

La modélisation mécanistique des microorganismes associés aux plantes

- design de communautés microbiennes pour le biocontrôle -

- Peyraud Rémi -



iMEAN
Life engineering using digital organisms



Dealing with life complexity



Biocontrol agent

**WEAK EFFICIENCY
LOW ROBUSTNESS IN FIELD**



Make the complexity a strength

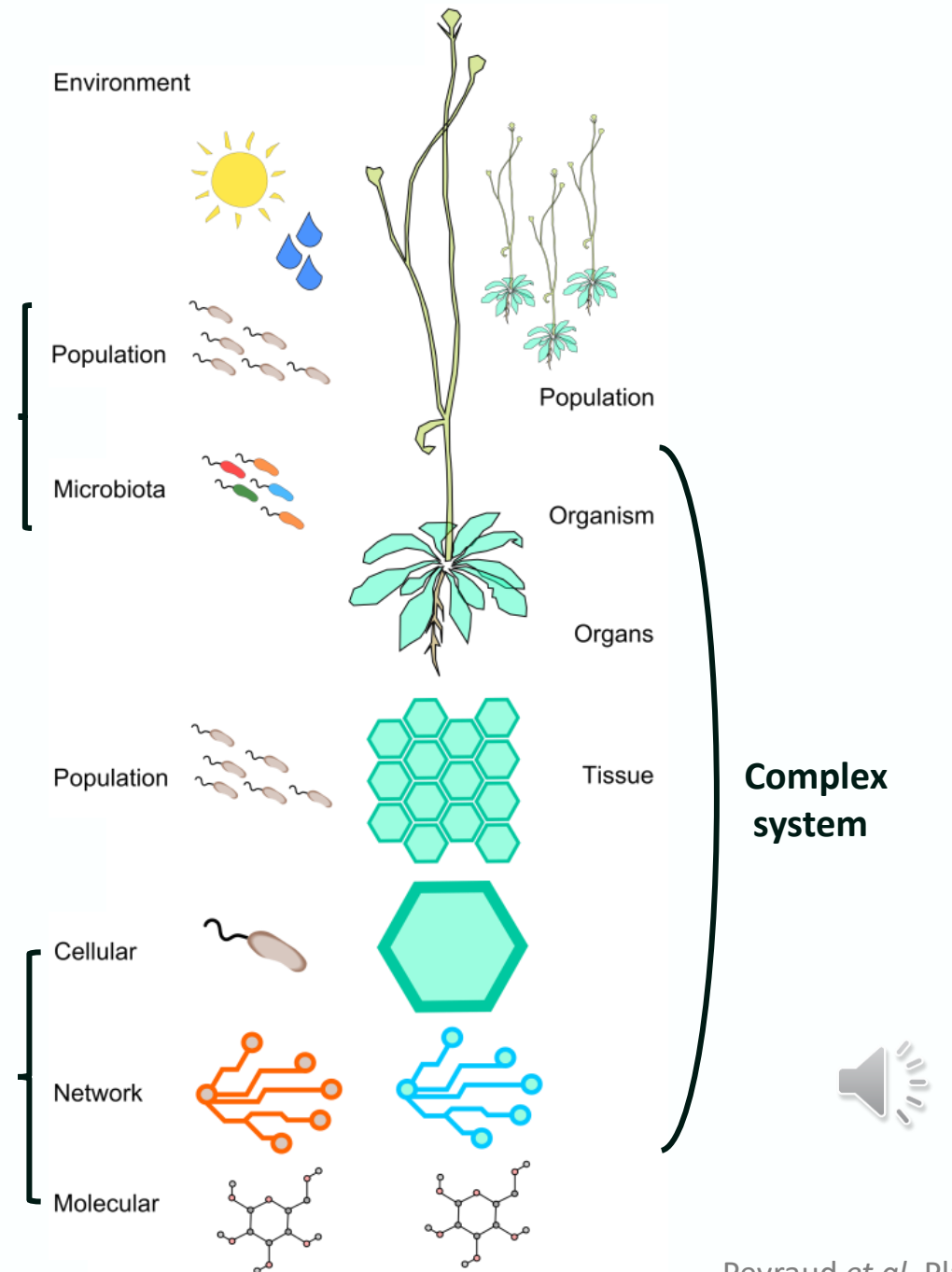
**SYNTHETIC COMMUNITIES
FOR BIOCONTROL**





