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## **Monitor and steer the microbiota to protect grapevines against downy mildew**

Corinne Vacher, Simon Labarthe

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Corinne Vacher, Simon Labarthe. Monitor and steer the microbiota to protect grapevines against downy mildew. 2025 Annual Meeting of the VITAE project, PPR 'Growing and Protecting Differently', Mar 2025, Angers, France. <hal-05300025>

**HAL Id: hal-05300025**

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Submitted on 6 Oct 2025

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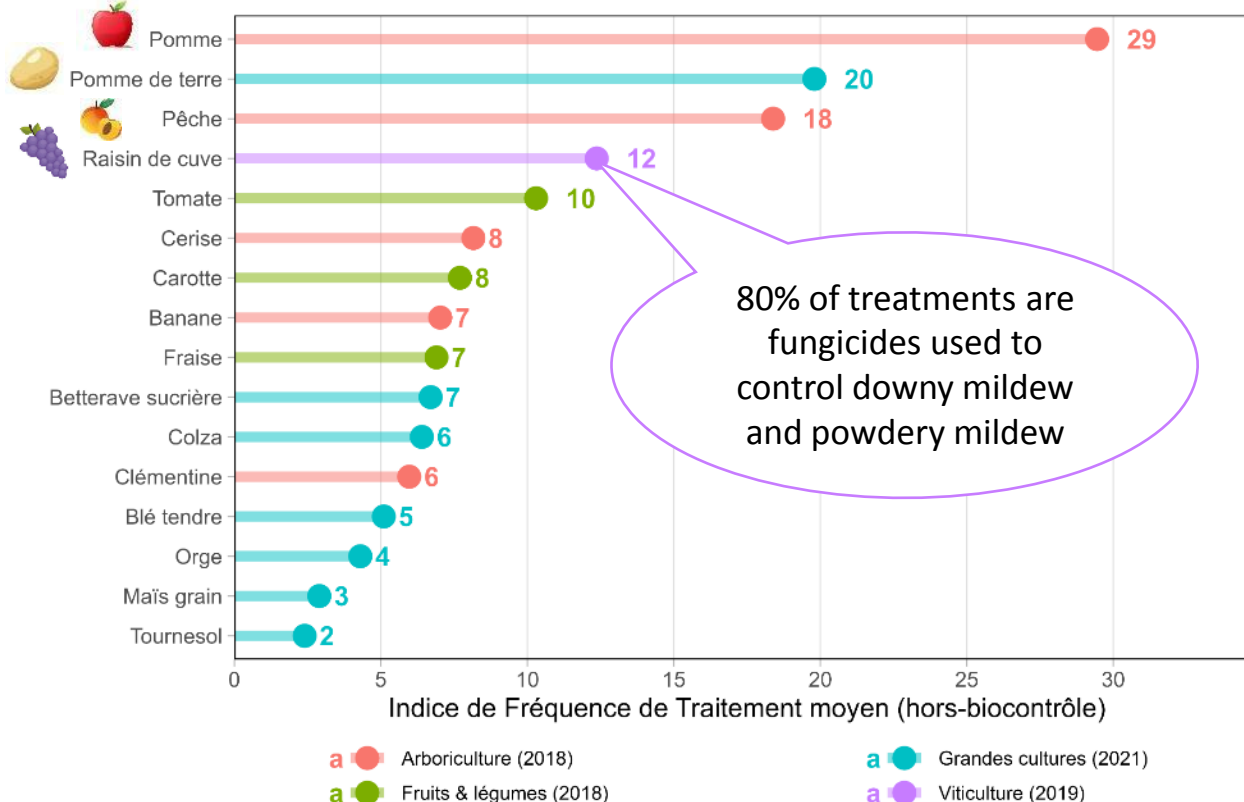


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# Monitor and steer the microbiota to protect grapevines against downy mildew

**Corinne Vacher**, INRAE, SAVE & **Simon Labarthe**, INRAE, Biogeco

# Grapevines are heavily treated



**Downy mildew**  
*Plasmopara viticola*  
(oomycete)



**Powdery mildew**  
*Erysiphe necator*  
(fungus)



**Image Source - Graph:** Simonovici & Caray. Agreste. 2023; modified by Olivier Nefti; **Diseased Leaves:** <http://ephytia.inra.fr/fr/D/1757>

# Towards zero-pesticide viticulture

**PROPHYLAXIS &  
GRAPEVINE MANAGEMENT**  
Reducing inoculum pressure and  
creating an unfavorable  
microclimate for aerial diseases



**EPIDEMIOLOGICAL MONITORING**  
Predict epidemic risk and optimize  
practices



**DISEASE BIOCONTROL**  
Protect the plant against  
diseases through natural  
regulations

**GRAPE BREEDING**  
Selecting plants with greater  
disease resistance



# Microbiota-based management



**PROPHYLAXIS & GRAPEVINE MANAGEMENT**  
Reducing inoculum pressure and creating an unfavorable microclimate for aerial diseases



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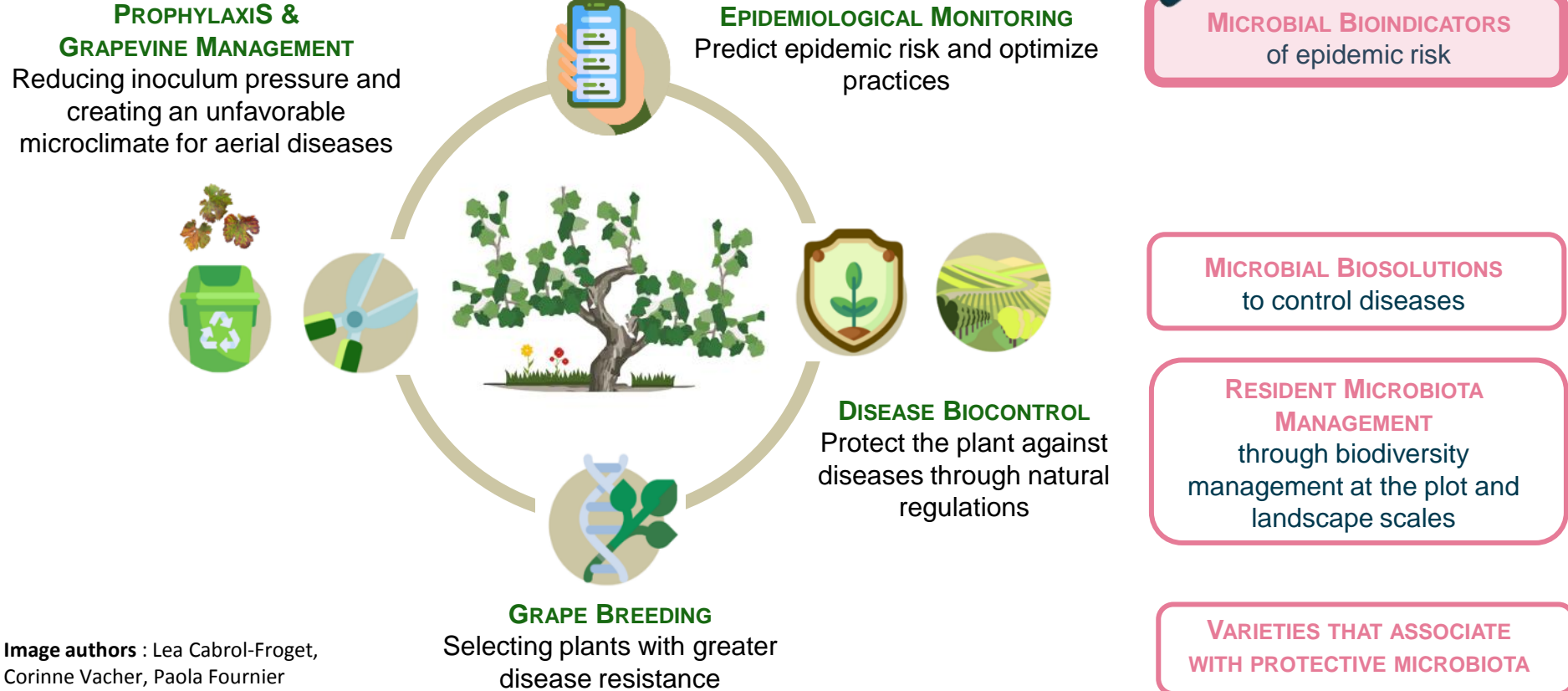
**MICROBIAL BIOINDICATORS**  
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**RESIDENT MICROBIOTA MANAGEMENT**  
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**VARIETIES THAT ASSOCIATE WITH PROTECTIVE MICROBIOTA**

