# Réservoirs insoupçonnés d'agents phytopathogènes : quelle importance pour la surveillance du territoire et pour la gestion de la santé des plantes ?

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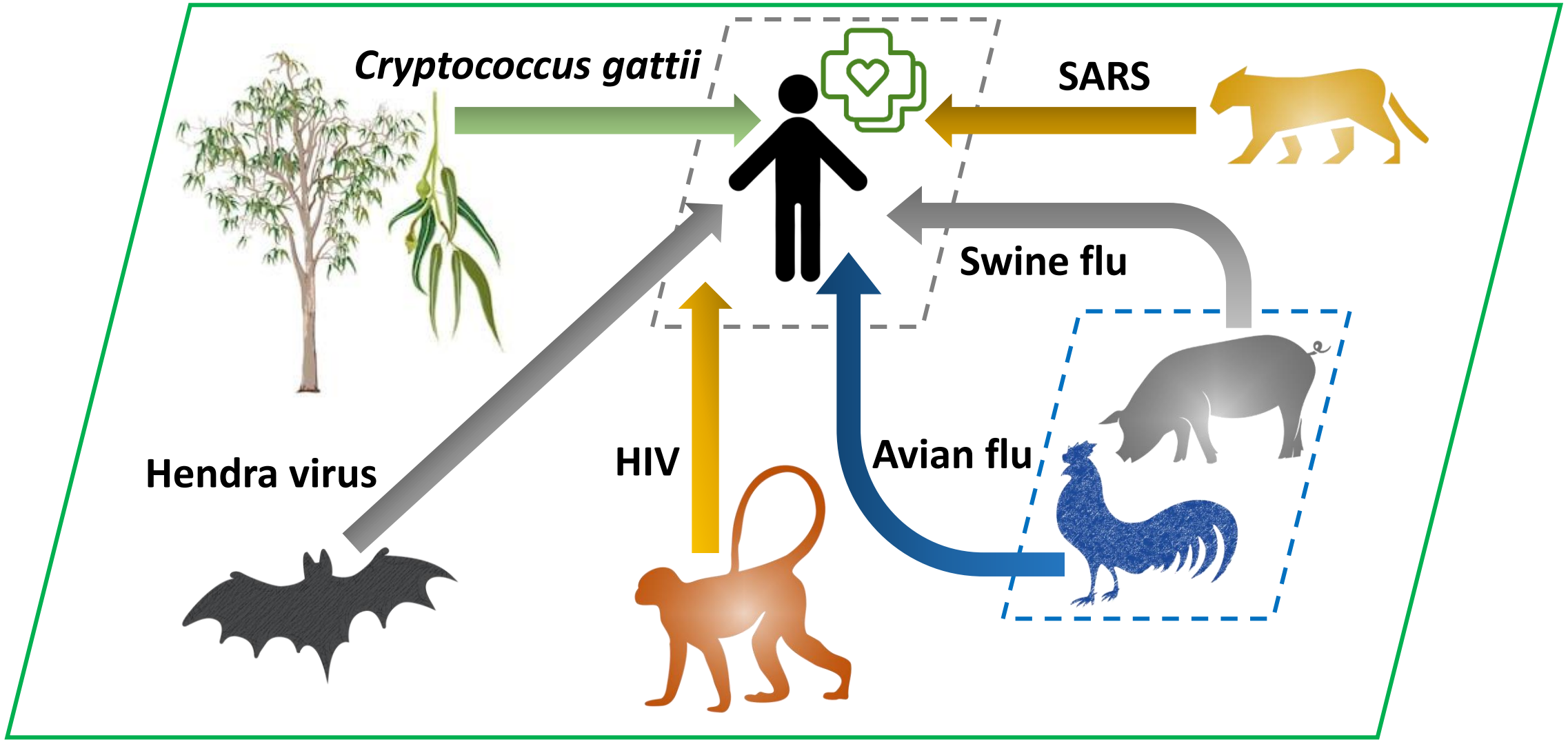
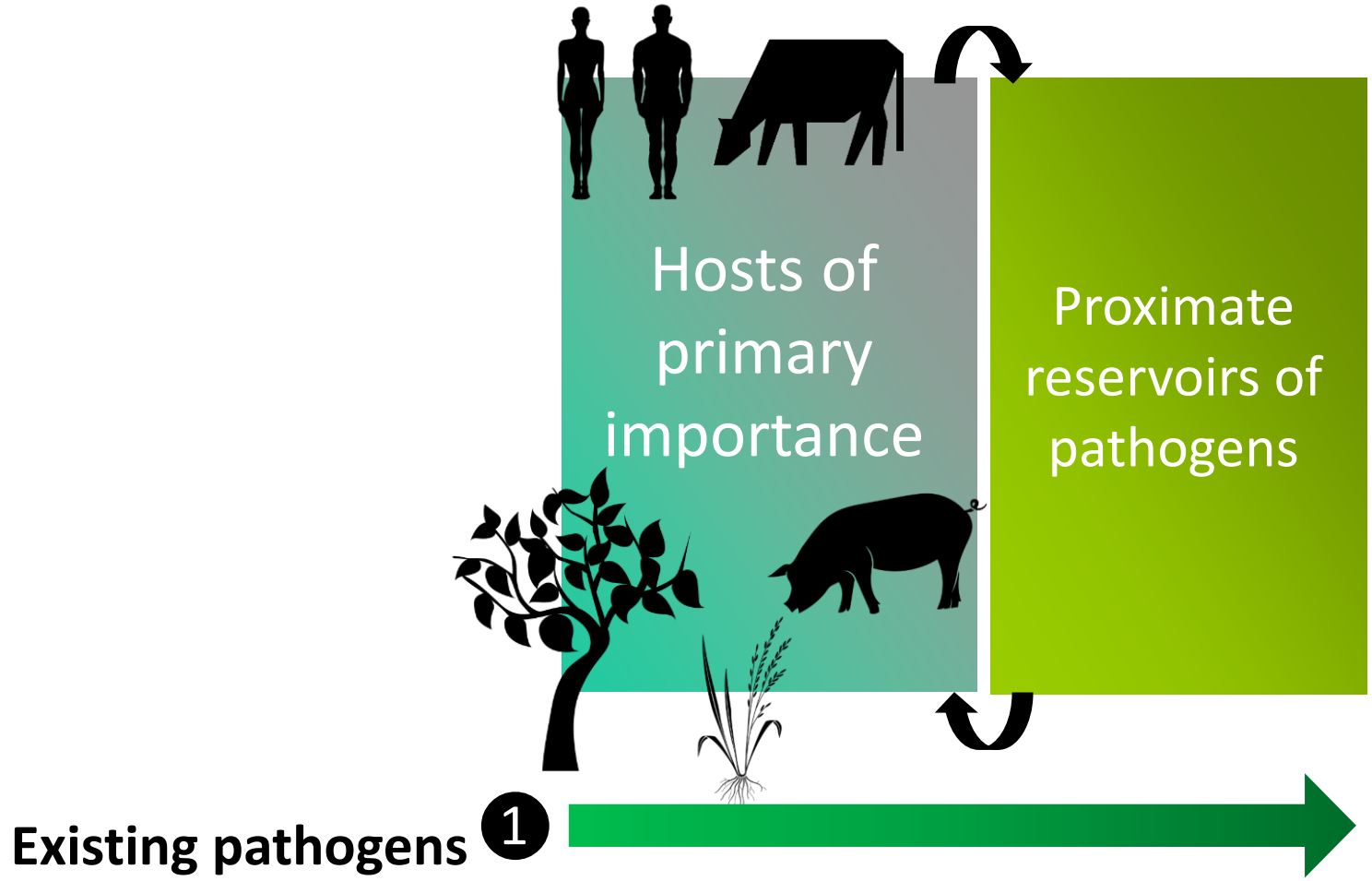
*Séminaire du 3 octobre 2018*
*La santé végétale dans le concept One Health : quelle contribution ?*

