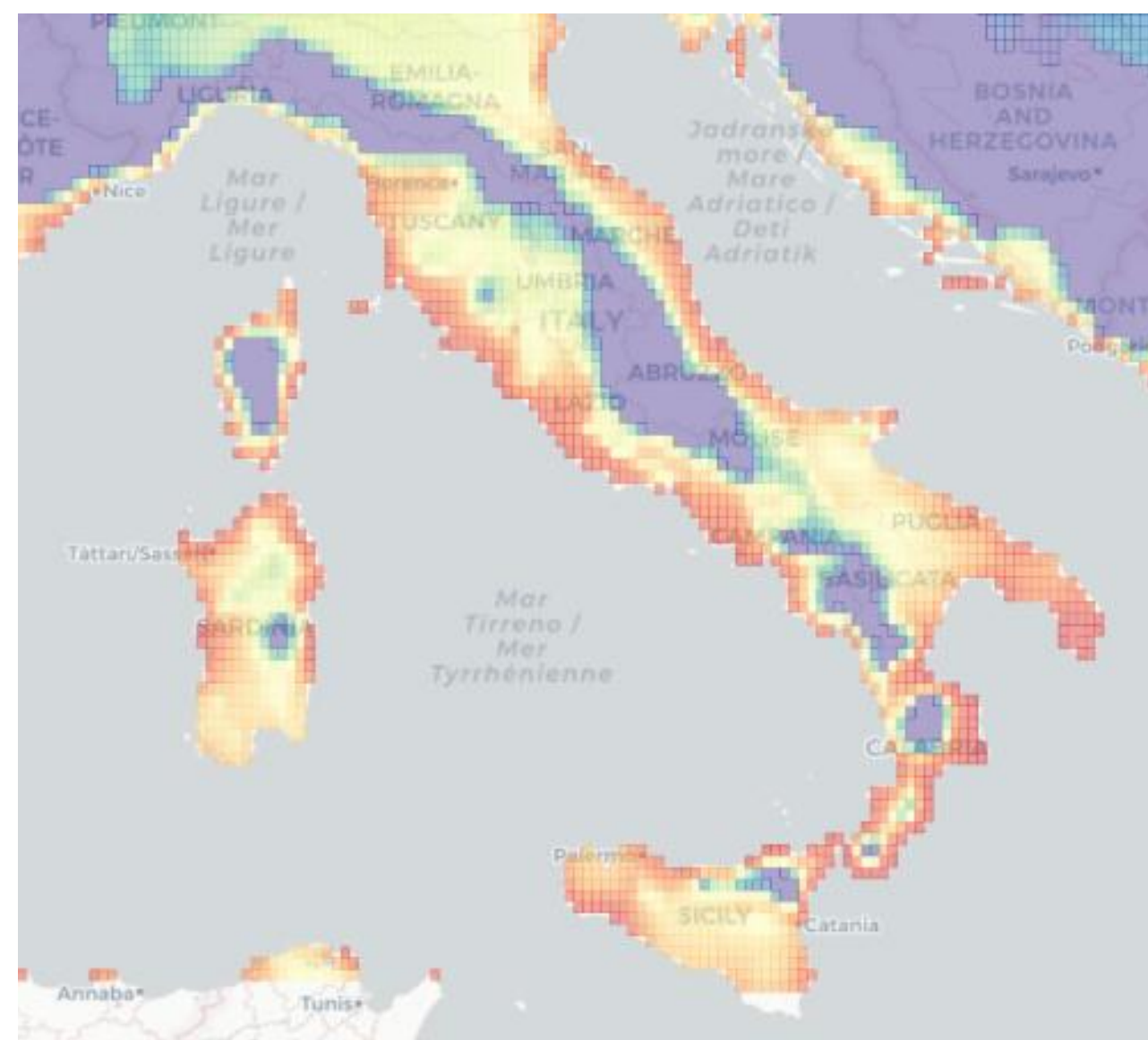


A SERVICE PROVIDED BY



MENU ▾

Risk at +1.5°C



WELCOME TO THE PIERCE'S DISEASE ESTABLISHMENT RISK DASHBOARD!

Pierce's Disease, caused by the bacterium *Xylella fastidiosa*, poses a significant threat to the health and productivity of various crops, particularly grapevines. In order to better understand and mitigate the risks associated with its establishment, a team of dedicated scientists have undertaken extensive research and developed a robust model. This webpage serves as a comprehensive resource that presents the findings of their study, offering valuable insights into the factors influencing Pierce's Disease establishment risk. By examining various environmental, biological, and climatic parameters, the model provides a predictive framework to assess the vulnerability of different regions to the disease. Through this webpage, researchers, policymakers, and stakeholders in the agricultural sector can access critical information, empowering them to make informed decisions and implement effective strategies to prevent and manage Pierce's Disease outbreaks.

MODEL & CURRENT RISK

Discover the present threat level! Uncover our groundbreaking assessment of the current risk of Pierce's Disease, providing vital insights for farmers and researchers alike. Explore our published article in Communications Biology for a deeper dive into our findings!