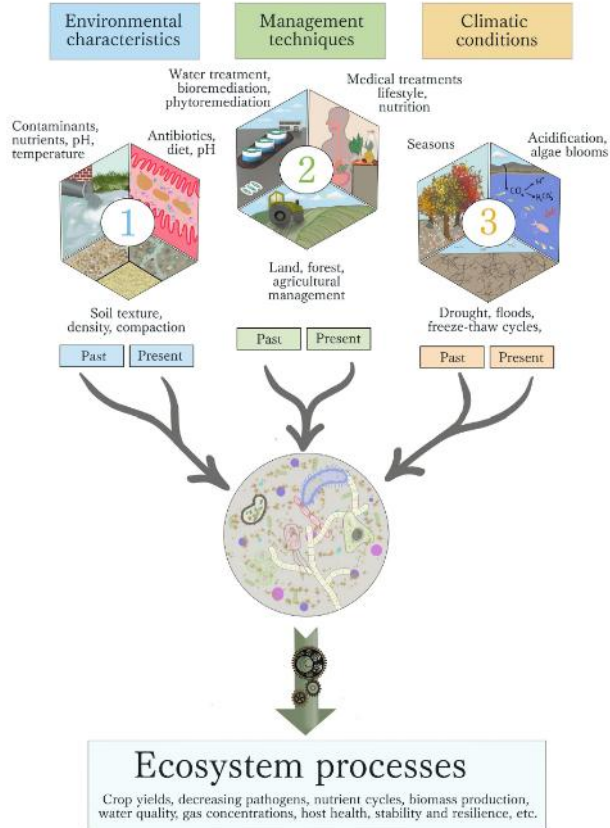
# Microbiota-based management



# Monitor the microbiota to predict risk of downy mildew epidemics

**Corinne Vacher**, INRAE, SAVE & **Simon Labarthe**, INRAE, Biogeco

# The predictive power of the microbiota



## Opinion

### The forecasting power of the microbiome

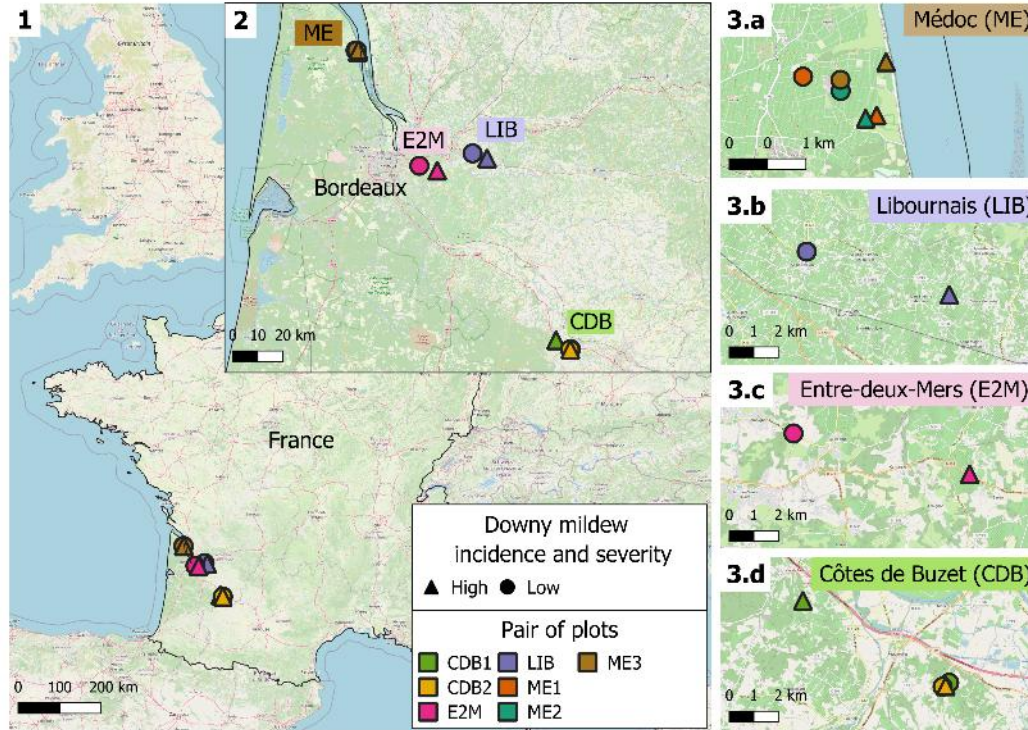
Sara Correa-Garcia <sup>1</sup>, Philippe Constant, <sup>1</sup> and Etienne Yergeau <sup>1,\*</sup>

Microbial communities **integrate** past and present ecosystem features (e.g. climate conditions, agricultural practices)

Microbial communities are directly **involved** in ecosystem processes (e.g. crop yield, protection against pathogens)