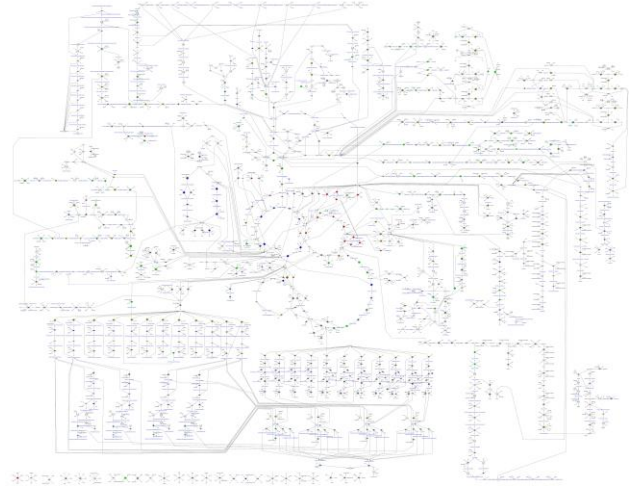
Phenotype/selection level

Interaction level



Understanding the interactions from molecular level

Methylobacterium extorquens

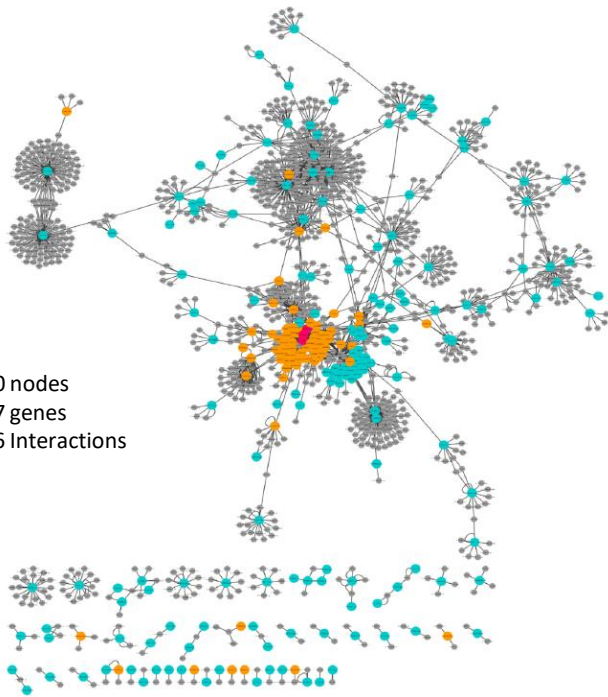


Genome-scale metabolic network

Peyraud *et al.* PNAS 2009

Peyraud *et al.* BMCsystbiol 2011

Arabidopsis thaliana
quantitative resistance



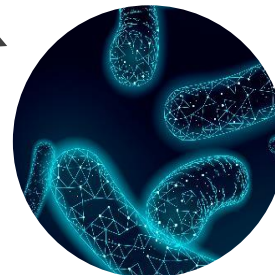
1330 nodes
1047 genes
1876 Interactions

Immune system network

Delplace *et al.* in press PNAS 2020



Crops
Horticultures



Environmental
microbes

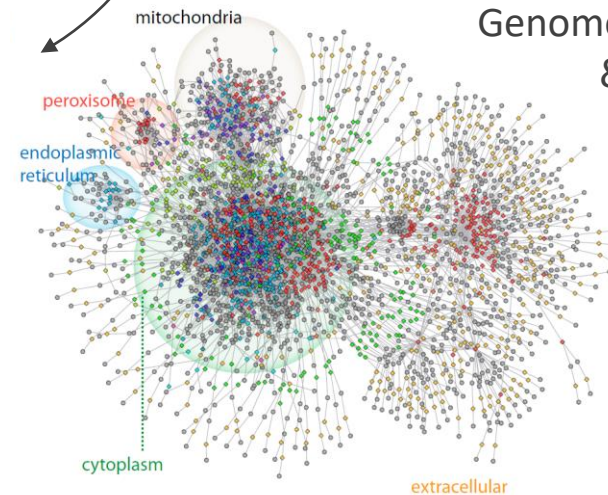


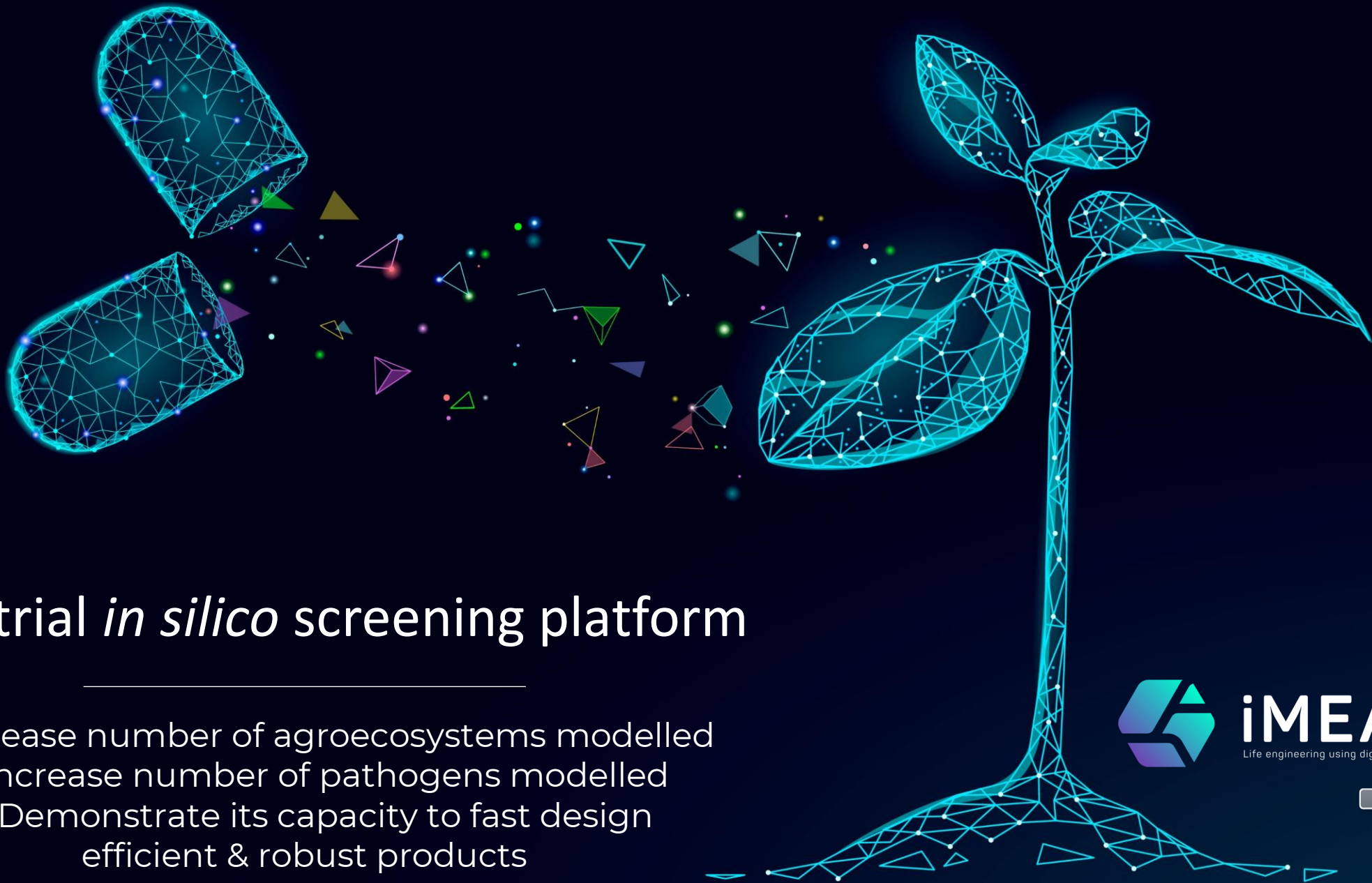
Pathogens

Sclerotinia sclerotiorum

Genome-scale metabolic network
& PCW degradation

Peyraud *et al.* PNAS 2019





Industrial *in silico* screening platform

- Increase number of agroecosystems modelled
 - Increase number of pathogens modelled
 - Demonstrate its capacity to fast design efficient & robust products