# **One Health** key concept: disease spill-over between environments



# **One Health**: a framework to understand disease emergence



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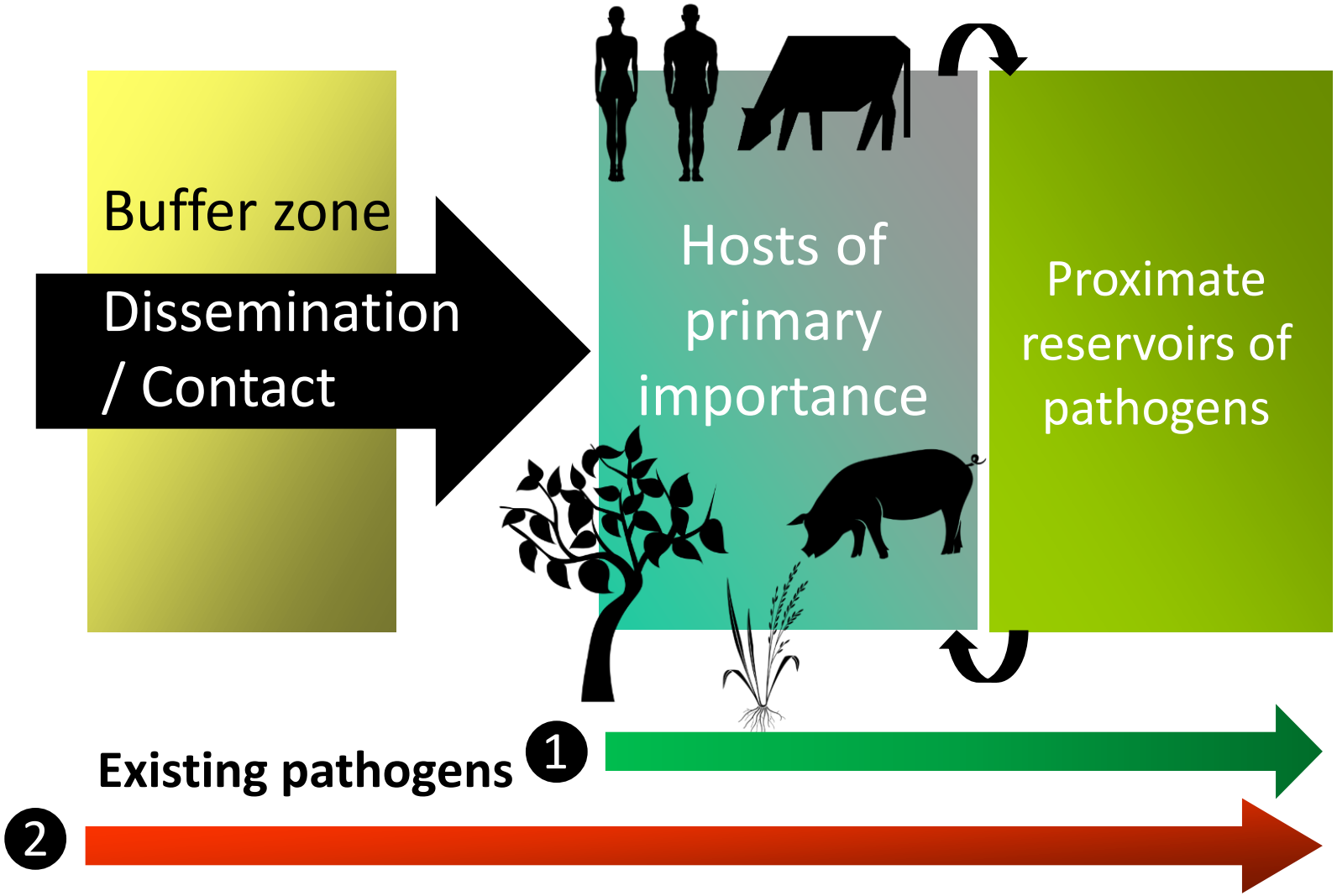