- Microbiome data can be used in forecasting models

# Can we predict downy mildew incidence and severity from microbiota data?

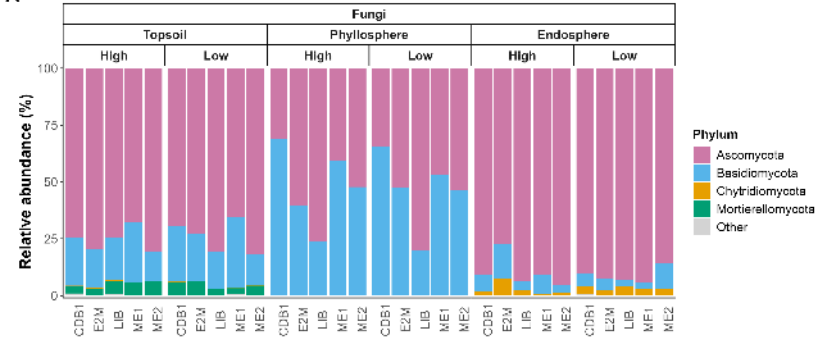


**Paola  
Fournier**

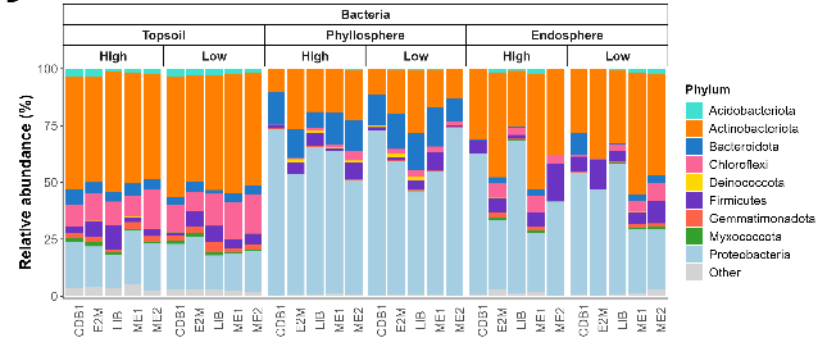
# Analysis of the early-season microbiota



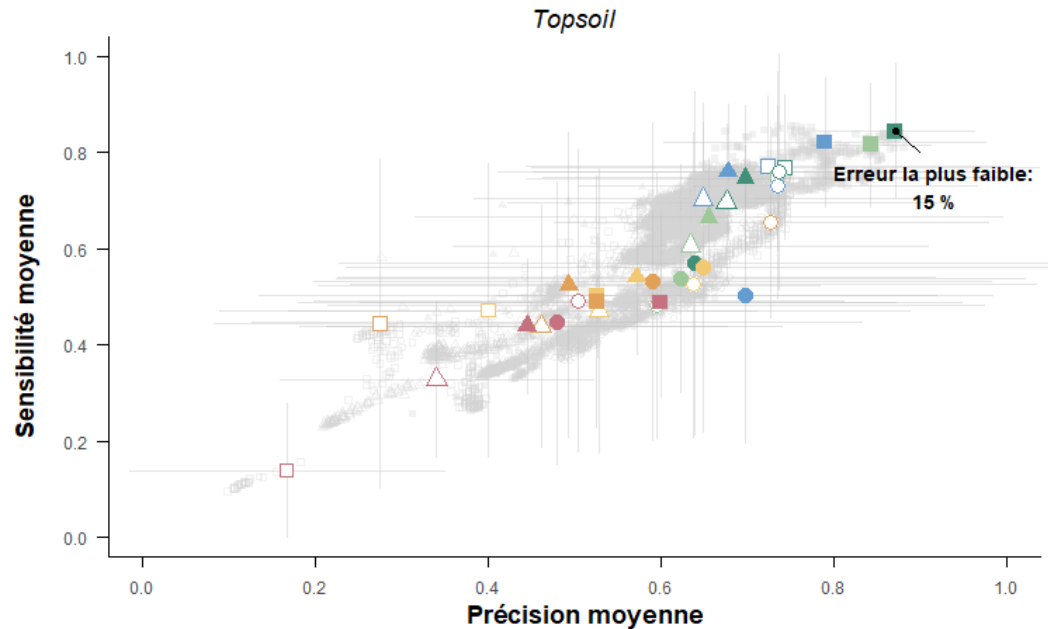
**A**



**B**



# Within-year predictions using RF algorithms



- Microbiota data:**
- Tous les champignons
  - ◇ Toutes les bactéries
  - △ Tous les champignons + bactéries
  - Champignons abondants
  - ◆ Bactéries abondantes
  - Champignons abondants + bactéries

- Niveau taxonomique:**
- ◆ ASV
  - ◆ Espèce
  - ◆ Genre
  - ◆ Famille
  - ◆ Ordre
  - ◆ Classe

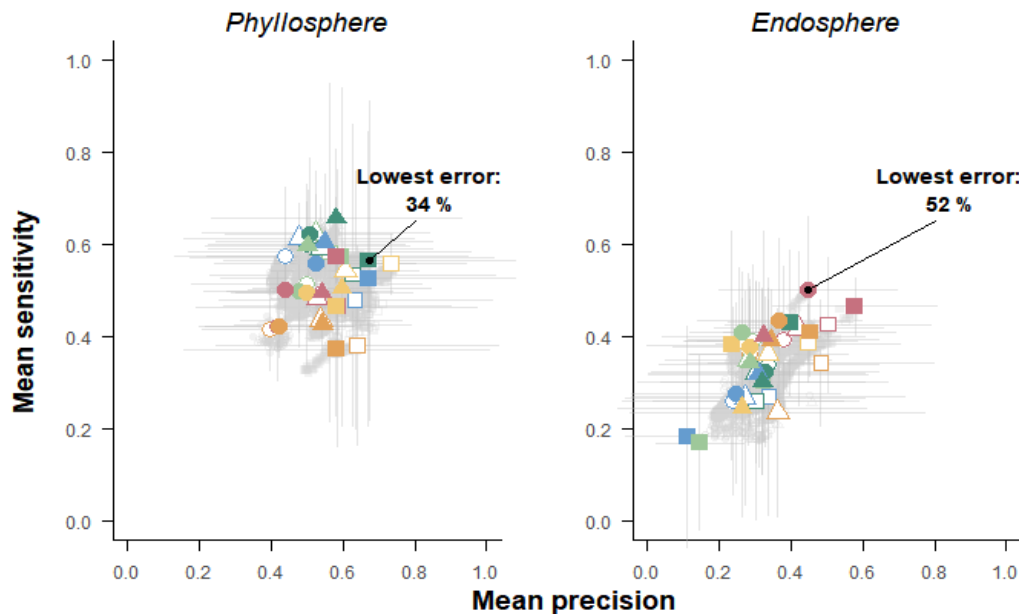
**Abundant fungi of the topsoil microbiota are good predictors of disease incidence and severity.**



**Paola Fournier**

Fournier et al. Environmental Microbiome. 2025  
Cambon et al. Molecular Ecology. 2023 (NGB project)

# Within-year predictions using RF algorithms



- Microbiota data:**
- All fungi
  - ◇ All bacteria
  - △ All fungi + bacteria
  - Abundant fungi
  - ◆ Abundant bacteria
  - ▲ Abundant fungi + bacteria

- Taxonomic level:**
- ◆ ASV
  - ◆ Species
  - ◆ Genus
  - ◆ Family
  - ◆ Order
  - ◆ Class