DASHBOARD

ARTICLE

CLIMATE CHANGE & FUTURE RISK

Peek into the future! Explore our cutting-edge assessment of the future risk of Pierce's Disease under diverse climatic projections. Gain valuable insights into the potential impact on vineyards and agricultural landscapes. Get ready to adapt and mitigate with our research findings!

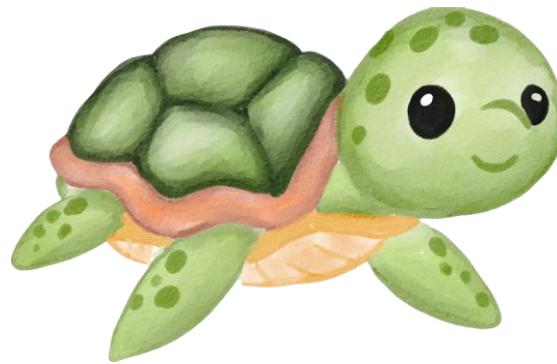
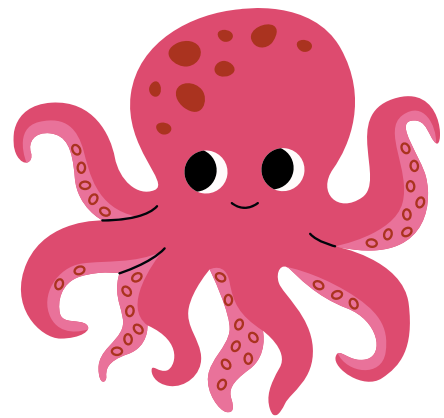
DASHBOARD

ARTICLE

WEB PAGE AUTHOR(S): ÀLEX GIMÉNEZ-ROMERO

<https://pdrisk.ifisc.uib-csic.es/>

Thank you



webpage



agimenezromero.bsky.social



agimenezromero.github.io



agimenezromero



Àlex Giménez Romero

@agimenezromero.bsky.social

472 followers 332 following 17 posts

Physicist. PhD in Physics of Complex Systems. Currently at CEAB-CSIC.

Interested in ecology, epidemiology, AI, remote sensing, quantitative finances, economy, philosophy of science... I code in Julia and Python.

agimenezromero.github.io





Xylella fastidiosa

5th European conference

Bari, Italy | 22-26 June 2026



REGIONE PUGLIA



UNIVERSITÀ
DEGLI STUDI DI BARI
ALDO MORO



**A novel and rapid *in vitro* method
for assessment of *Vitis vinifera* susceptibility to
Xylella fastidiosa subsp. *fastidiosa***



Xylella fastidiosa
subsp. *fastidiosa*

Marwa Mourou⁺, Giuseppe Incampo⁺, Giovanna Bottalico, Flora Spataro, Vito Montilon*,