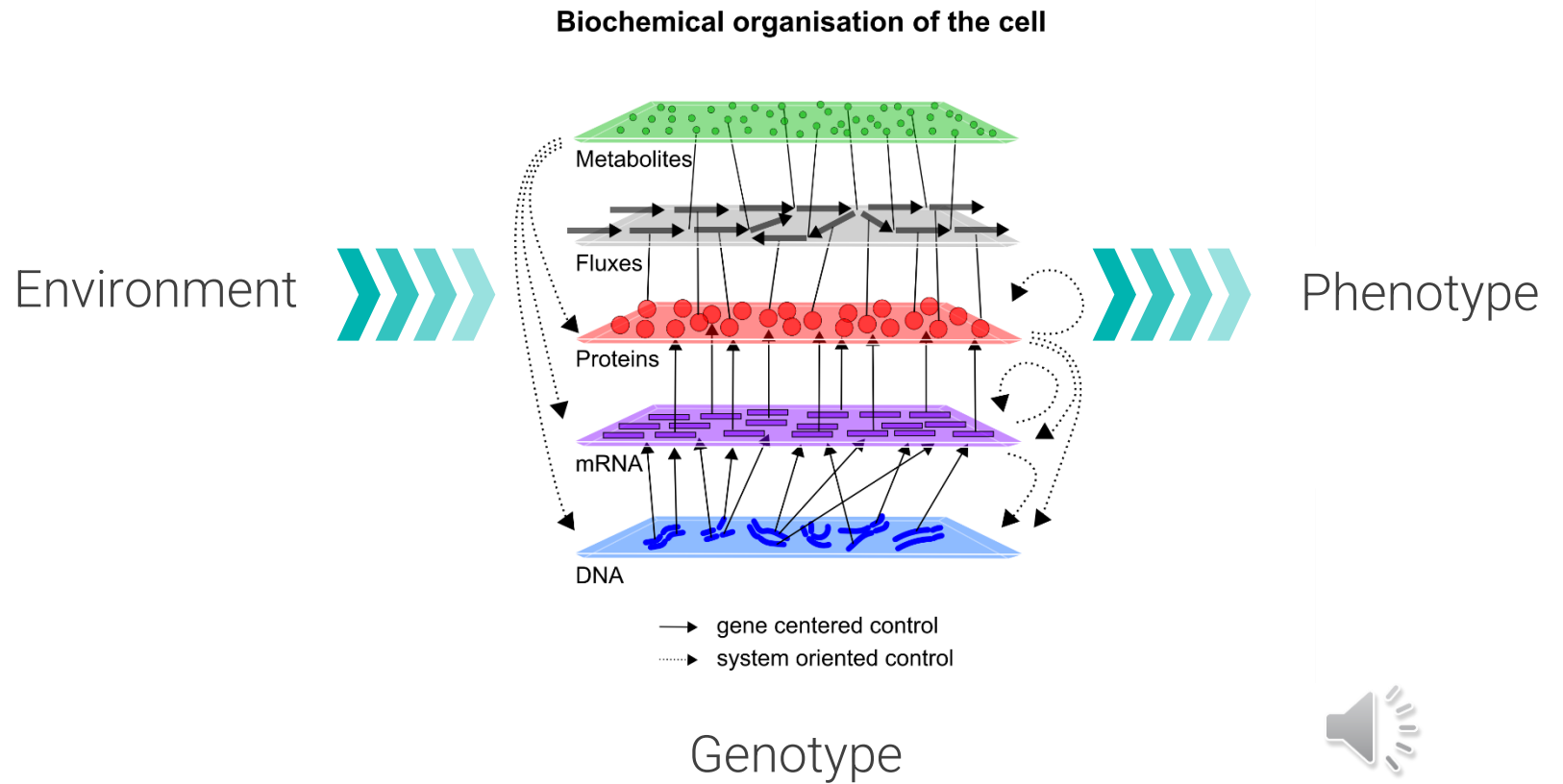


Modelling life complexity



Life modeling

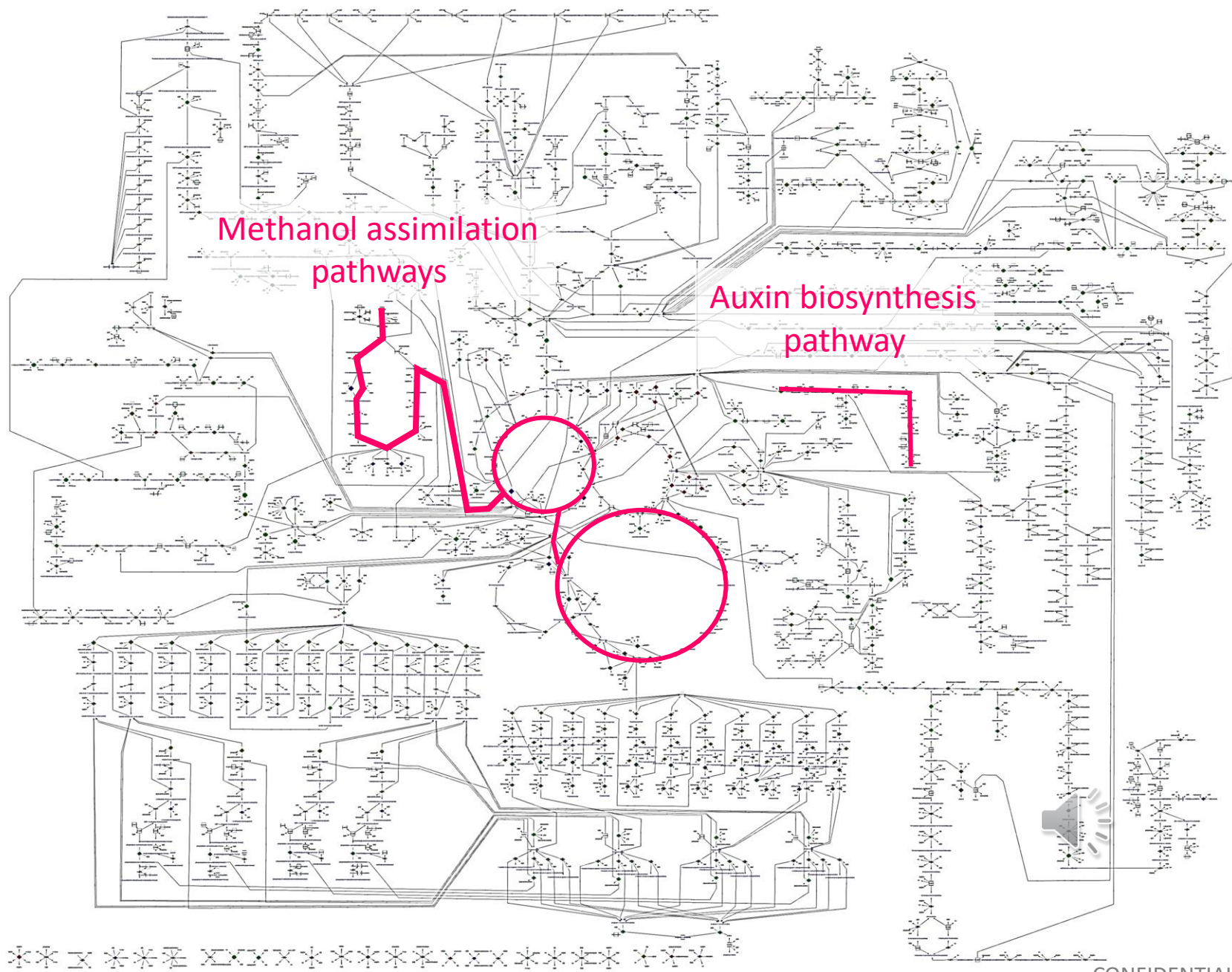
We build *in silico* organisms



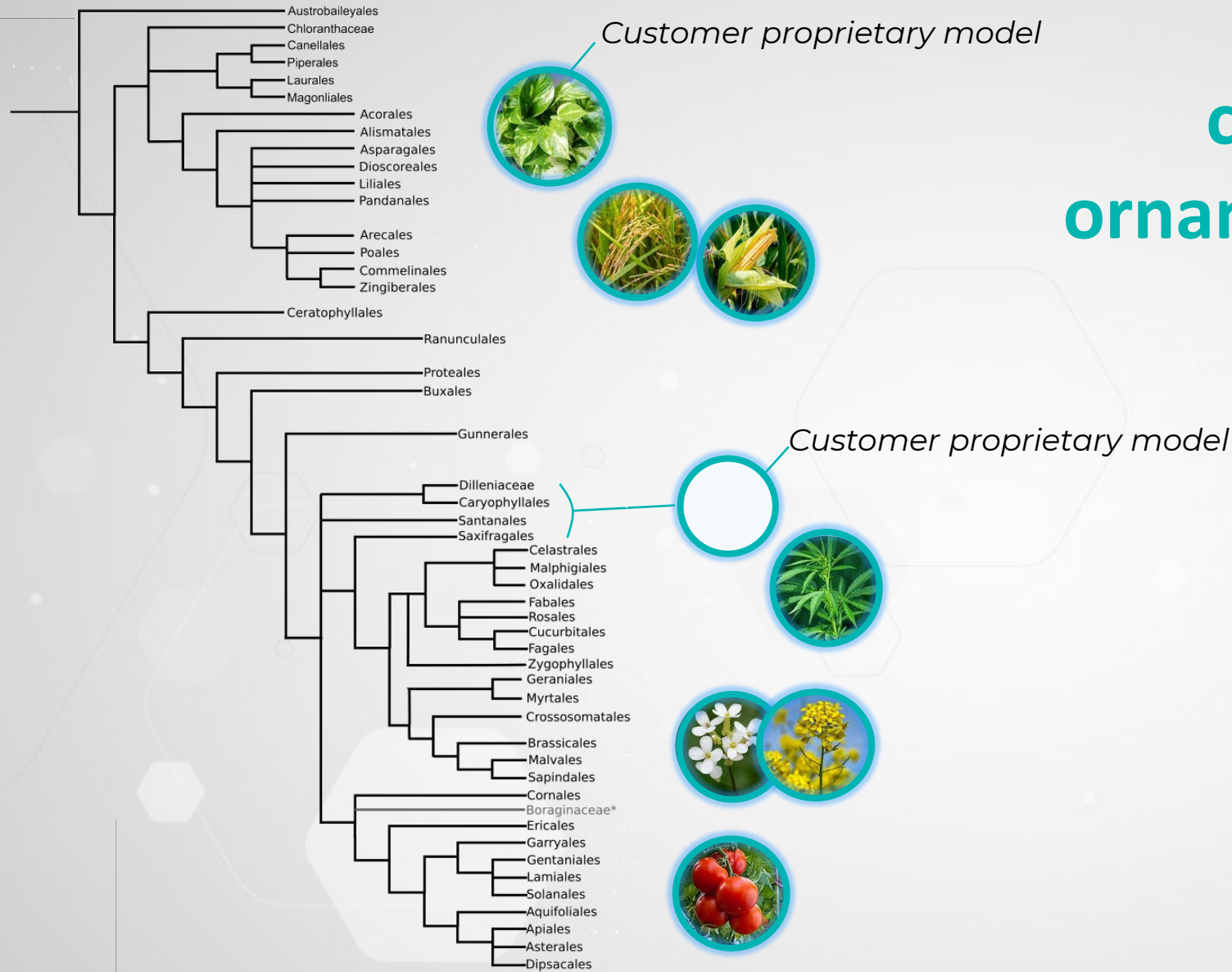
Life modelling

Peyraud *et al.* PNAS 2009
Peyraud *et al.* BMCsystbiol 2011
Sonntag *et al.* Metab Eng. 2015
Ochsner *et al.* Curr Biol. 2017

Genome-scale metabolic network of *Methylobacterium extorquens*



Modelling crops, vegetables ornamental plants, weeds



Available models

Arabidopsis thaliana
Oryza sativa japonica
Solanum lycopersicum
Cannabis sativa
Epipremnum aureum
Zea mays

On going

Brassica napus
Brassica rapa
Medicago truncatula
Phaseolus vulgaris
Glycine max
Amaranthus