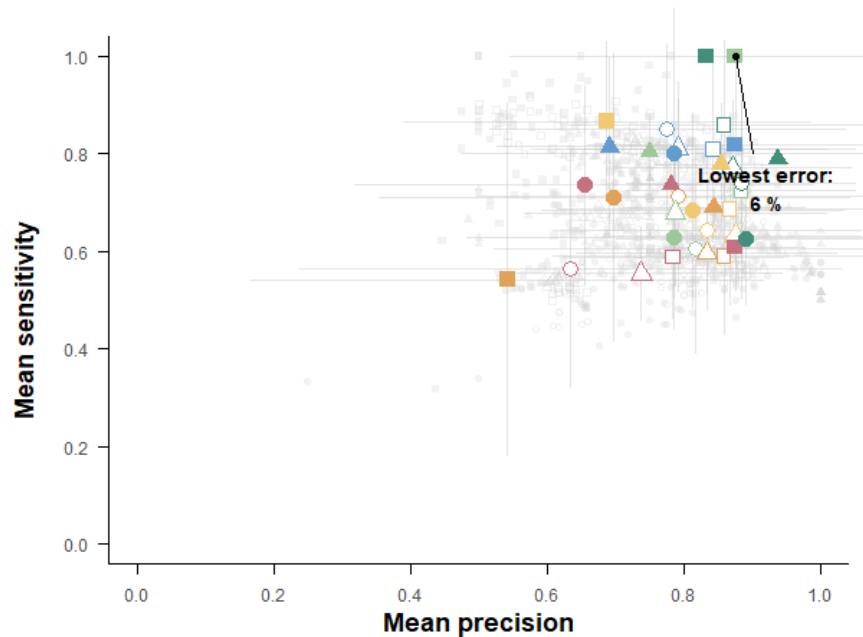
**Foliar microbial communities cannot predict disease incidence and severity.**



**Paola Fournier**

Fournier et al. Environmental Microbiome. 2025

# Between-year predictions using RF algorithms



- Microbiota data:**
- All fungi
  - ◇ All bacteria
  - △ All fungi + bacteria
  - Abundant fungi
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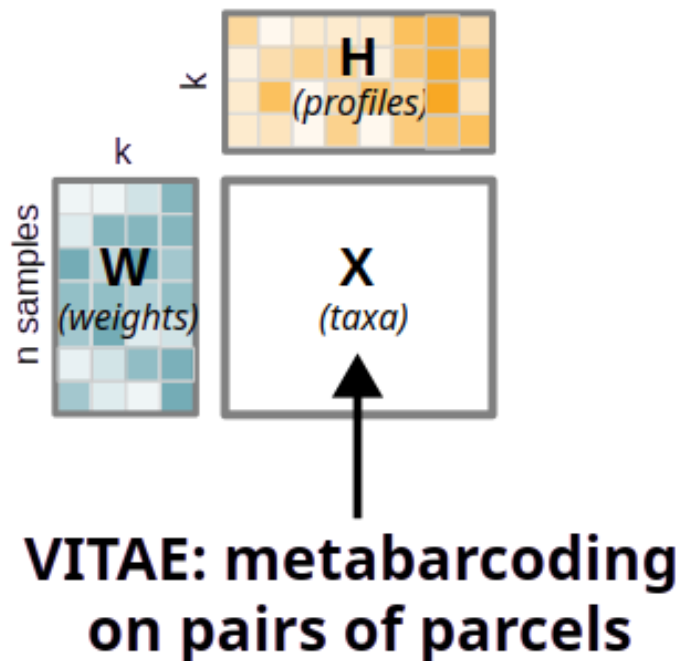
**Algorithms trained with 2022 microbiota data can be used to predict disease incidence and severity in 2023.**



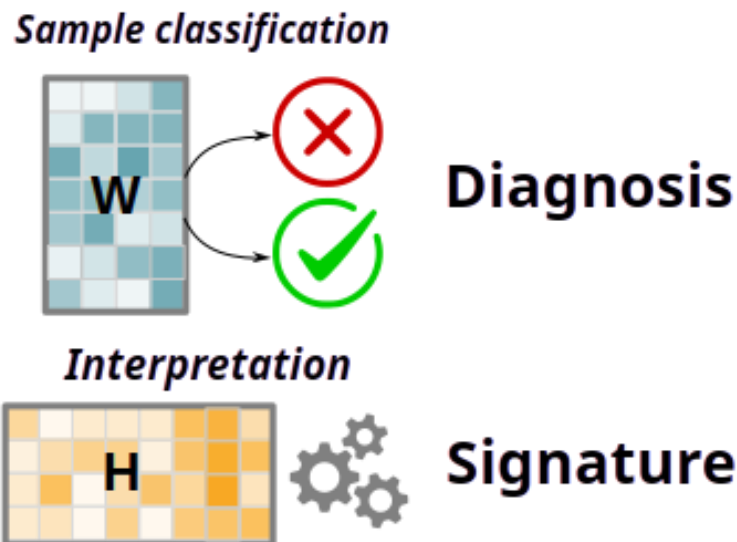
**Paola Fournier**

Fournier et al. Environmental Microbiome. 2025

# Perspectives – Improving predictions using dimension reduction methods

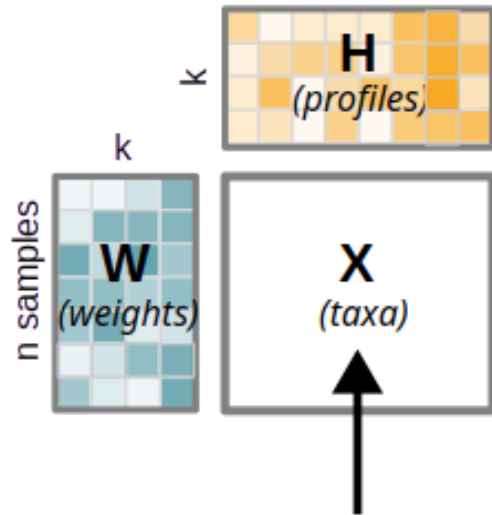


## Classical dimension reduction



# Perspectives – Improving predictions using dimension reduction methods

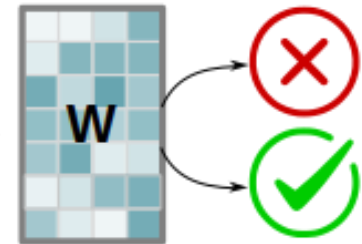
## Optimized dimension reduction for classification



**VITAE: metabarcoding on pairs of parcels**

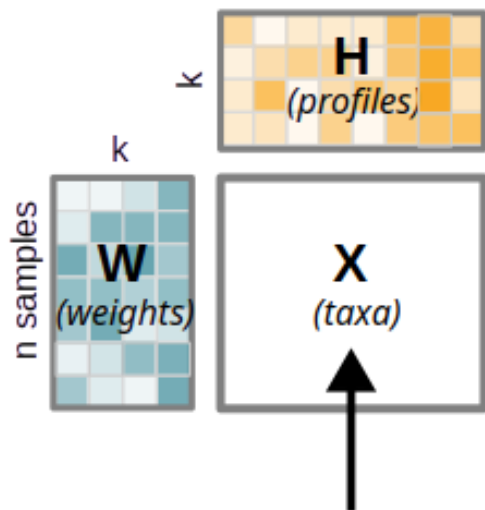


*Optimal reduction basis for classification*



# Perspectives – Selecting sentry microorganisms of epidemic risk

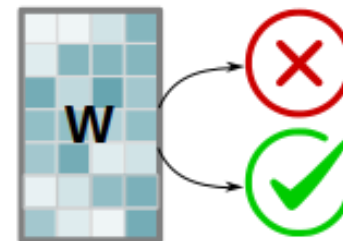
## Selection of sentry microorganisms for classification