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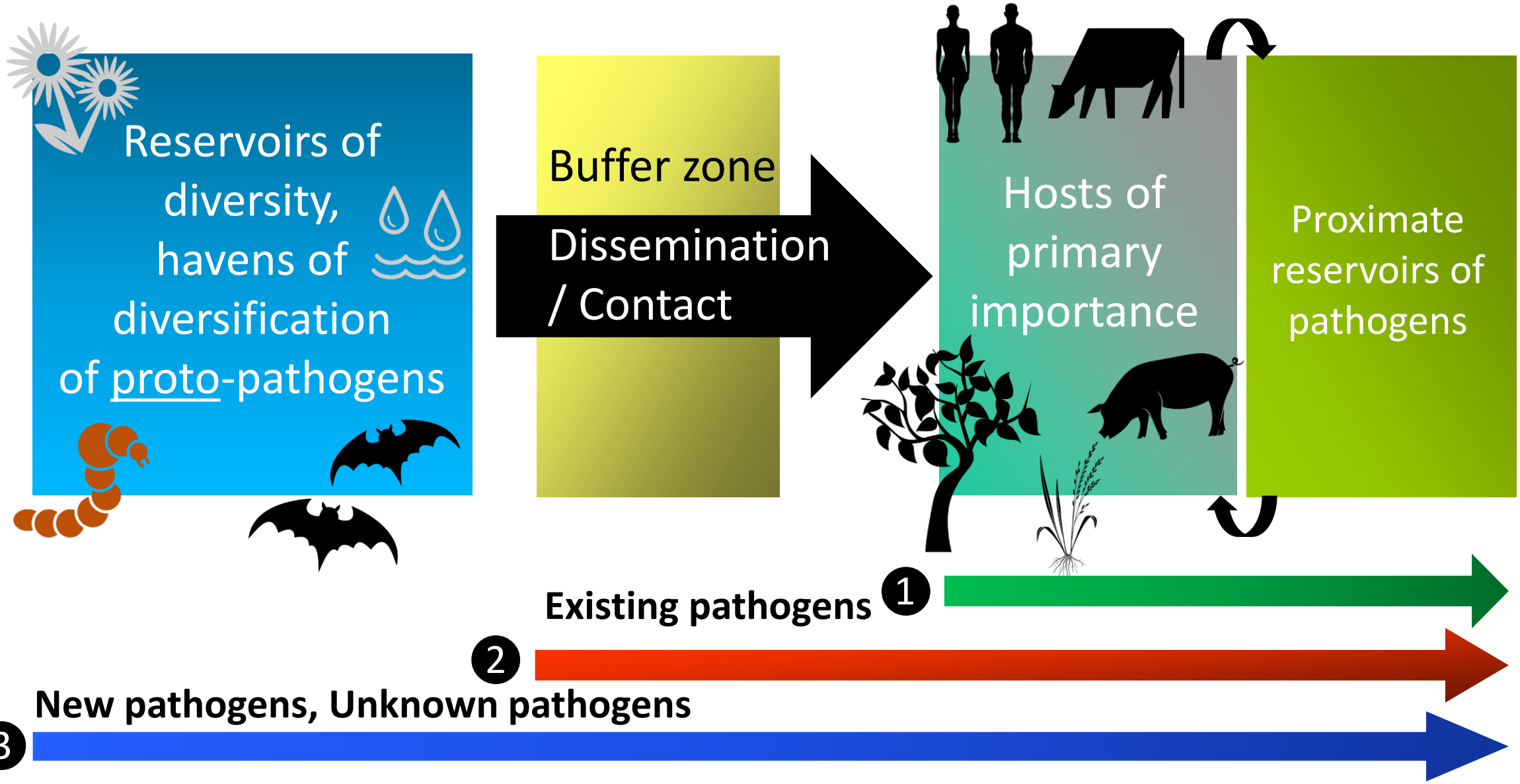


# How is surveillance used to anticipate emergence of **plant diseases** ?

❶&❷ Resurgence of known pathogens

- Surveillance of crops in the field (symptoms and/or diagnostic tests)
- Surveillance of transported plant materials
- Surveillance of major reservoirs (when known)
- Disease forecasting models

❸ Emergence of new pathogens never reported previously for a given plant host

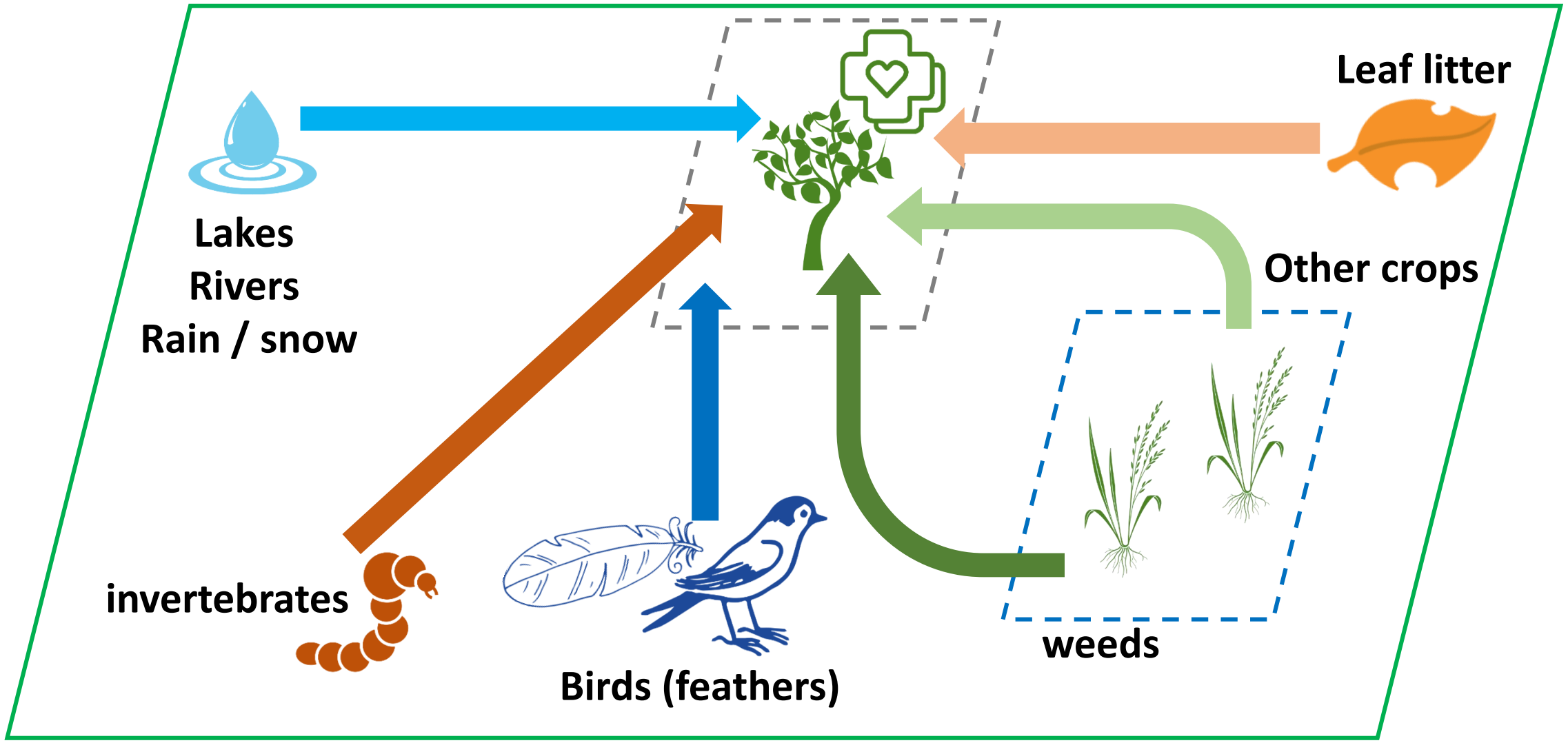
- There is no paradigm* in Plant Pathology for anticipating new diseases
- There is no official strategy to anticipate the risk of emergence of new plant diseases

*concepts, thought patterns, theories, research methods, postulates, standards for what constitutes legitimate contributions

**Environments outside of agriculture:** Reservoirs of plant pathogens?

Risk for spill-over to agriculture? How to survey?