Francesco Faretra, Franco Nigro and Stefania Pollastro

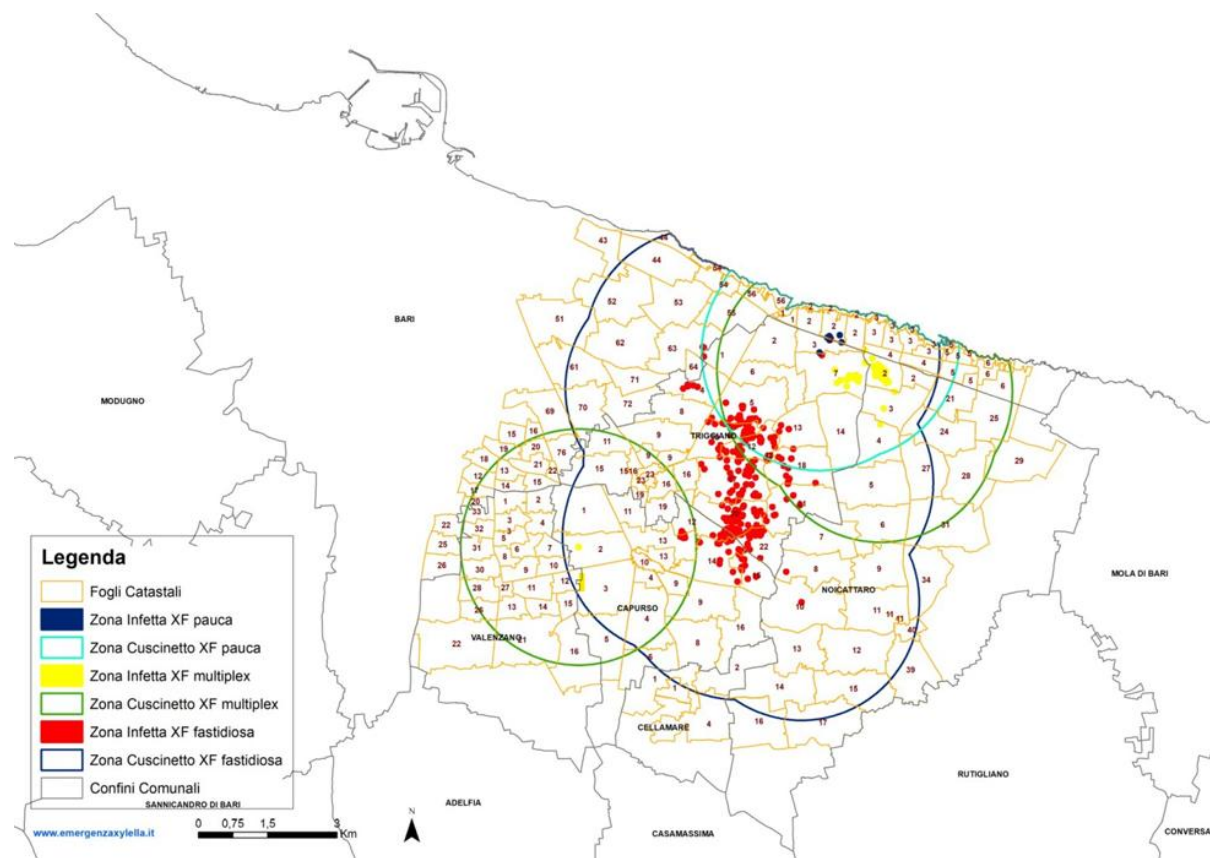
⁺ These authors share first authorship

Department of Soil, Plant and Food Sciences, University of Bari Aldo Moro, via Amendola

165/A 70126 Bari, Italy

Introduction

- One of the most destructive phytopathogens worldwide
- Firstly detected in California
- Reported in Apulia in 2024 on Vitis and Almond trees



1. *In vitro* plants

Objective:

- In vitro evaluation of the response of grapevine varieties deriving from the DiSSPA *ex situ* germplasm collection to controlled infections with *Xylella fastidiosa subsp. fastidiosa* ST1

To make this:

- Single-nodes cutting from *in vivo* plants were cultured on a nutrient medium (Quoirin and Lepoivre 1978)
- After 5 subcultures, individual shoots were transferred to the same medium without plant growth regulators
- Twelve biological replicates were used

Varieties

Aglanico
Bianca Antica
Gaglioppo
Greco Bianco
Lacrima Nera
Magliocco Dolce
Magliocco Canino
Zagarese

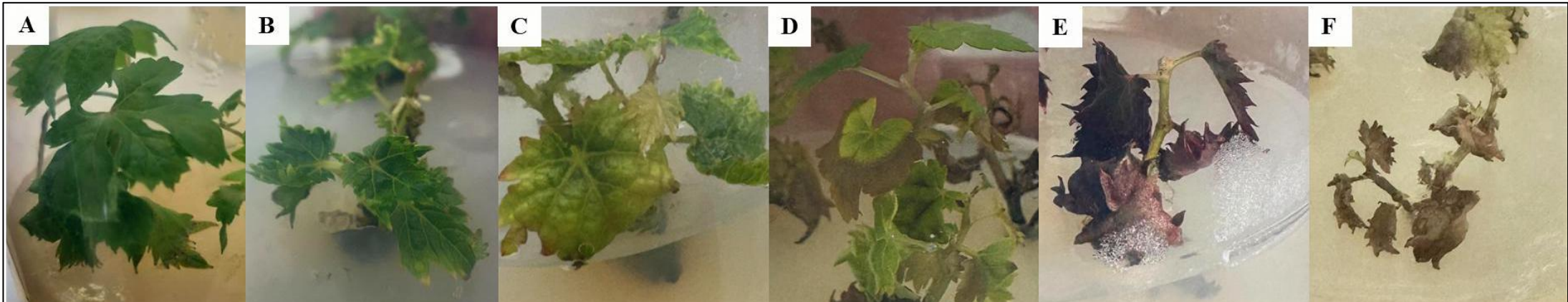


2. Inoculation

- Inoculation was performed using a hypodermic syringe.
- A suspension of Xff in PD3 broth was injected into the basal part of each plant.

2.1 Severity index scale

Symptoms were assessed at 15-day intervals after inoculation, up to 60 days post-inoculation. The severity index ranged from 0, corresponding to asymptomatic plants, to 5, corresponding to dead plants, as shown in panels A–F.



3. qPCR assays

qPCR assays were performed on the apical portions of the plants

- to determine the percentage of positive plants at different time points
- to estimate the bacterial load in each variety.