**VITAE: metabarcoding on pairs of parcels**



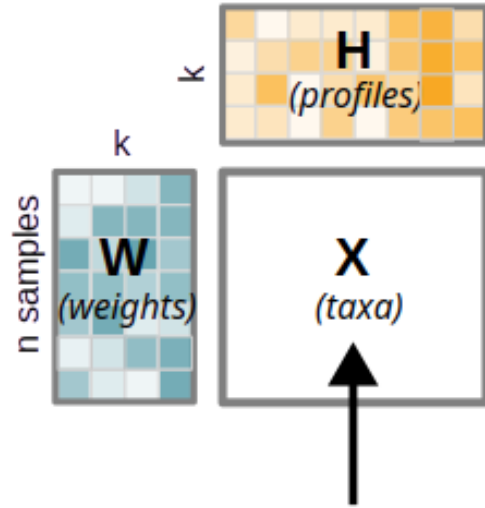
*Optimal reduction basis for classification*  
+  
*feature selection*



**=> optimized q-PCR chip**

# Perspectives – Selecting sentry microorganisms of epidemic risk

## Selection of sentry microorganisms for classification



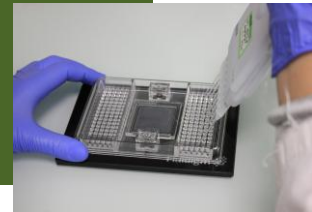
**VITAE: metabarcoding  
on pairs of parcels**