# Can we identify risks of spill-over of plant pathogens and create surveillance strategies?



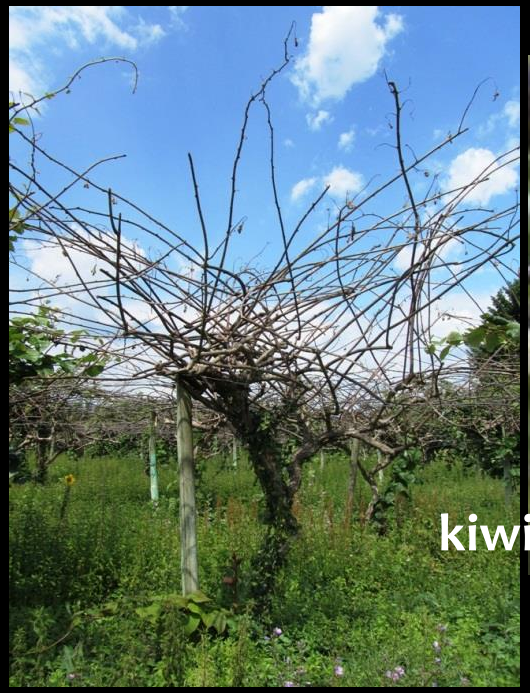
Example of a plant pathogen with wide-spread and diverse environmental reservoirs . . . . . .

# *Pseudomonas syringae*: an important plant pathogen . . . .


cantaloupe


horse chestnut


crucifers

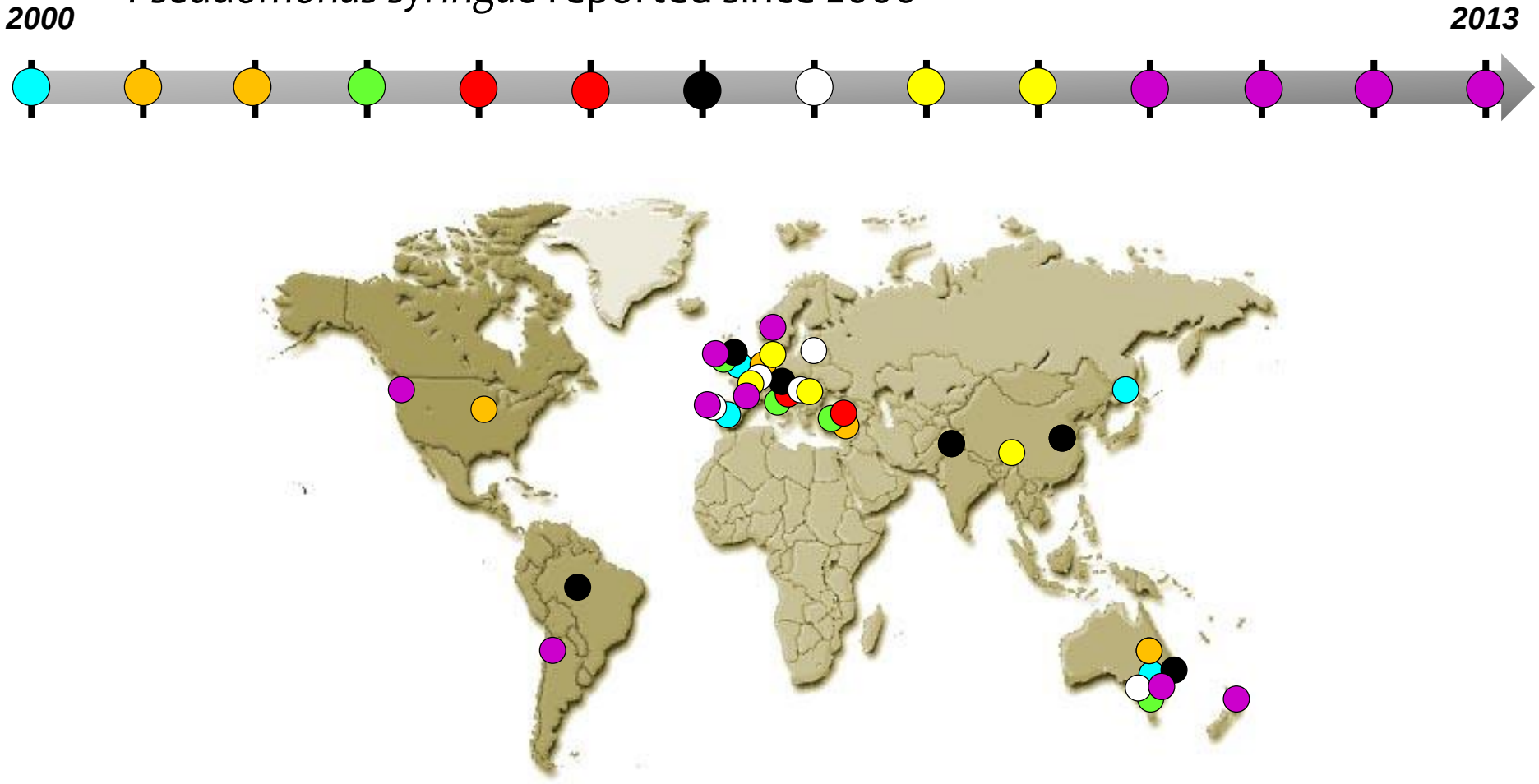

kiwifruit


tomato


hazelnut

# . . . . causing emerging diseases world-wide

**Examples** of disease outbreaks on woody plants caused by *Pseudomonas syringae* reported since 2000




**New outbreaks on > 20 woody crop species**

# In search of reservoirs of *P. syringae* outside of agriculture


# Reservoirs of *P. syringae*

Crops

Wild plants - healthy

Epilithic biofilms

Leaf litter



Cloud water

(Sands 1982, Amato 2007)