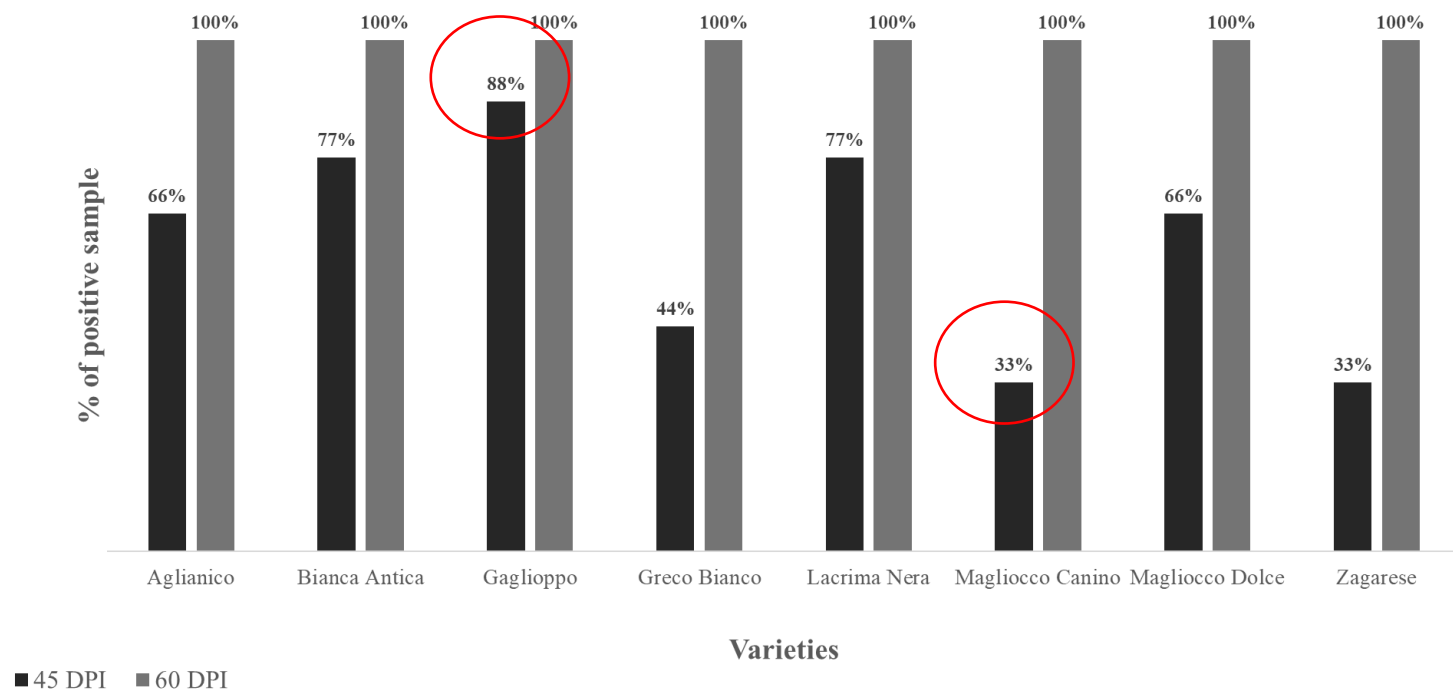


Figure 1. Percentage of positive samples after 45 and 60 DPI