Model reconstruction
by iMEAN





bpifrance

iCORN project



iMEAN
Life engineering using digital organisms

x

Limagrain 
de la terre à la vie



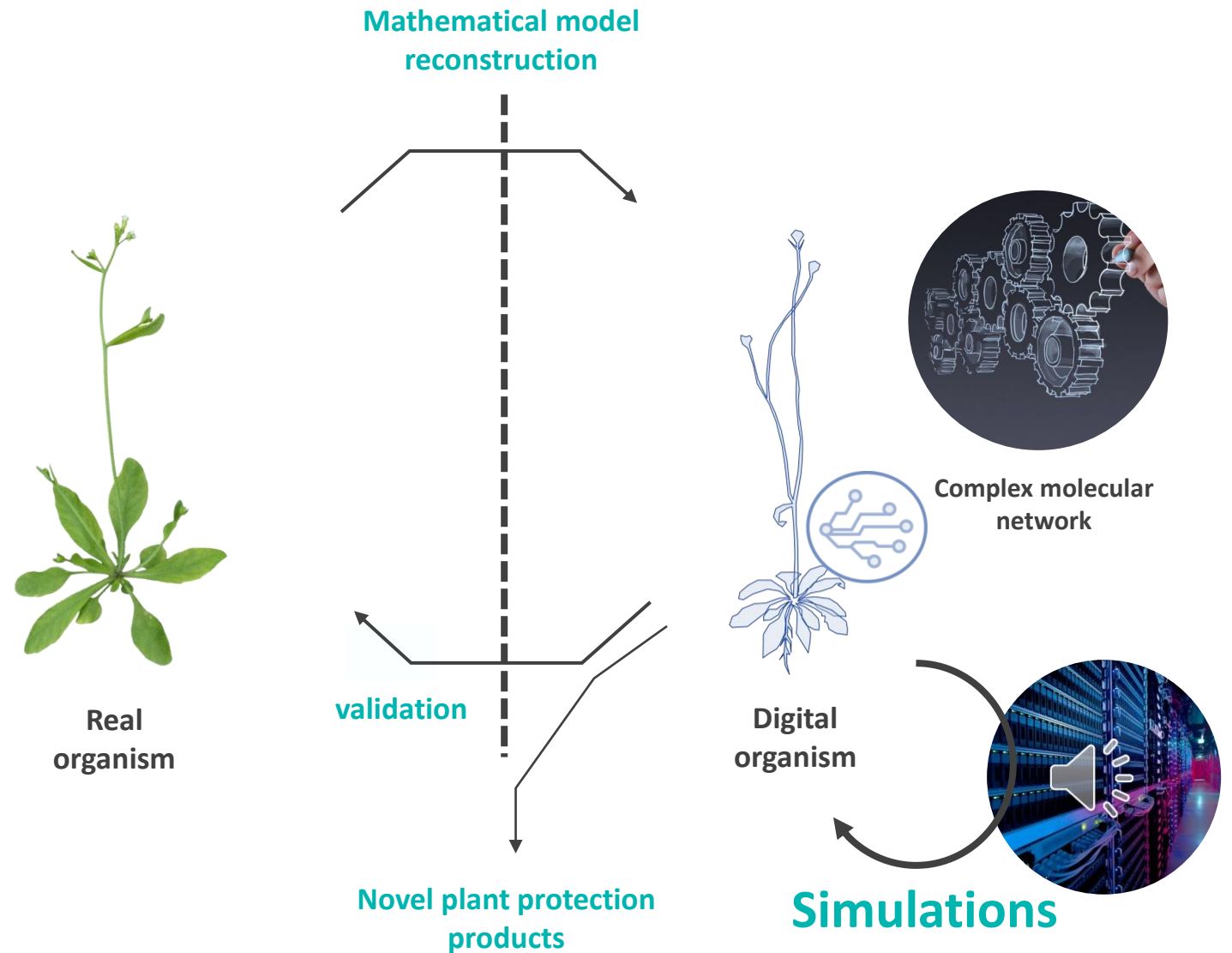


Industrial *in silico* screening platform





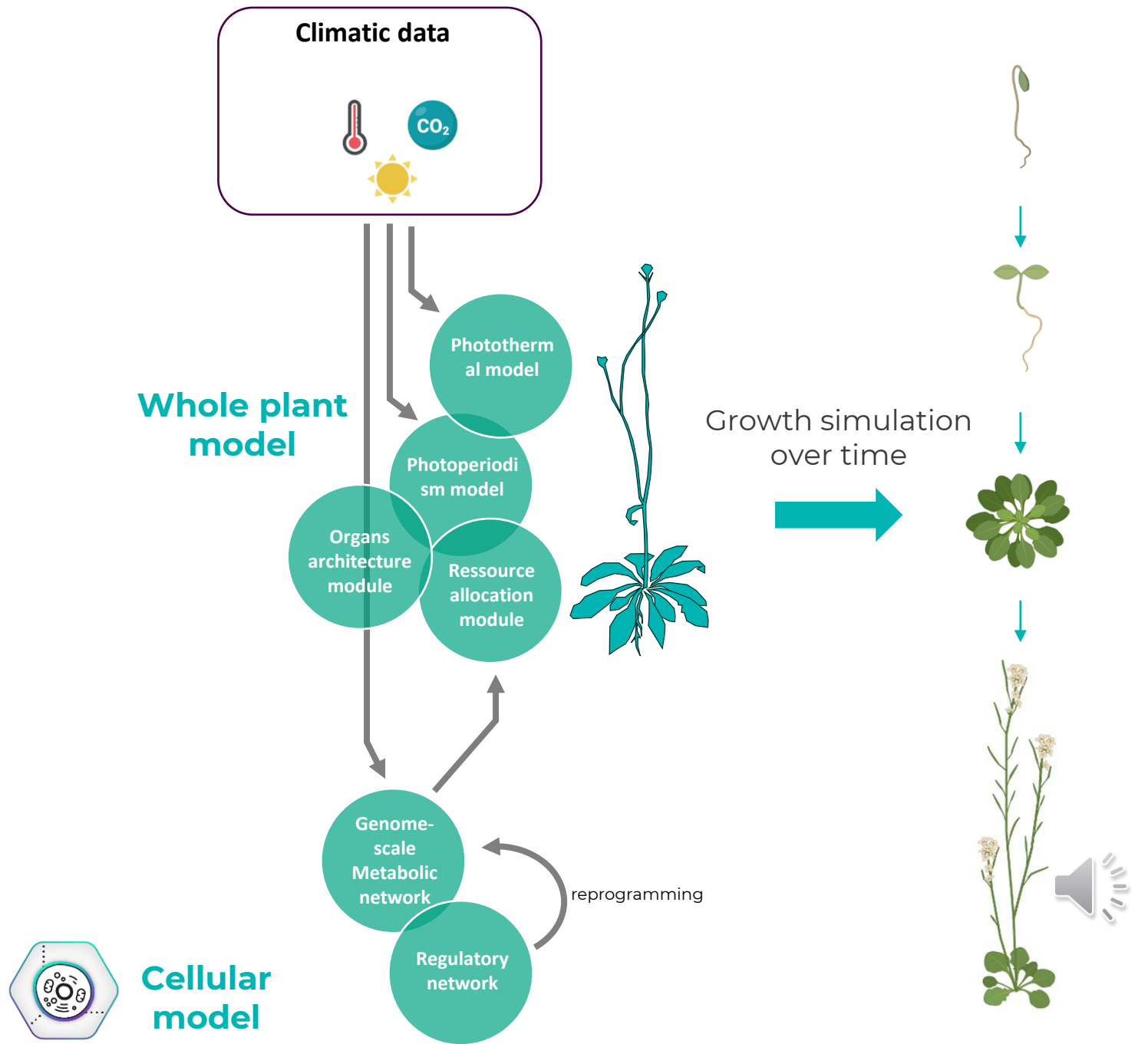
In silico screening platform

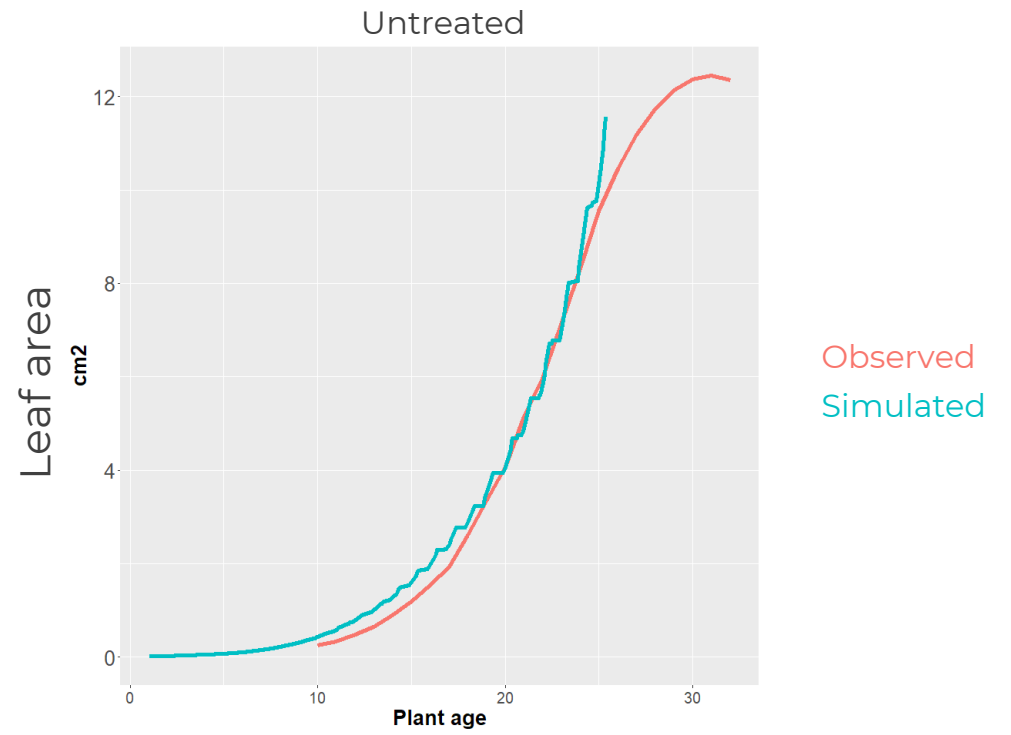


A close-up photograph of several young green seedlings with two leaves each, growing out of a bed of light brown soil. The background is softly blurred, showing more of the same plants. The overall lighting is natural and bright.

MODELLING PLANT & ENVIRONMENT







Models accuracy
> 95%

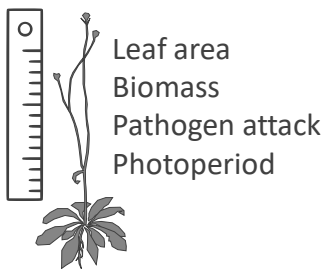
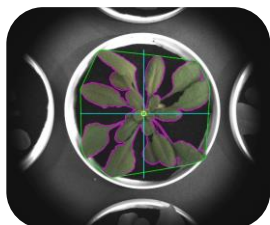