Yannis Ben  
Bassite

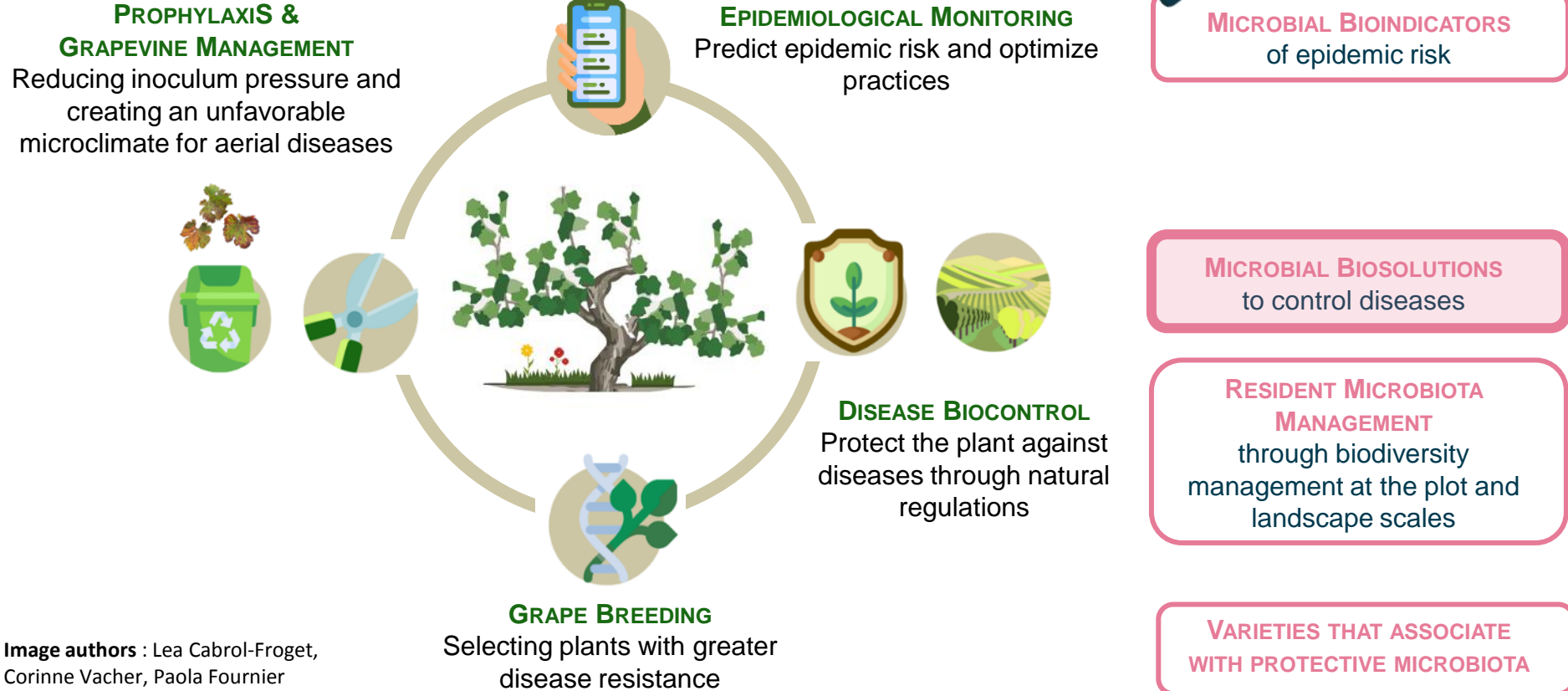


Manon  
Chargy



**=> optimized q-PCR chip**

# Microbiota-based management



# Steer the microbiota using biosolutions to strengthen protection against downy mildew

**Corinne Vacher**, INRAE, SAVE & **Simon Labarthe**, INRAE, Biogeco

# Few biocontrol products are available

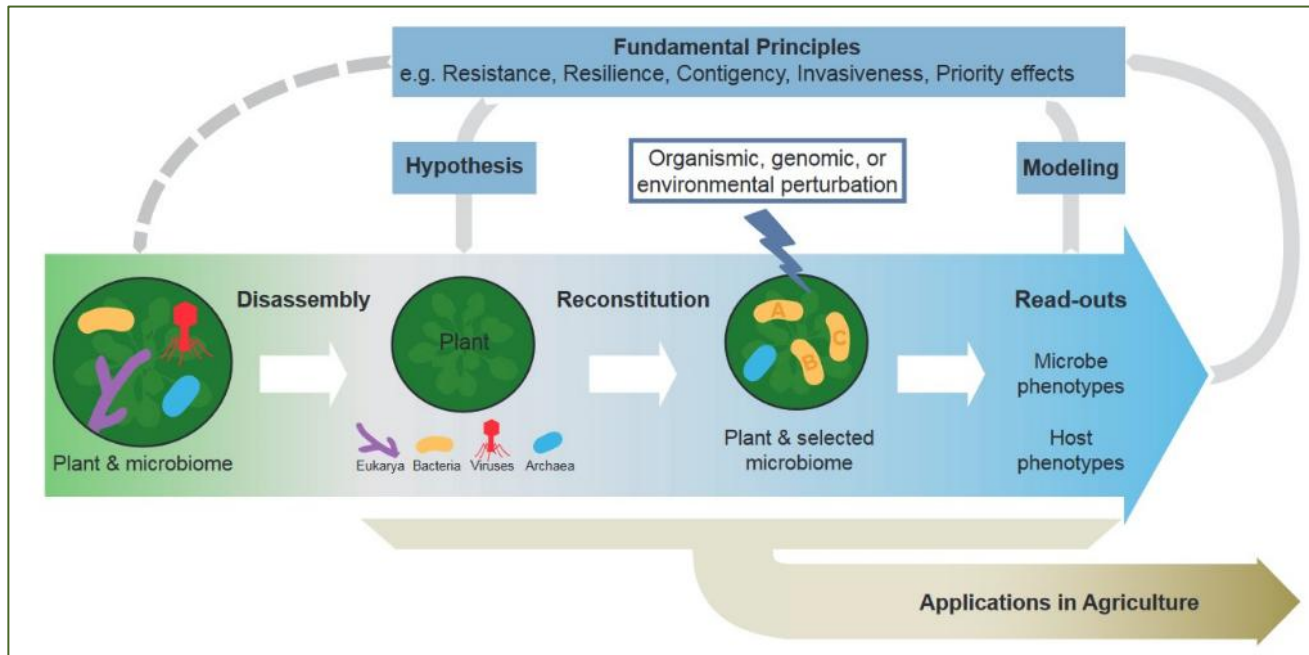
Les produits disponibles

Noms commerciaux	Catégorie	Principe actif	Mode d'action	Utilisable en AB
LBG-01F34 / Etonan / Pertinan / Alucinan / Facinan	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Phytosarcan/ Kerala	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Fosika / Milfos	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Savial Forte / Mikonos/ Cuneb	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Ceraxel / BCPC358FC	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Redeli / Sirius / Fructial	Substance naturelle	Phosphonate de potassium	Fongicide et SDP	
Messenger/ Blason / Bastid / Bstim	Substance naturelle	COS-OGA	Stimulateur des défenses (SDP)	AB
Fytosave /Esdéaine	Substance naturelle	COS-OGA	Stimulateur des défenses (SDP)	AB
Romeo / Actileaf	Substance naturelle	Cerevisane (parois de levures)	Stimulateur des défenses (SDP)	AB
Essen'ciel/ Limocide/ Auran'ciel /Limoil	Substance naturelle	Huile essentielle d'orange	Fongicide	AB
Taegro*	Micro-organisme	<i>Bacillus amyloliquefaciens</i> s. FZB24	Antibiose et SDP	AB

\* Homologué mais non commercialisé pour cet usage

# Synthetic Microbial Communities (SynComs)

Synthetic microbial communities (SynComs) are microbial consortia designed to **test hypotheses** and to mimic, to some extent, the role of a particular microbiome



Useful **tool** to **understand** plant-microbiome-pathogen interactions

Design commercial **multi-strain biocontrol products** for application in the field

# Hypotheses

**H1 : A SynCom composed of a combination of microbial species prevalent in the phyllosphere and species with known individual biocontrol effects is able to resist invasion of the leaf by the pathogen.**

H2 : SynComs with higher alpha diversity exhibit greater biocontrol efficacy.

H3 : SynComs with higher phylogenetic diversity exhibit biocontrol efficacy.

H4 : Cross-kingdom SynComs exhibit greater biocontrol efficacy

**Aarti  
Jaswa**



**Valérie  
Martin**

*In collaboration with  
**IRHS** (Marie  
Simonin) and **IGEPP**  
(Nathan Vannier)*

# Experimental design

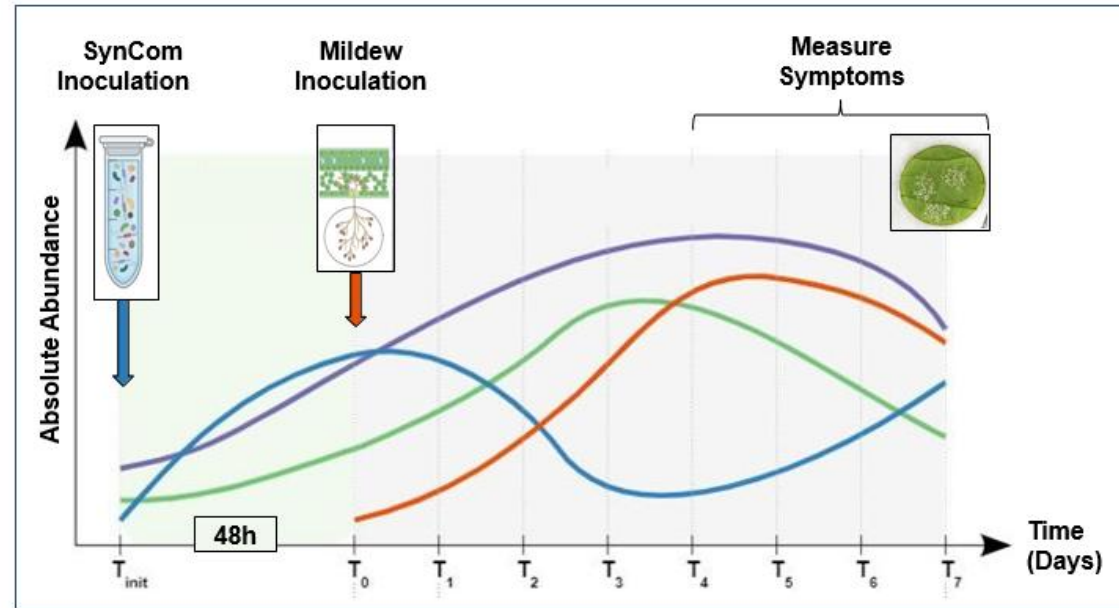
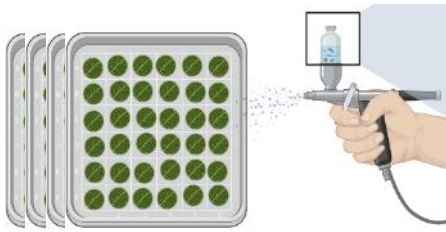
SynCom A (n=42): all isolates

SynCom B (n=22): Species with known biocontrol activity in literature

Four Modalities + Two Controls:

1. SynCom A only
2. SynCom A + mildew
3. SynCom B only
4. SynCom B + mildew
5. Mildew only
6. Saline only

320 discs per modality divided into 4 replicate plates



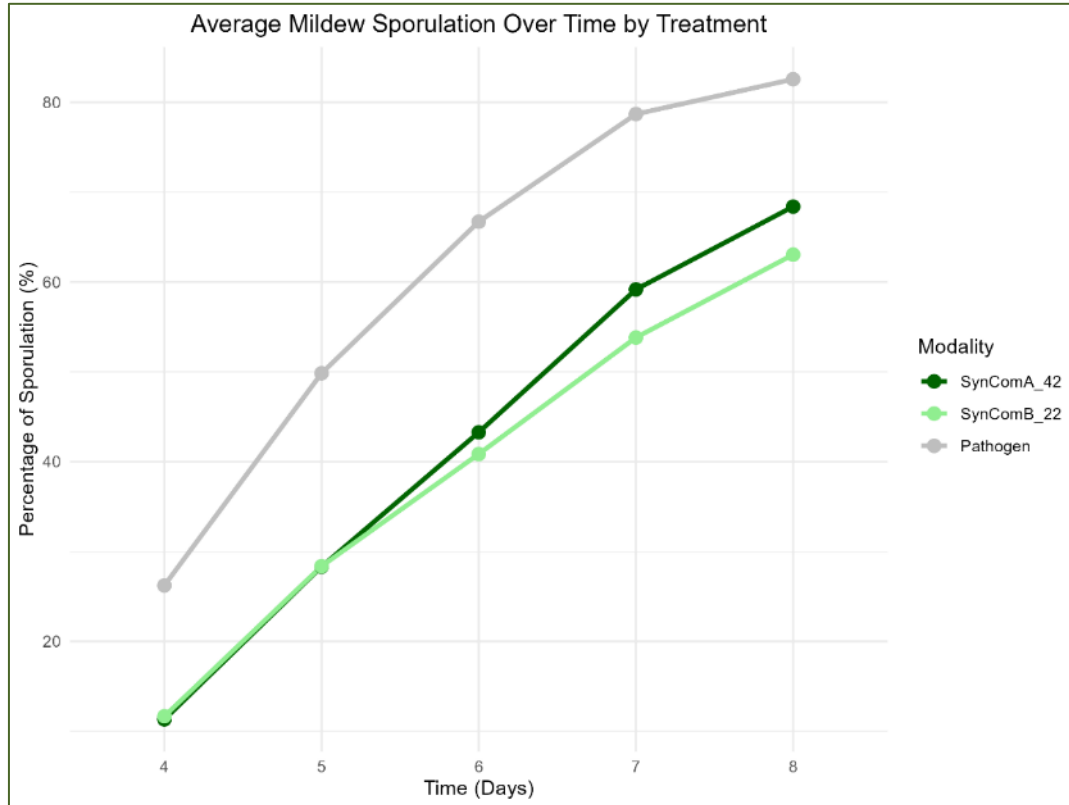
## Ongoing Analyses :

Quantification of disease symptoms  
qPCR Microfluidic chip  
Metabolomics  
Metatranscriptomics



**Aarti  
Jaswa**

# Consistently lower mildew sporulation with SynCom treatments



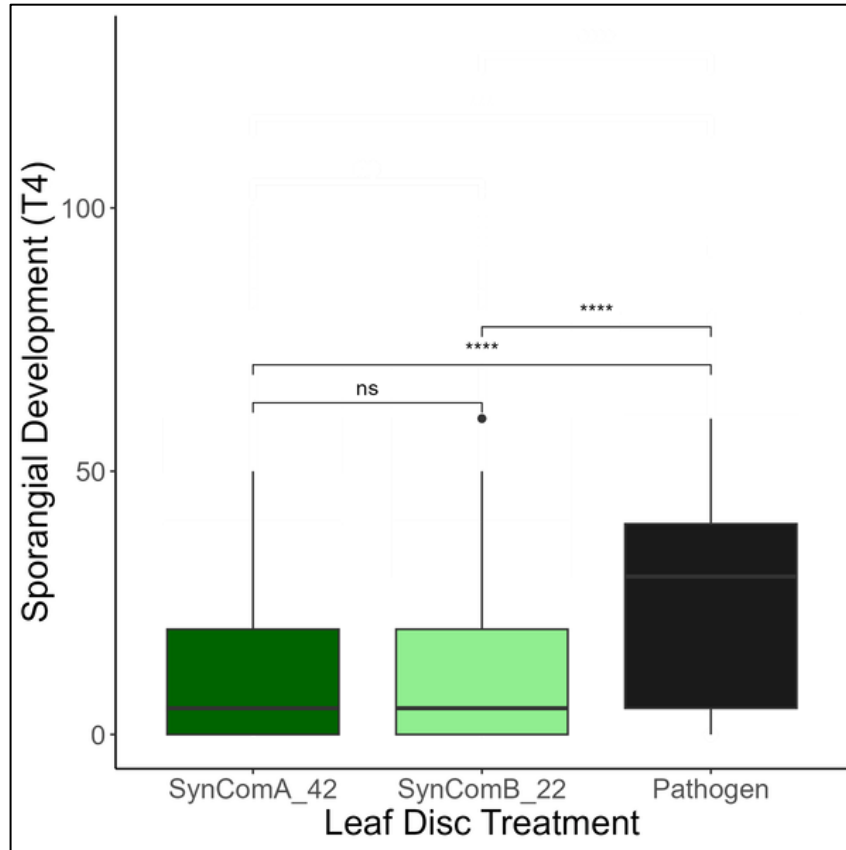
## Notable observations:

- First visible mildew symptoms on T4
- Mildew development appeared to be slower on the plates with SynComs



**Aarti  
Jaswa**

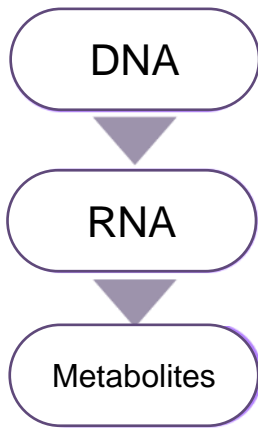
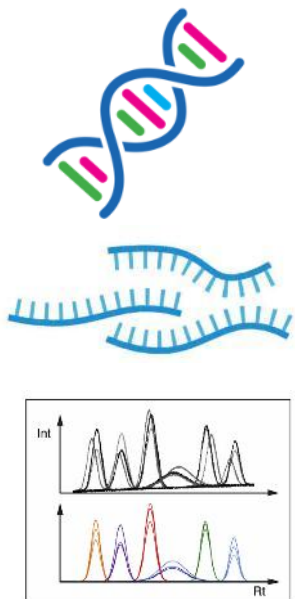
# Consistently lower mildew sporulation with SynCom treatments



**Aarti  
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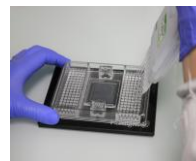
**Valérie  
Martin**