Rain

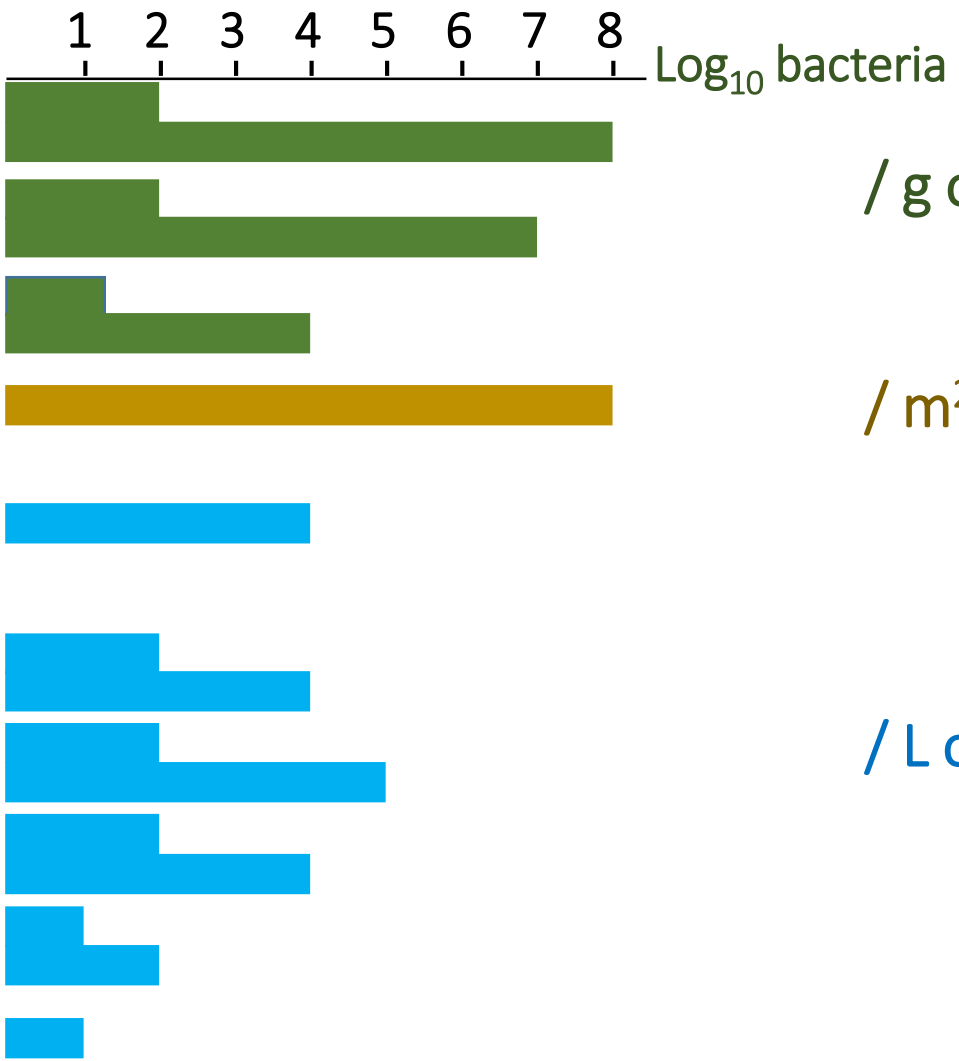
Snow

Alpine lakes & rivers

Irrigation basins

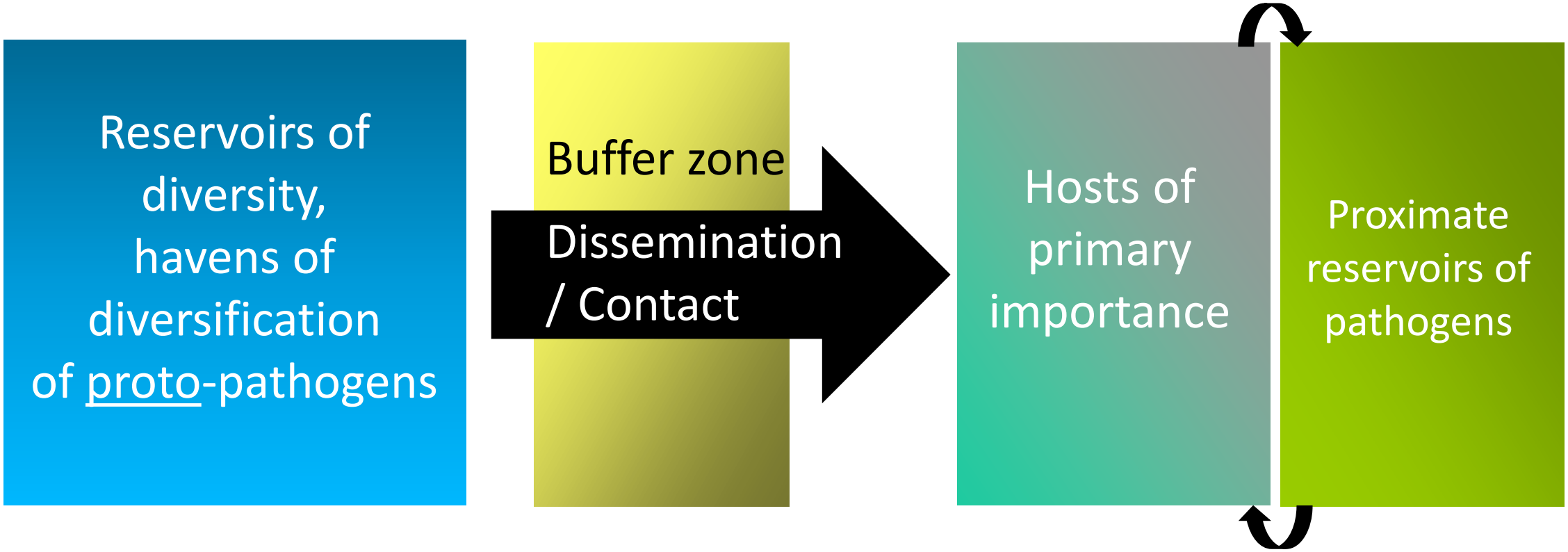
Ground water: 7 m b.g.l.

Aerosols (Lindemann 1982)



# **One Health**: a framework to understand disease emergence

What are the parameters and variables of this framework that can be characterized and quantified to help anticipate emergence and to make surveillance more robust?