Assesment of robustness to climate change



INRAE

High definition imaging



**Robotized
phenotyping
platform**

220 k€

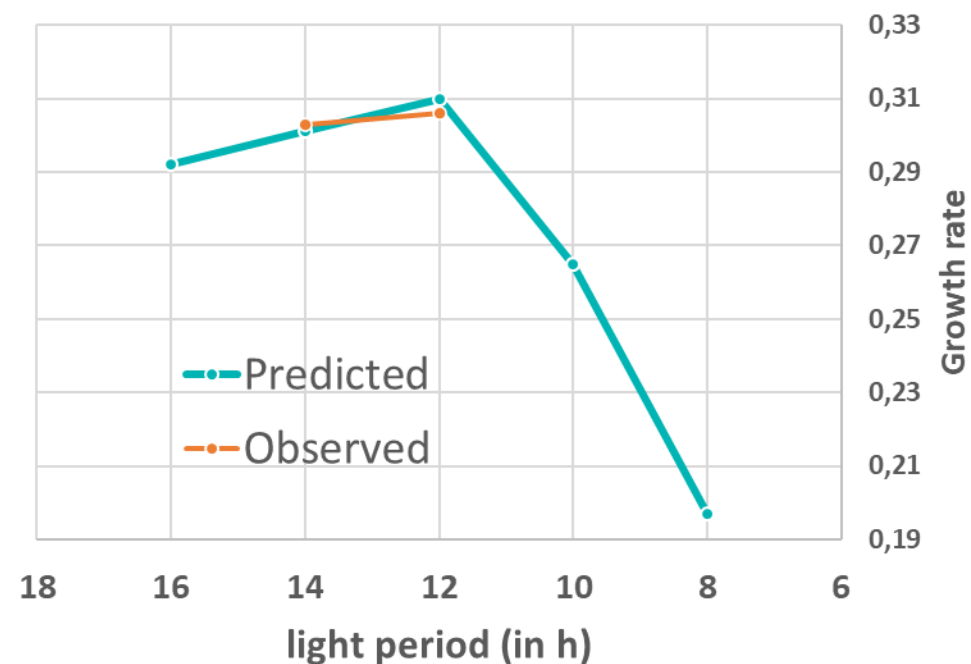
**Experimental
Phenotyping
(8 months)**



20 k€

in silico

**Phenotyping
(1 month)**

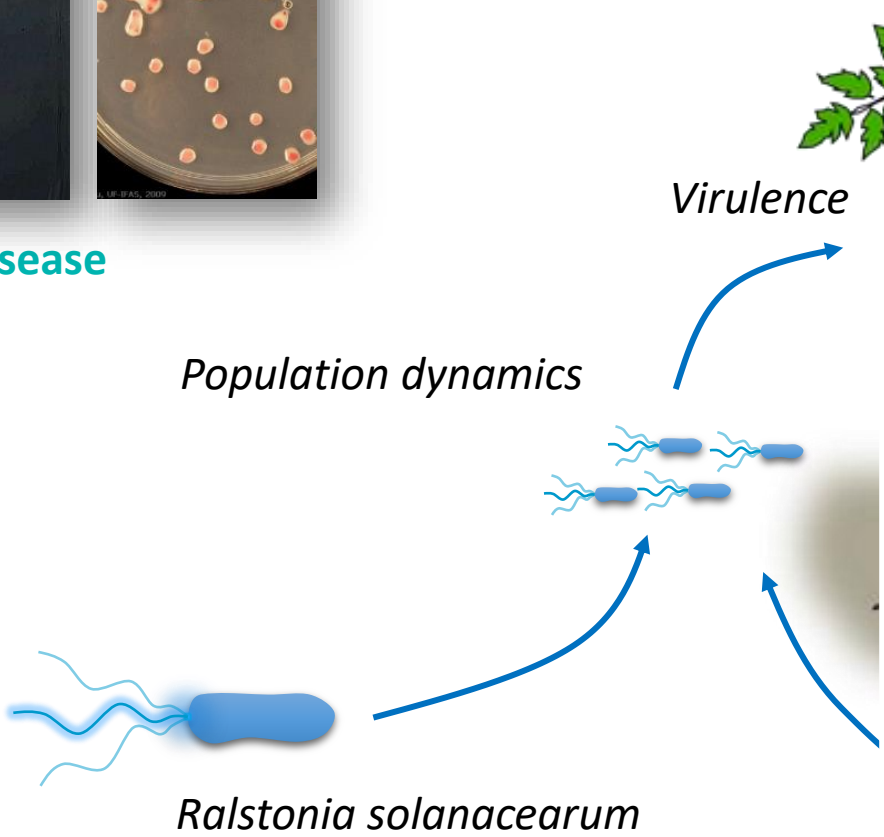


MODELLING PATHOGEN INFECTION

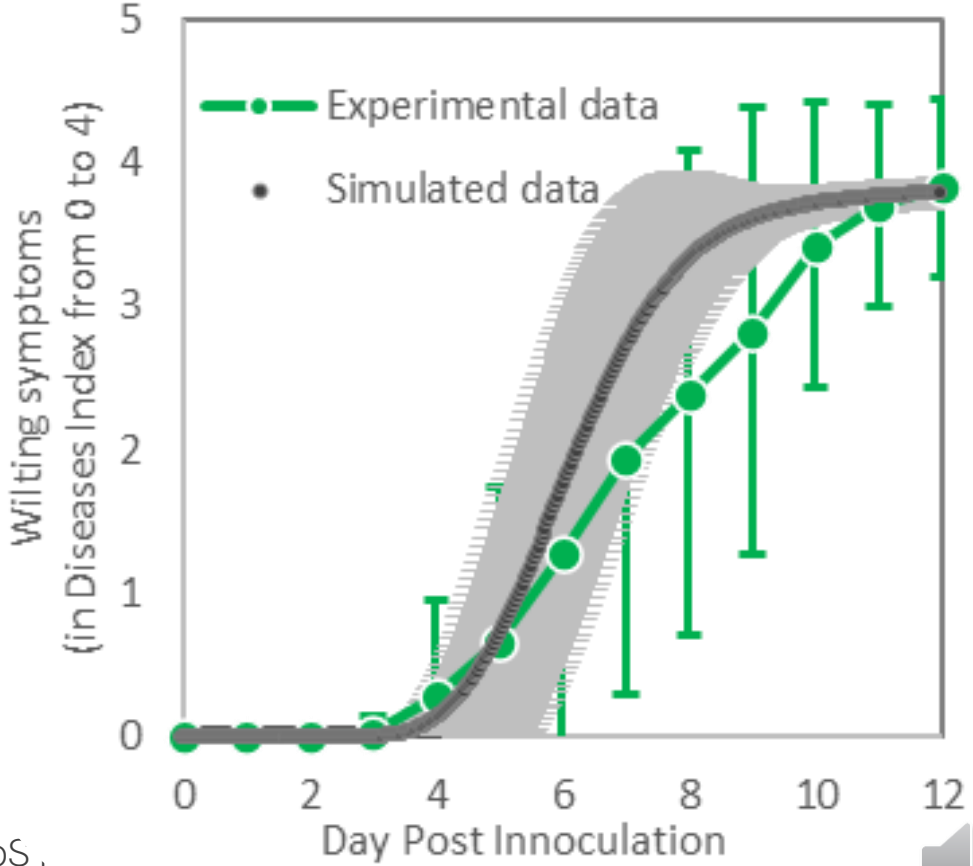




Bacterial wilt disease

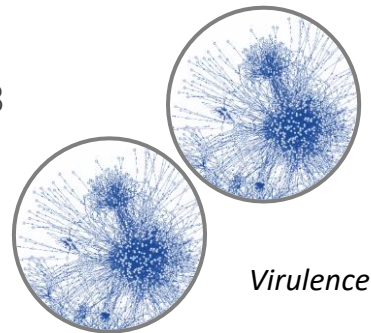


Resistance or susceptibility?



work

Infection model derived from Jiang and peyraud *et al.* BioRxiv 2018



Genome-scale metabc
 Peyraud *et al.* PloS .
 Peyraud *et al.* Nat Commun. 2010