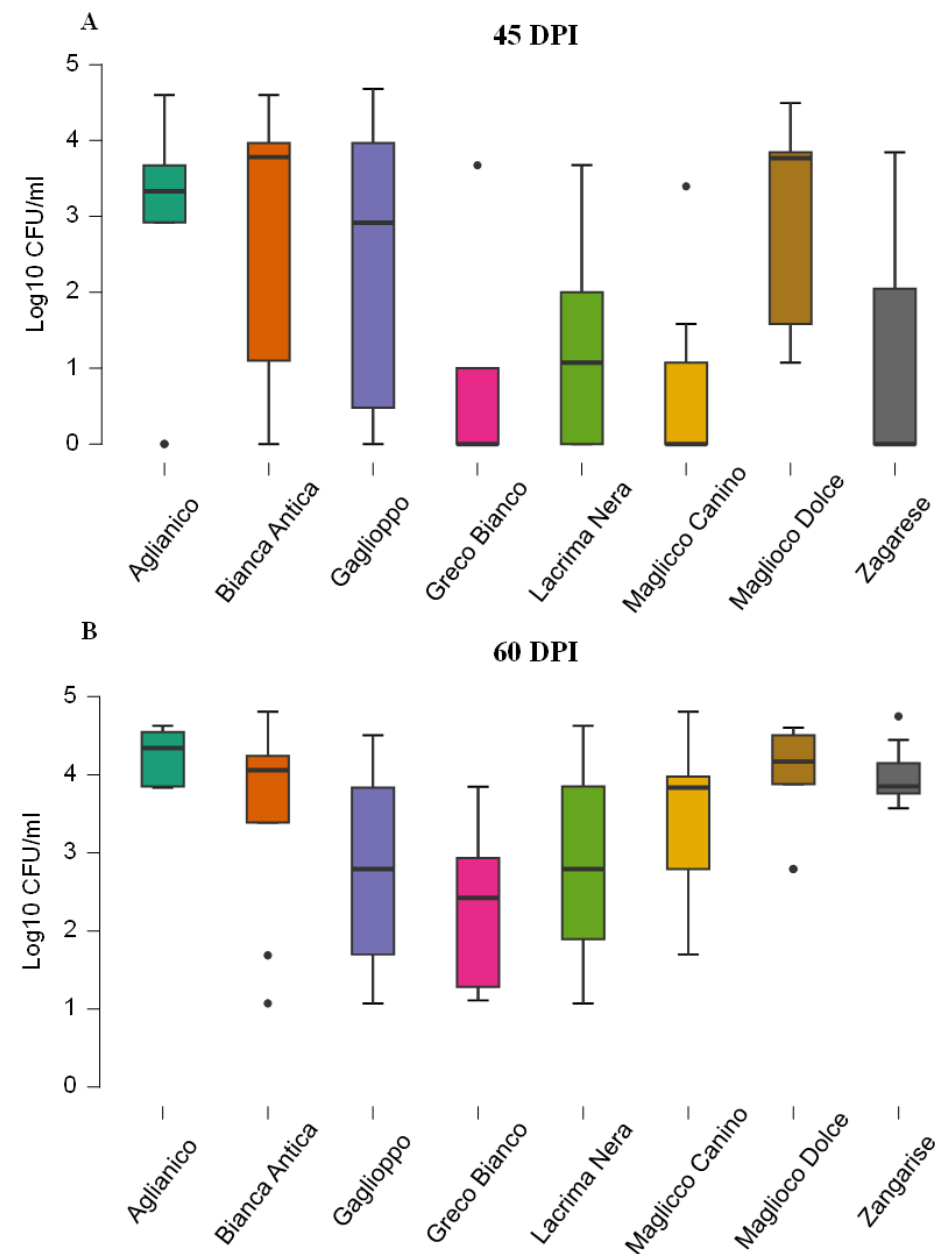
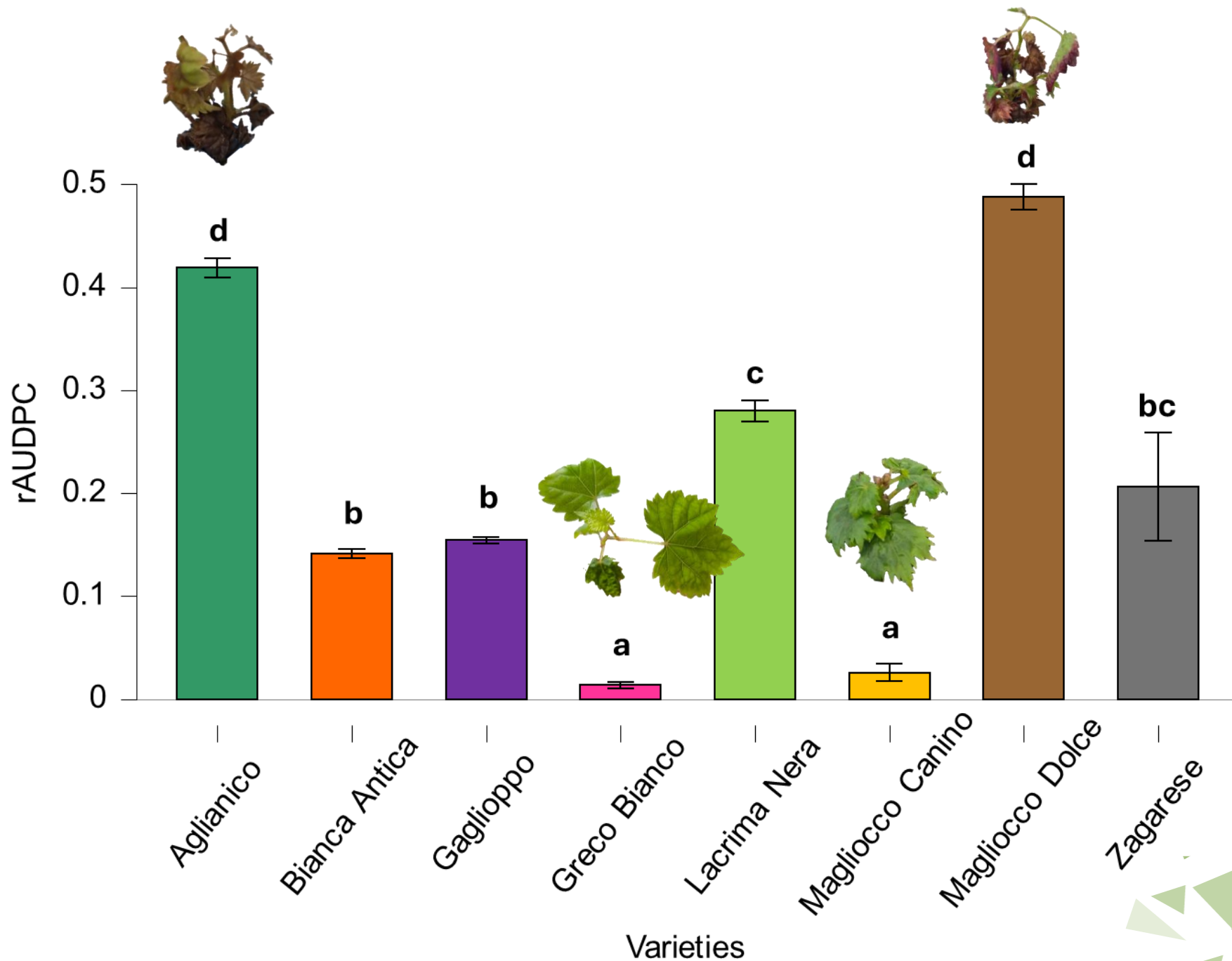