# Parameters and variables

## Pathogen reservoirs

- **Metapopulation size**
- **Genetic and phenotypic diversity**
- **Localization/distribution**
- **Arms for overcoming plant defenses**

**Dissemination**

**Probability for encounter with crops**

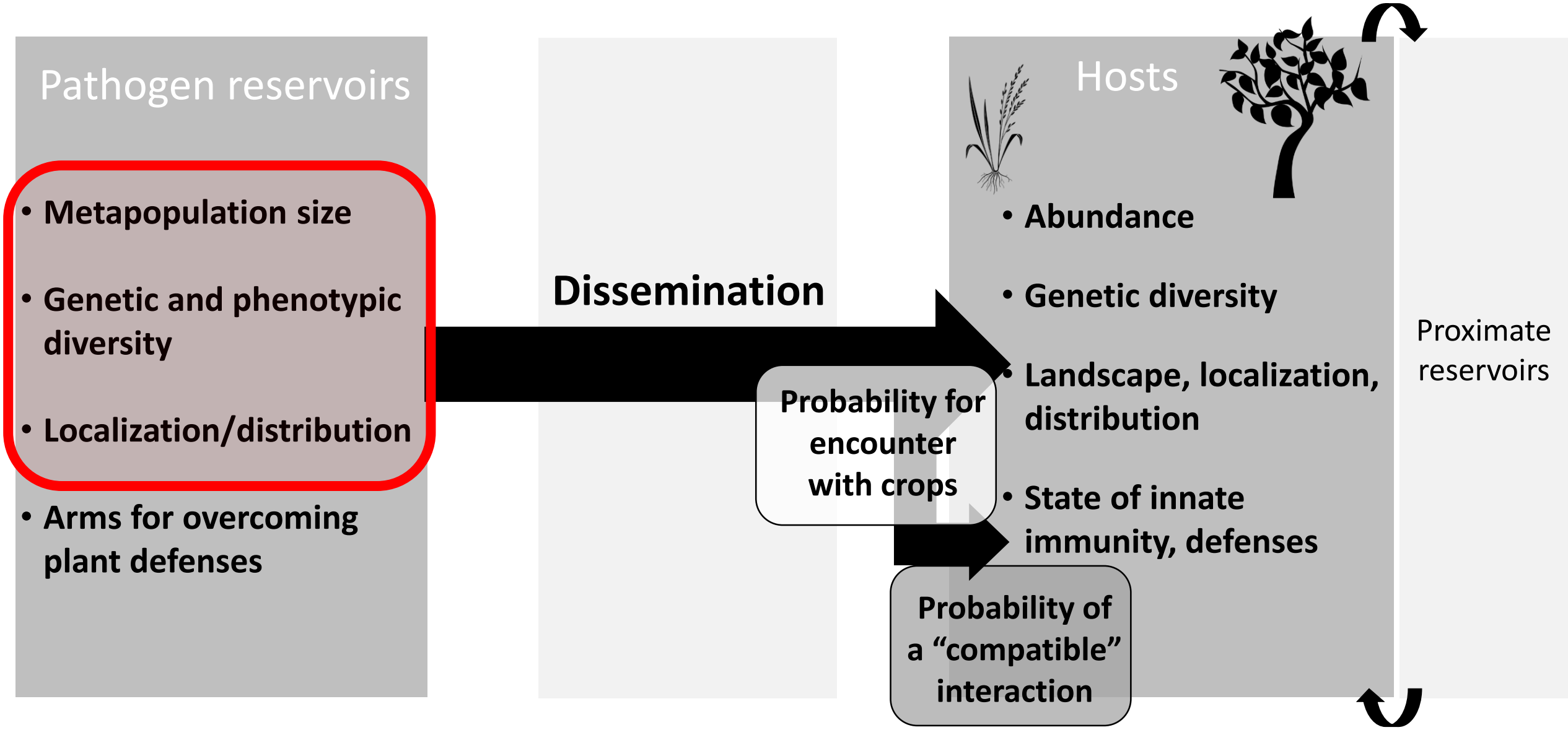
## Hosts

- **Abundance**
- **Genetic diversity**
- **Landscape, localization, distribution**
- **State of innate immunity, defenses**

**Probability of a “compatible” interaction**

Proximate reservoirs

# Parameters and variables



# Reservoirs of *P. syringae* and the size of the metapopulation

Crops

Wild plants - healthy

Epilithic biofilms

Leaf litter



Cloud water

(Sands 1982, Amato 2007)

Rain

Snow

Alpine lakes & rivers

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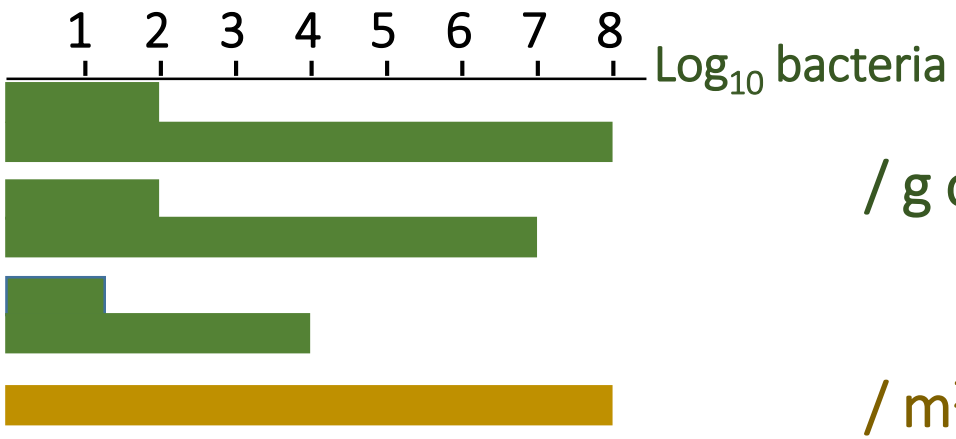
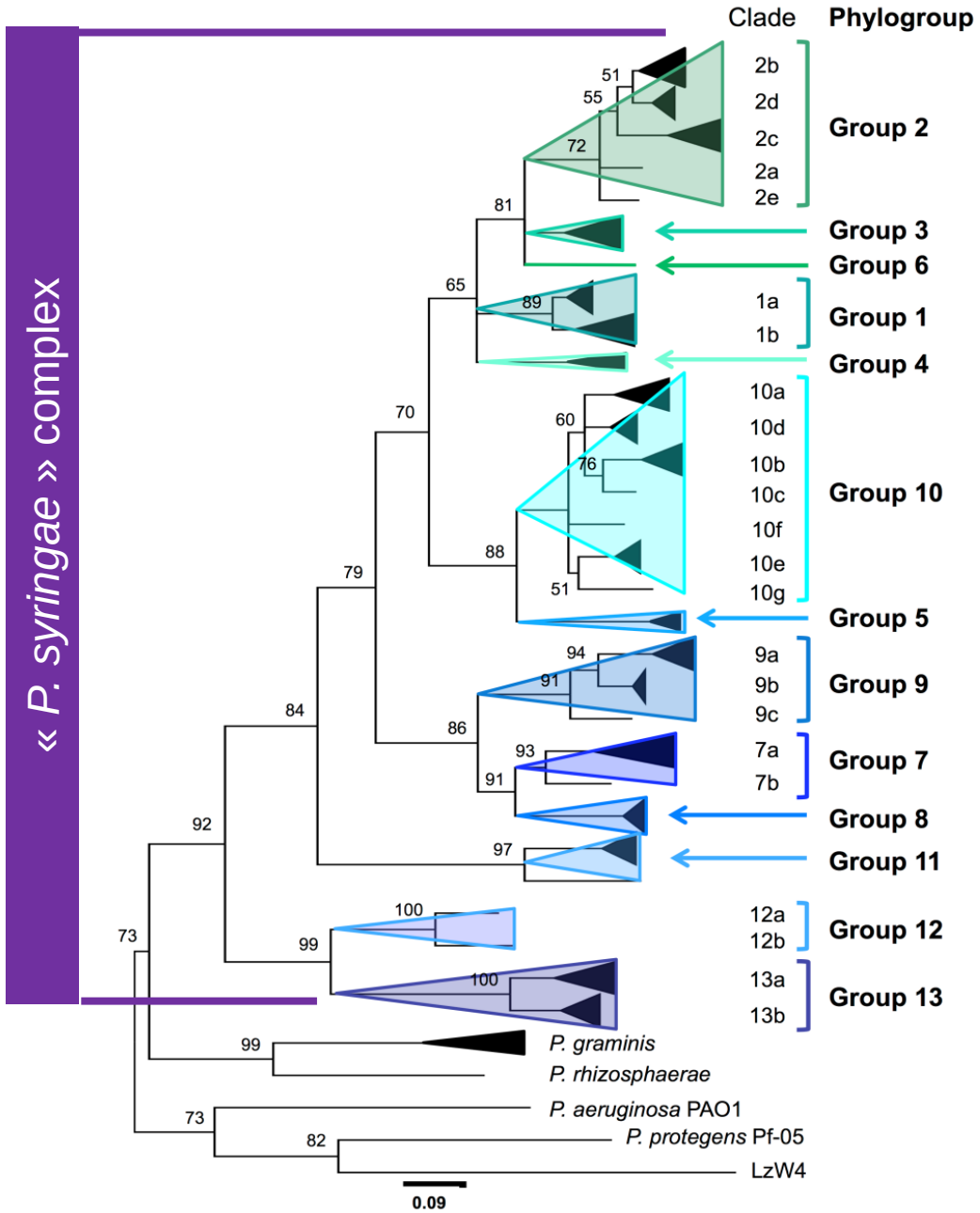