Virulence regulatory network

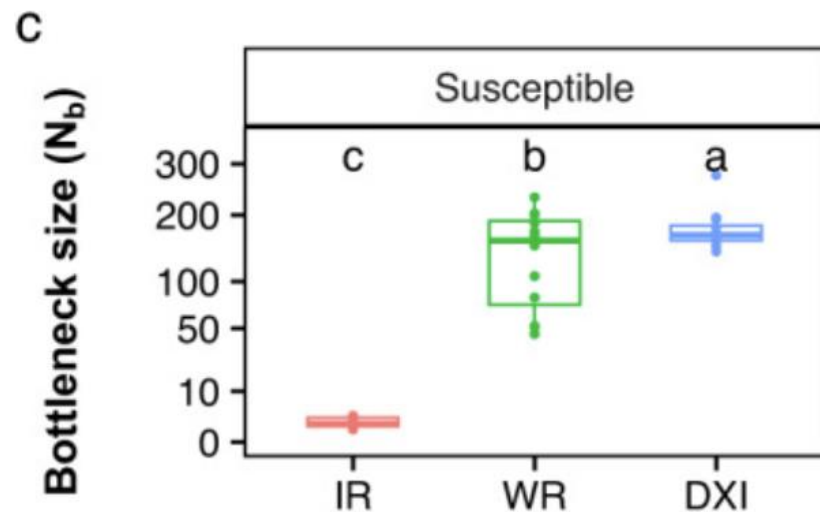


Effects of plant tissue permeability on invasion and population bottlenecks of a phytopathogen

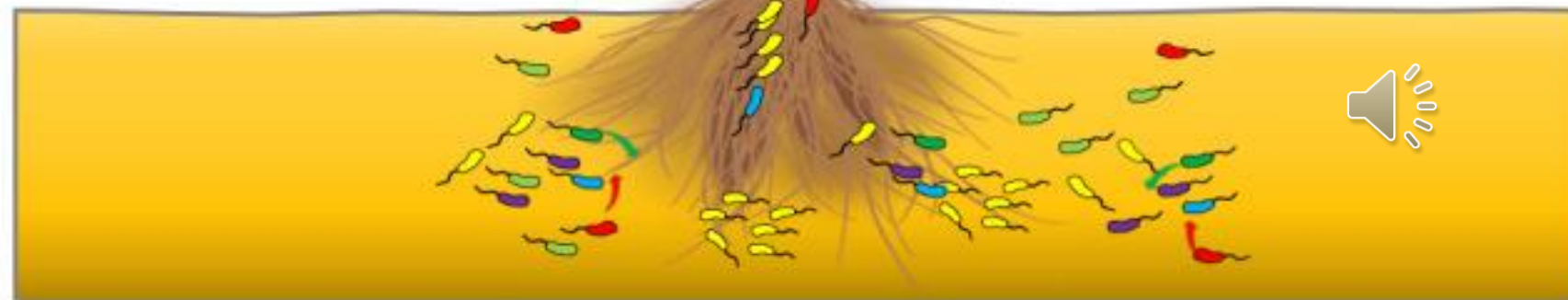
Jiang *et al.* Nat Commun. 2024
Jiang and peyraud *et al.* BioRxiv 2018



Bacterial wilt disease



**1-10 cells are
infecting plants**

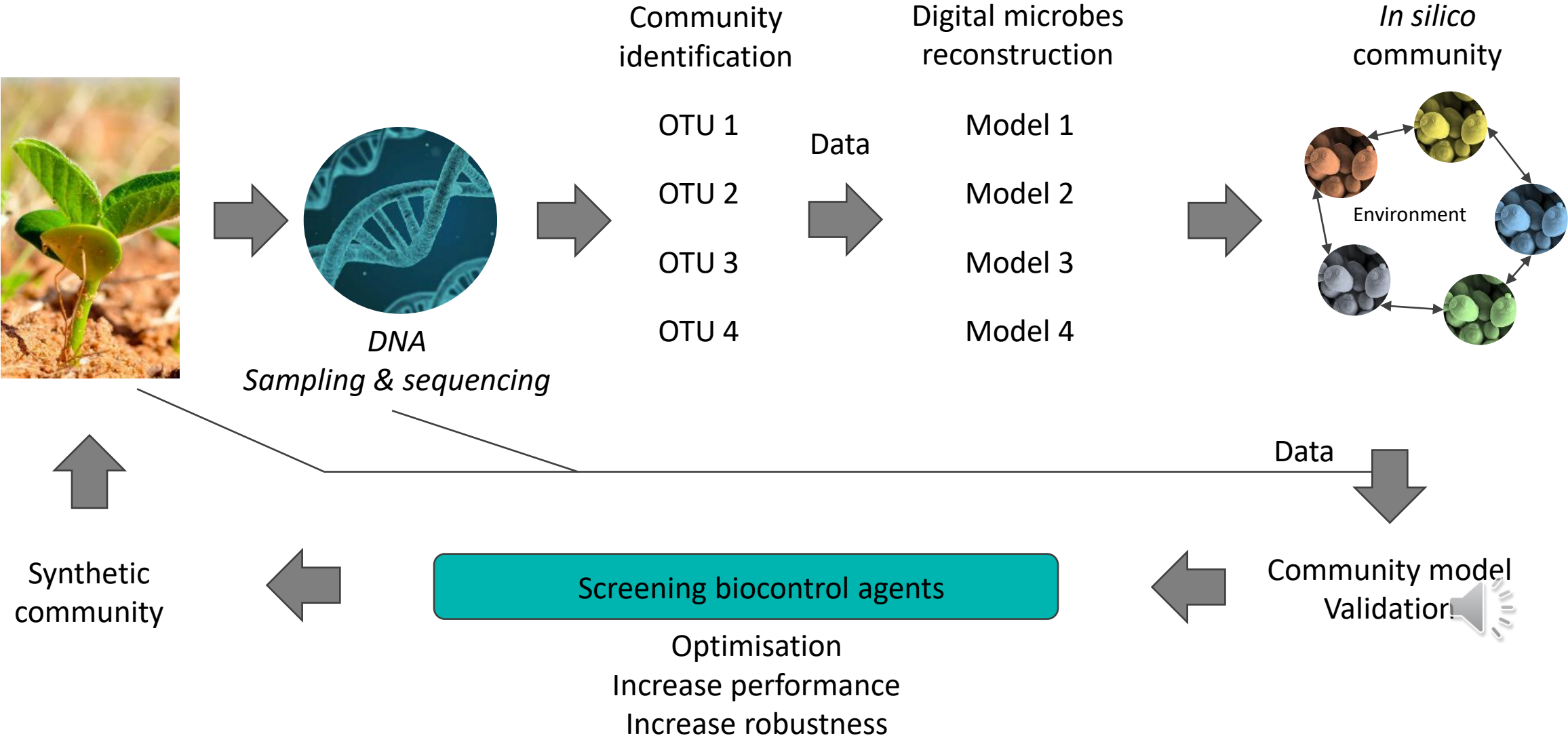


A close-up photograph of several young green seedlings with two leaves each, growing out of a bed of light-colored soil. The background is softly blurred, showing more plants and soil. The overall lighting is natural and bright.