Figure 2. Log10 CFU/ml at 45 and 60 DPI

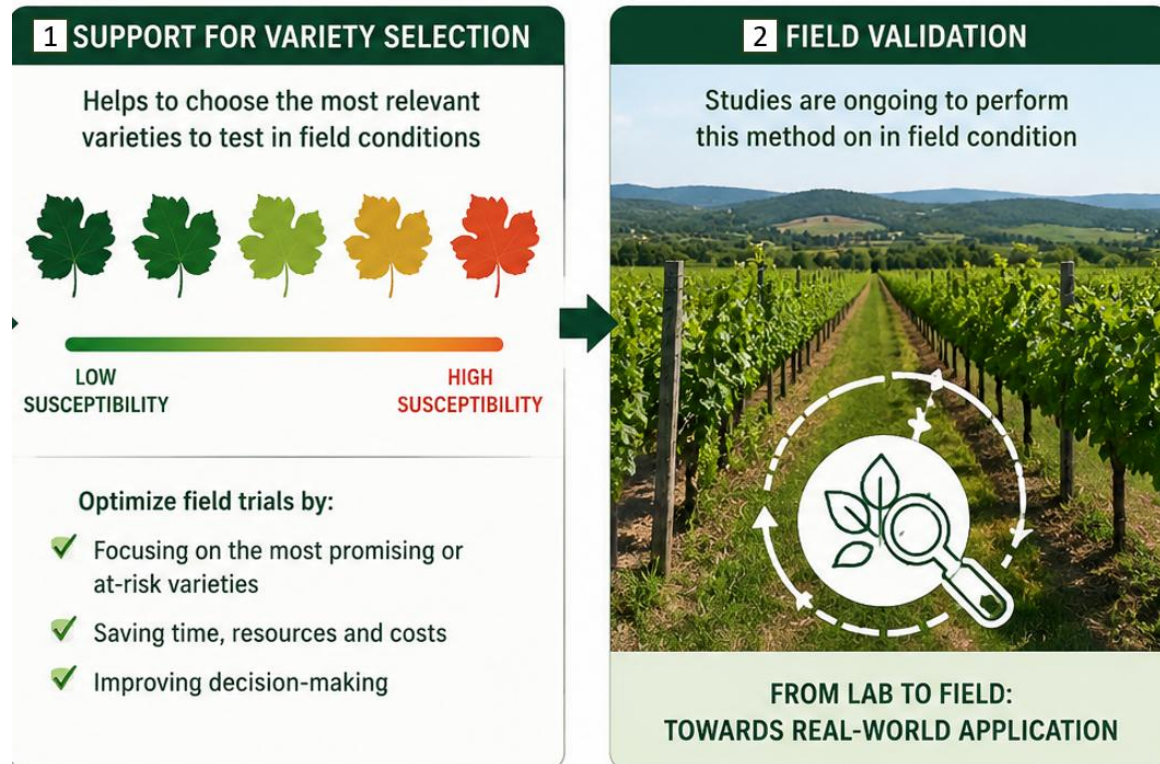
4. rAUDPC

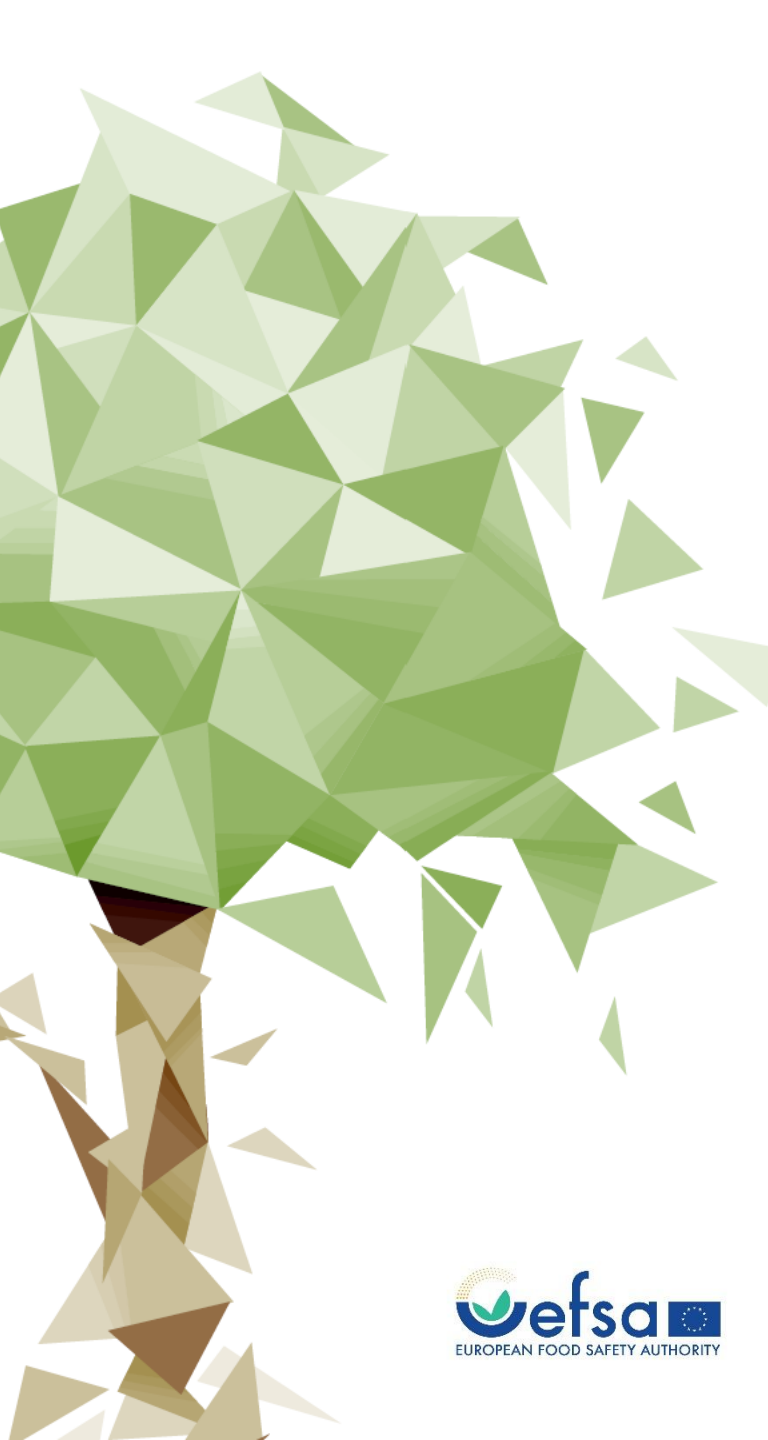
- The rAUDPC was performed at 60 DPI
- Based on symptoms
- Statistically significant differences were found between the different varieties