**Estimated size of the planetary metapopulation: ca. $10^{22}$ cells**

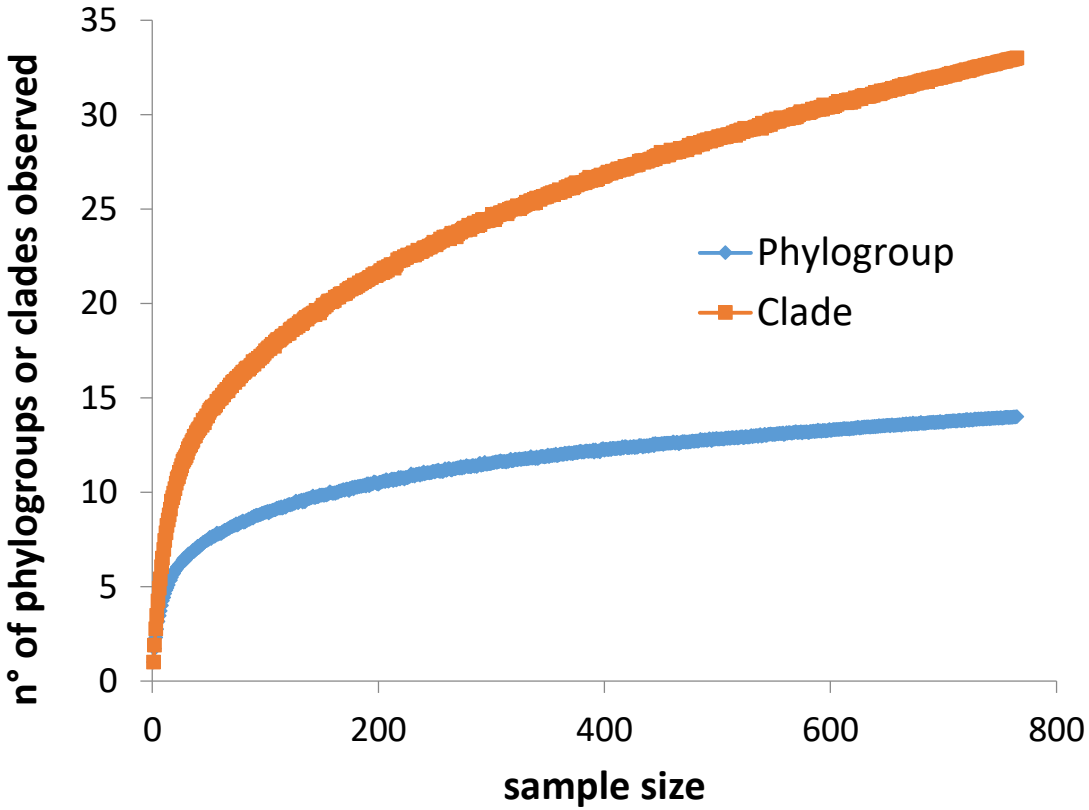
/ $m^2$ / sec ↑

# Phylogeny based on known strains

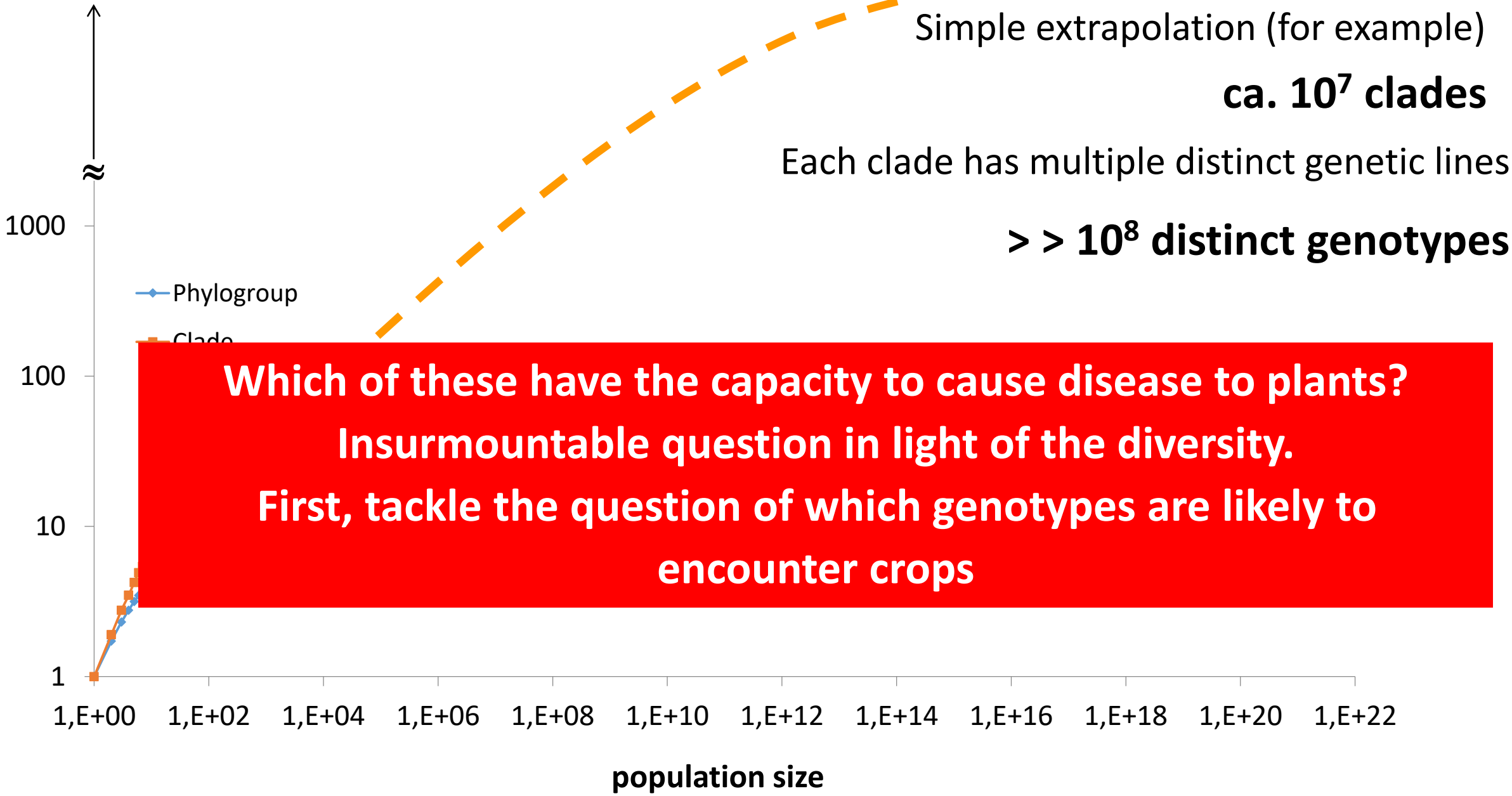



# How many different genotypes of *P. syringae*?

Rarefaction with 765 strains . . . . .



## How many different genotypes of *P. syringae* for $10^{22}$ individuals?




**Which of these have the capacity to cause disease to plants?**
**Insurmountable question in light of the diversity.