MODELLING MICROBIOTA & SYNTHETIC COMMUNITIES



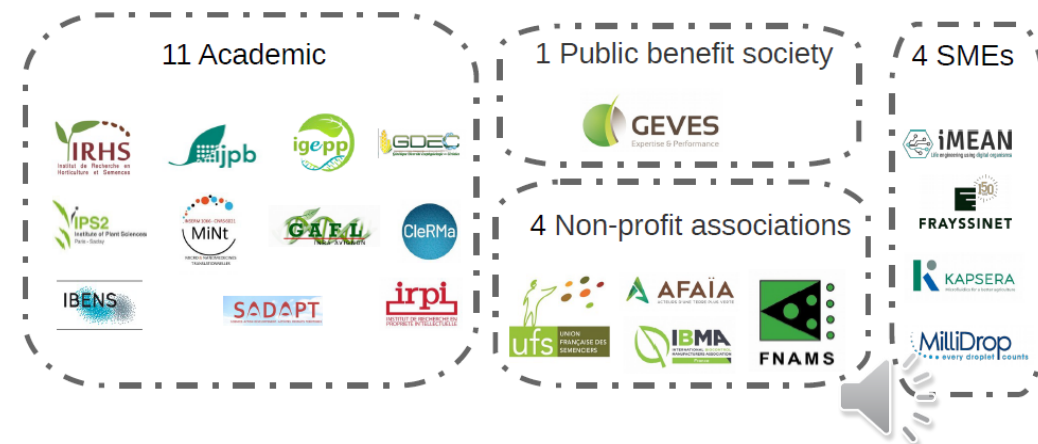
Integration of microbiome effect in field

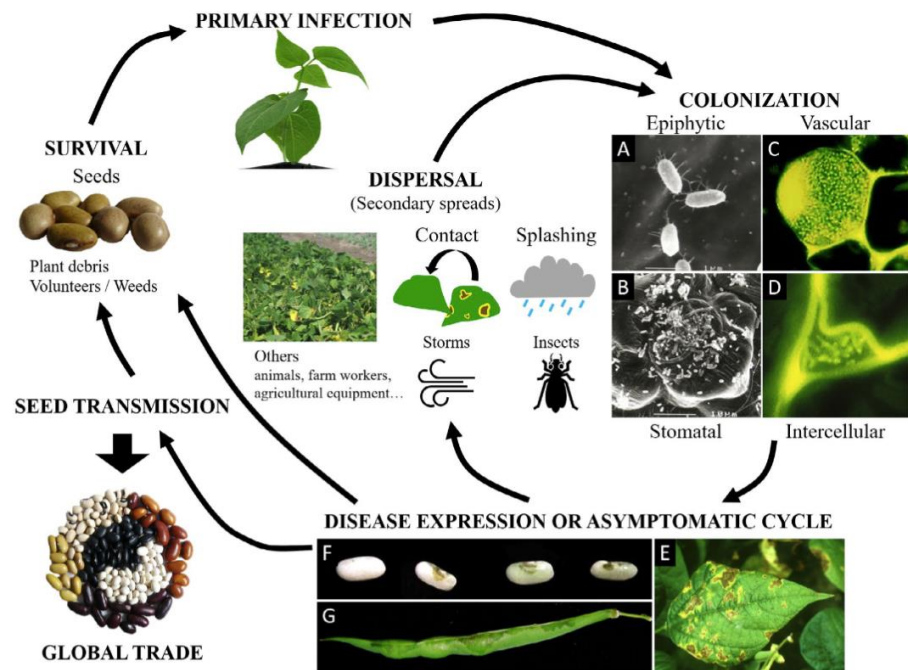




SUCSEED

Design biosolutions against damping-off

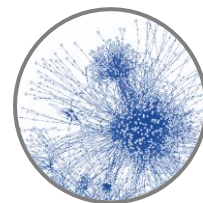




bacterial blight of bean



Xanthomonas. citri pv fuscans model



Genome-scale metabolic network
Heiske *et al.* unpublished



Margit Heiske

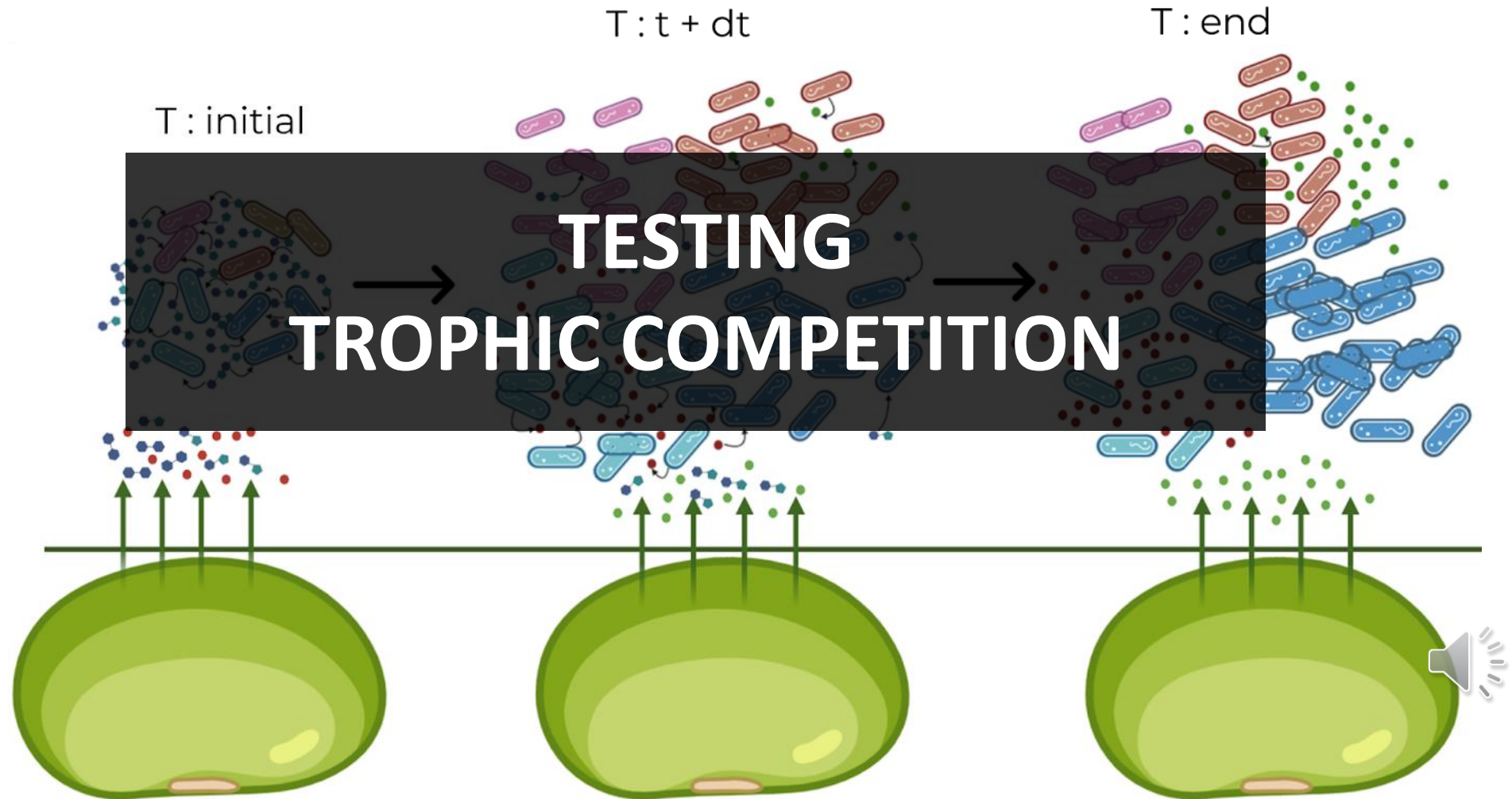
Number of reactions with confidence score*					
total	No assignment	modelling	Genomic & physiology	genetic	biochemistry
2642	0	614	1945	54	27