5. Conclusions

- This method may provide a reliable approach for assessing *Vitis vinifera* susceptibility and for selecting varieties for subsequent field evaluation.
- Future studies will focus on validating the method across additional cultivars and under field conditions.
- Moreover, this approach may also be useful for the study of other vector-borne quarantine pathogens.





Introducing the project **XYL-o-VINE: Ecology, ethology and transmission biology of *Xylella fastidiosa* by insect vectors in table grape vineyards**

5th European conference

Bari, Italy | 25 June 2026

Pitch talk presenter: Michela Chiumenti (IPSP, CNR)



ECOLOGY, ETHOLOGY AND TRANSMISSION BIOLOGY OF XYLELLA FASTIDIOSA BY INSECT VECTORS IN TABLE GRAPE VINEYARDS

Funding institution: European Food Safety Authority (EFSA)

Grant Agreement: EUBA-EFSA-2025-PLANTS-01-Lot1

Period: 48 months, starting from 19th February 2026



Consortium:



Prof. Daniele Cornara



Michela Chiumenti



Berkeley
UNIVERSITY OF CALIFORNIA

Prof. Rodrigo Almeida

Focus: Table grape

Key Knowledge gaps:

1. the **tendone training** system widely used in Apulian table grape vineyards creates unique microclimatic and structural conditions that may significantly affect the insect–bacterium–plant interaction.
2. the **primary insect vector**: spittlebugs (family Aphrophoridae) differ significantly in phenology, ecology, and behavior from the sharpshooters (family Cicadellidae)



These differences likely lead to distinct patterns of bacterial spread and must be taken into account when developing **monitoring** and **containment strategies**.

XYLOVINE - Objectives

Objective 01

Task 1

Vector ecology

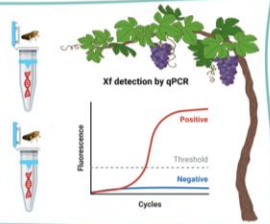
Field survey and collection of data about climate, landscape, agronomic practices and vector movement



Task 2

Vector infectivity

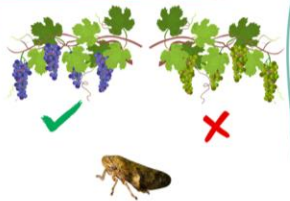
Collection of data about vector infectivity in table grape vineyards through qPCR and sequence type identification



Task 3

Vector preference

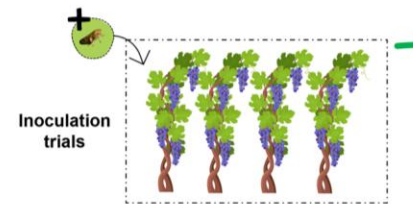
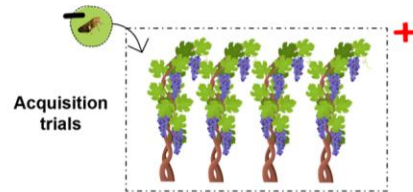
Collection of data about vector preference for different table grape cultivars through behavioral trials



Objective 02

Vector transmission efficiency

Evaluation of transmission efficiency by spittlebugs to different table grape cultivar throughout the seasons