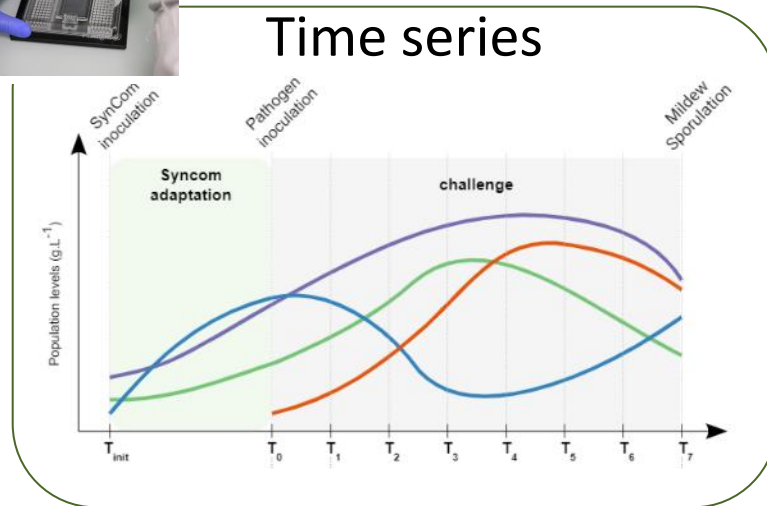
**Genomic data**

**Transcriptomic data**

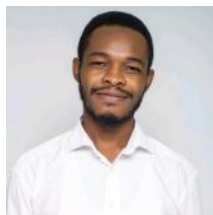
**Metabolomic data**



**Time series**

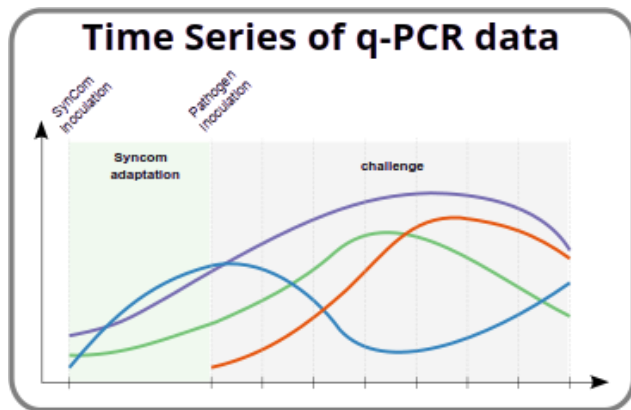


**Sthyve  
Tatho**

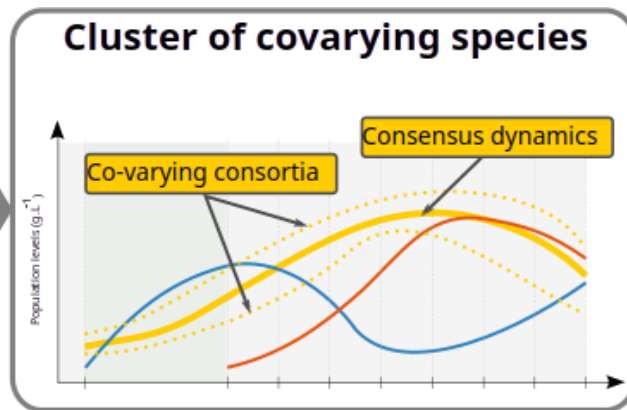


**=> Modelling plant-microbiota-pathogen  
interaction networks**

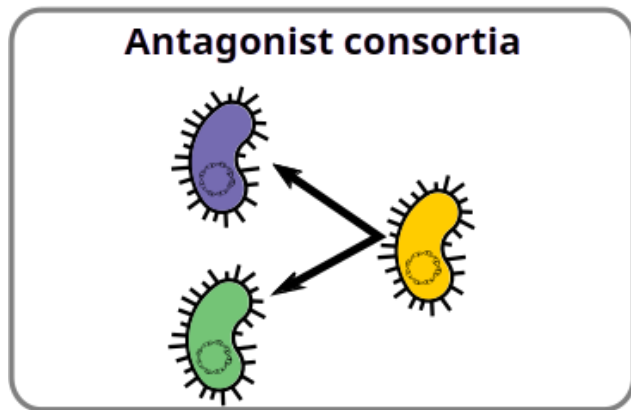
# Identifying microbial antagonists in the Syncom



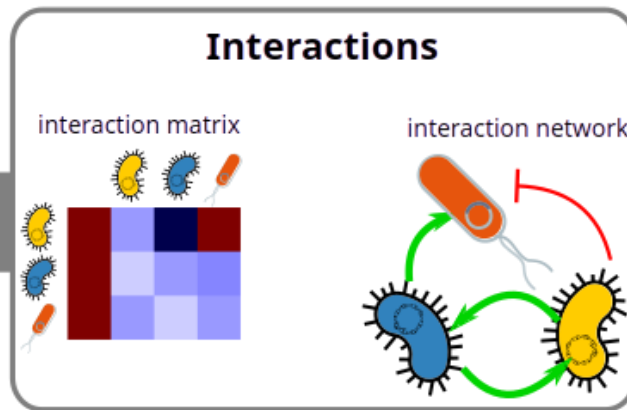
Clustering



Inference

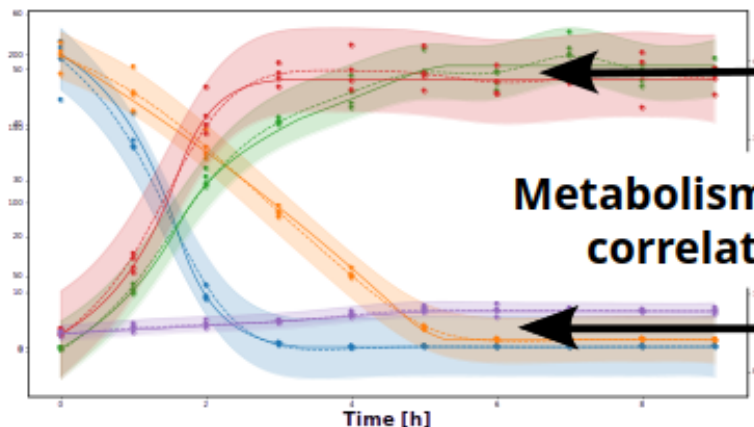


Selection



# Trophic interactions in the SynCom

## Multi-omic time series



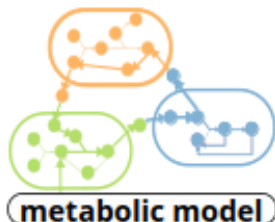
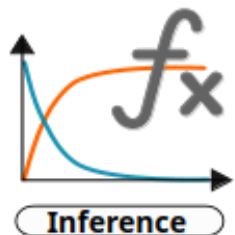
Metabolism-based correlations



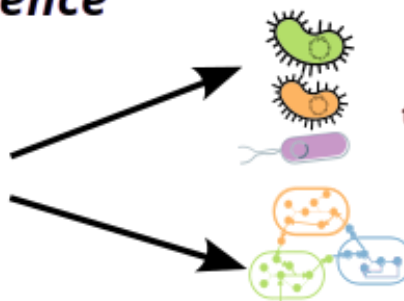
**Sthylve Tatho**  
PhD Mystic



## Goal : metabolism-informed inference



+



individual contributions, trophic interactions

Individual metabolism

# Perspectives (GetUp project)



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Reducing inoculum pressure and creating an unfavorable microclimate for aerial diseases



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# Acknowledgements



**SAVE Microbiota Team  
(+ BC2Grape)**



**PLEIADE Team**

**AGAP** (Patrice This)  
**OENO** (Guilherme Martins, Isabelle Masneuf-Pomarède)  
**BFP** (Thierry Candresse, Armelle Marais)  
**Univ. Birmingham** (Marine Cambon)  
**IRHS** (Marie Simonin)  
**IGEPP** (Nathan Vannier)  
**Moët-Hennessy IFV**  
**PGTB**  
**MetaboHub**