Amélie Caddéo
PhD student

Population dynamics on the seed

Caddéo *et al.* unpublished



Unpublished Data

Initial Concentration : 0,003 gDW/L

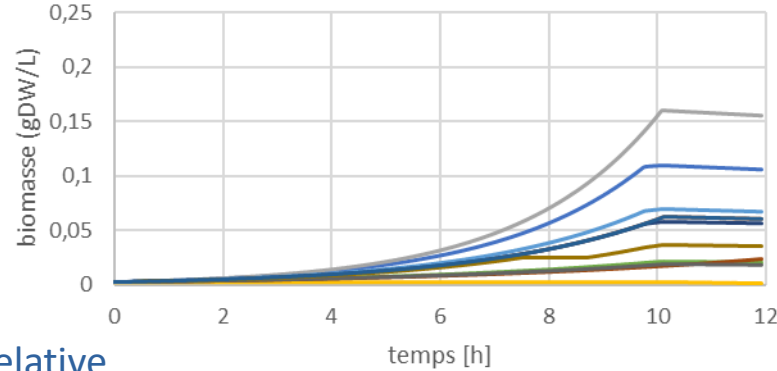
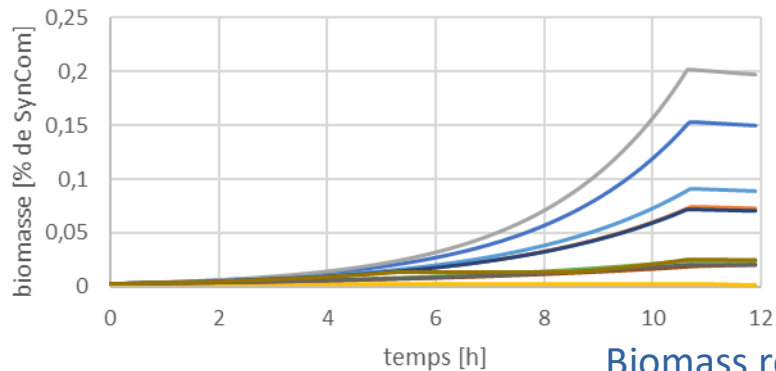
For each SynCom members

Environnement: 87 metabolites

Found on bean seed

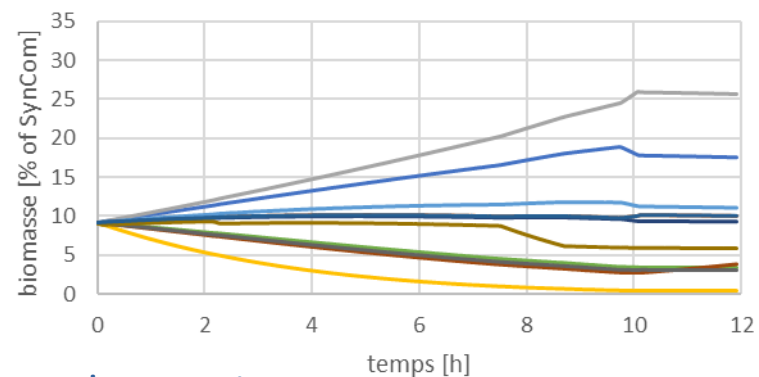
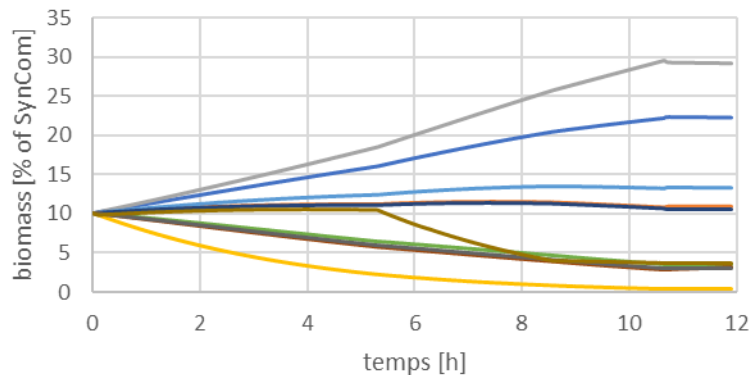
10 souches

Biomass

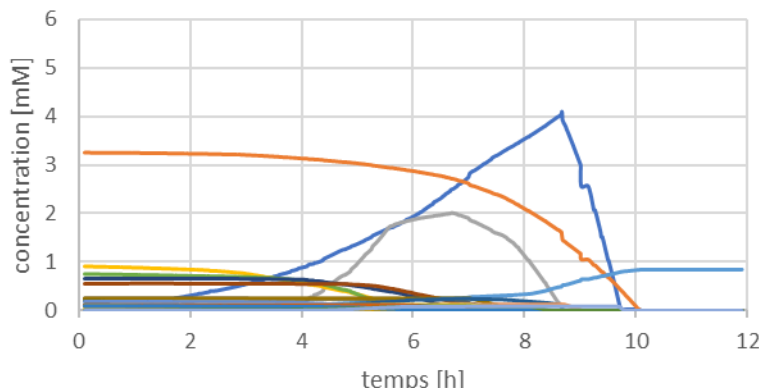
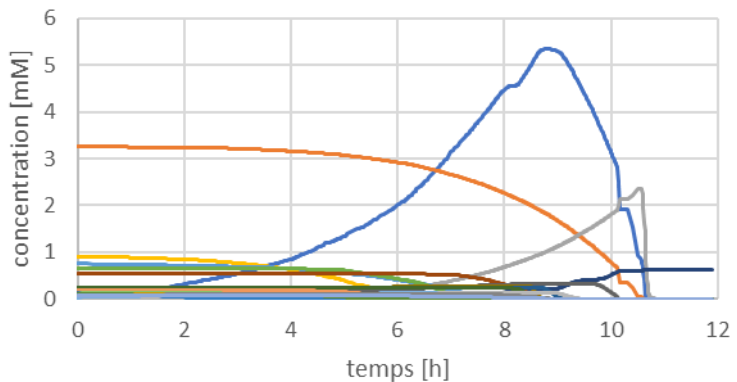


- Leclercia sp
- Pantoea agglomerans
- Bacillus thuringiensis
- Frigoribacterium sp
- Massilia sp.
- Pseudomonas coleopterorum
- Pseudomonas fluorescens
- Rhizobium sp SUCSEED
- Sphingomonas sp
- Stenotrophomonas rhizophila
- Xanthomonas citri pv. fuscans

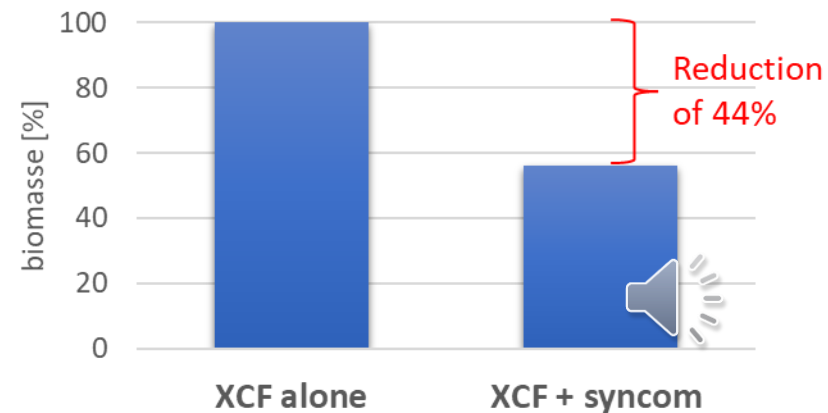
Biomass relative



Metabolites in the environment



biomasse xanthomonas
(t = 12h)



Unpublished Data



Industrial *in silico* screening platform



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Life engineering using digital organisms





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remi.peyraud@imean-biotech.com