Objective 3

Dissemination of project activities

Task 1

Publication of open access scientific articles, protocols and raw datasets



Task 2

Dissemination of results through social media



Task 3

Participation to national and international conferences



Task 4

Organization of the European Pierce's disease Symposium



Task 5

Podcast dedicated to Pierce's disease and project activities



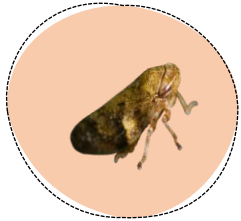
(i) elucidate the ecology, seasonal dynamics, and host preferences of potential insect vectors in table grape vineyards, including the influence of agronomic, climatic, and landscape factors on vector activity

(ii) assess vector transmission efficiency and cultivar susceptibility through field-based transmission trials conducted throughout the growing season

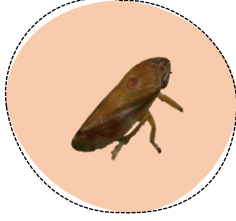
(iii) disseminate findings to stakeholders and the scientific community

EXPECTED RESULTS

To generate foundational **KNOWLEDGE** on the ecology and population dynamic of insect vectors of *Xylella fastidiosa*, and on the transmission biology of the fastidious bacterium, in **TABLE GRAPE VINEYARDS**.



*Philaenus
spumarius*



*Neophilaenus
campestris*

$$P_{nt} = 1 - (1 - iE)^{nt}$$

Purcell, 1981

**Better understanding of Xff-ST1
vector-pathogen-host interactions**
in table grape systems,
identification of key risk factors,
and **generation of data to support
EFSA risk assessment.**

Objective 1 Task 2

To determine **INFECTIVITY** (*i*) **TRENDS** throughout
the year in table grape vineyards

Objective 1 Task 1 and 3

To assess populations
dynamics, host plant
preference and the influence
of exogenous factors
including agronomic
practices on **VECTOR
ACTIVITY** (*nt*) in table grape
vineyards

n=Abundance
t=Time spent on plants

Objective 2

To characterize transmission **EFFICIENCY** (*E*)
and transmission dynamic throughout the year
under semi-field/field conditions

Poster 157

INTRODUCING THE PROJECT XYL-O-VINE: ECOLOGY, ETHOLOGY AND TRANSMISSION BIOLOGY OF XYLELLA FASTIDIOSA BY INSECT VECTORS IN TABLE GRAPE VINEYARDS

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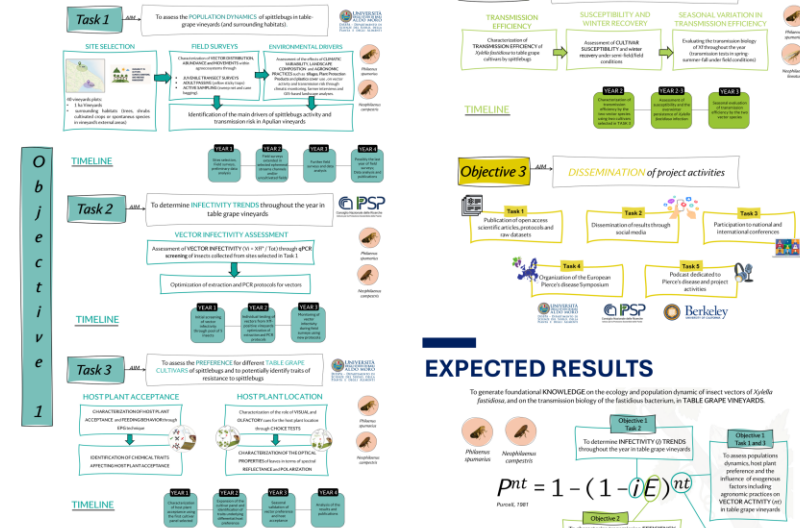
INTRODUCTION

The emergence of *Xylella fastidiosa* subsp. *fastidiosa* Sequence Type 1 (Xff-ST1) in table grape vineyards in Apulia, Southern Italy, poses a significant new threat to European viticulture. Unlike well-studied outbreaks in olives, the epidemiology of Xff-ST1 in table grape systems remains poorly understood. Preliminary evidence suggests a bimodal transmission pathway involving *Neophilaenus campestris* (almond-to-grapevine) and *Philaenus spumarius* (grapevine-to-grapevine), but current data are spatially and temporally limited.

In this context, the **XYLOVINE** project, funded by the **European Food Safety Authority (EFSA)** under grant agreement number EUBA-EFSA-2025-PLANTS-01-Lot1, aims to:

- **Objective 1:** elucidate the ecology, seasonal dynamics, and host preferences of potential insect vectors in table grape vineyards, including the influence of agronomic, climatic, and landscape factors on vector activity;
- **Objective 2:** assess vector transmission efficiency and cultivar susceptibility through field-based transmission trials conducted throughout the growing season;
- **Objective 3:** disseminate findings to stakeholders and the scientific community.

METODOLOGY



CONCLUSIONS

A better understanding of Xff-ST1 vector-pathogen-host interactions in table grape systems, will allow the identification of key risk factors, and the generation of data to support EFSA risk assessment. XYL-o-VINE will provide data to help protect European table grape production and strengthen preparedness against future outbreaks.

For further details and to know more about the ongoing activities check our poster (157)!

Thank you for the attention!