**
**First, tackle the question of which genotypes are likely to encounter crops**

# Parameters and variables

## Pathogen reservoirs

- **Metapopulation size**
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**Dissemination**

**Probability for encounter with crops**

**Probability of a “compatible” interaction**

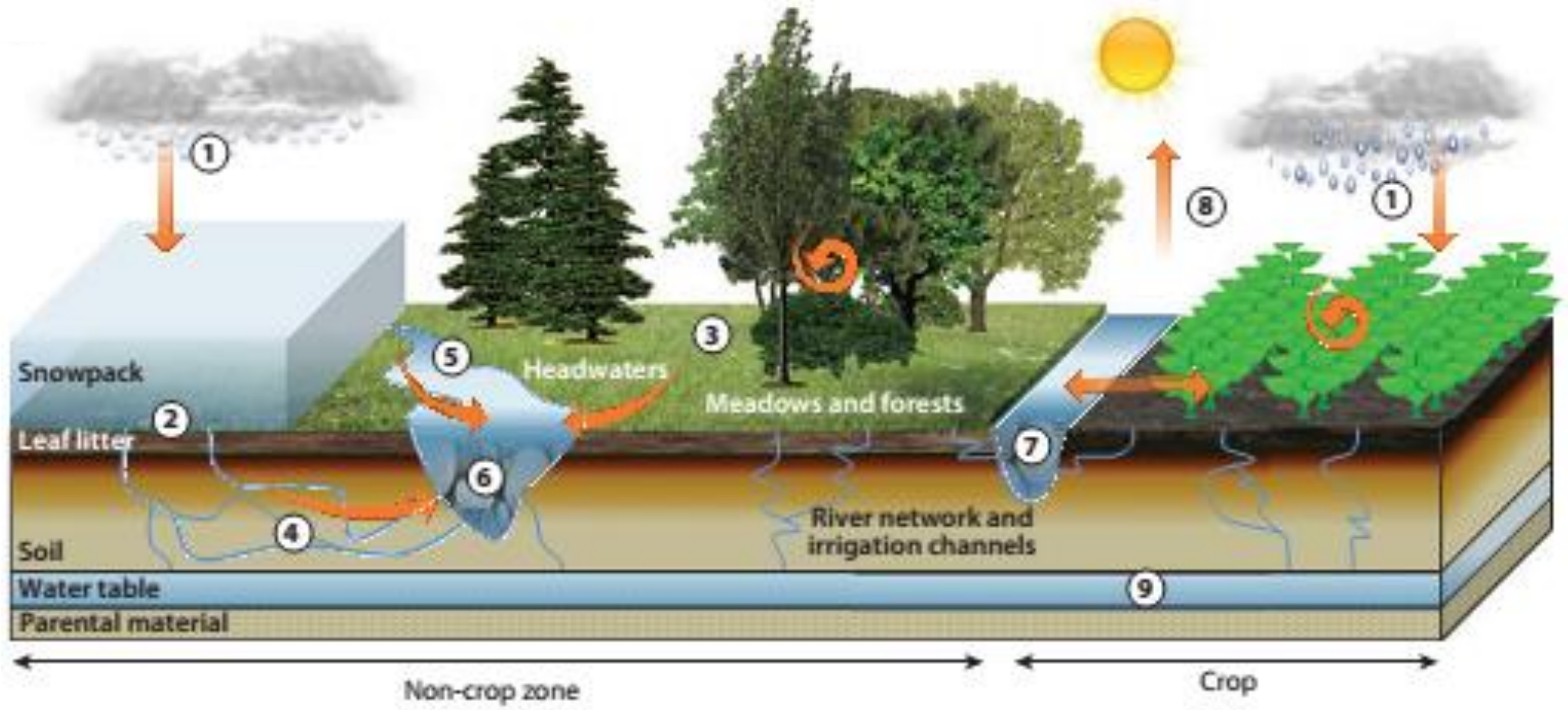
## Hosts

- **Abundance**
- **Genetic diversity**
- **Landscape, localization, distribution**
- **State of innate immunity, defenses**

Proximate reservoirs

# *P. syringae* persists in and is disseminated among a wide range of habitats

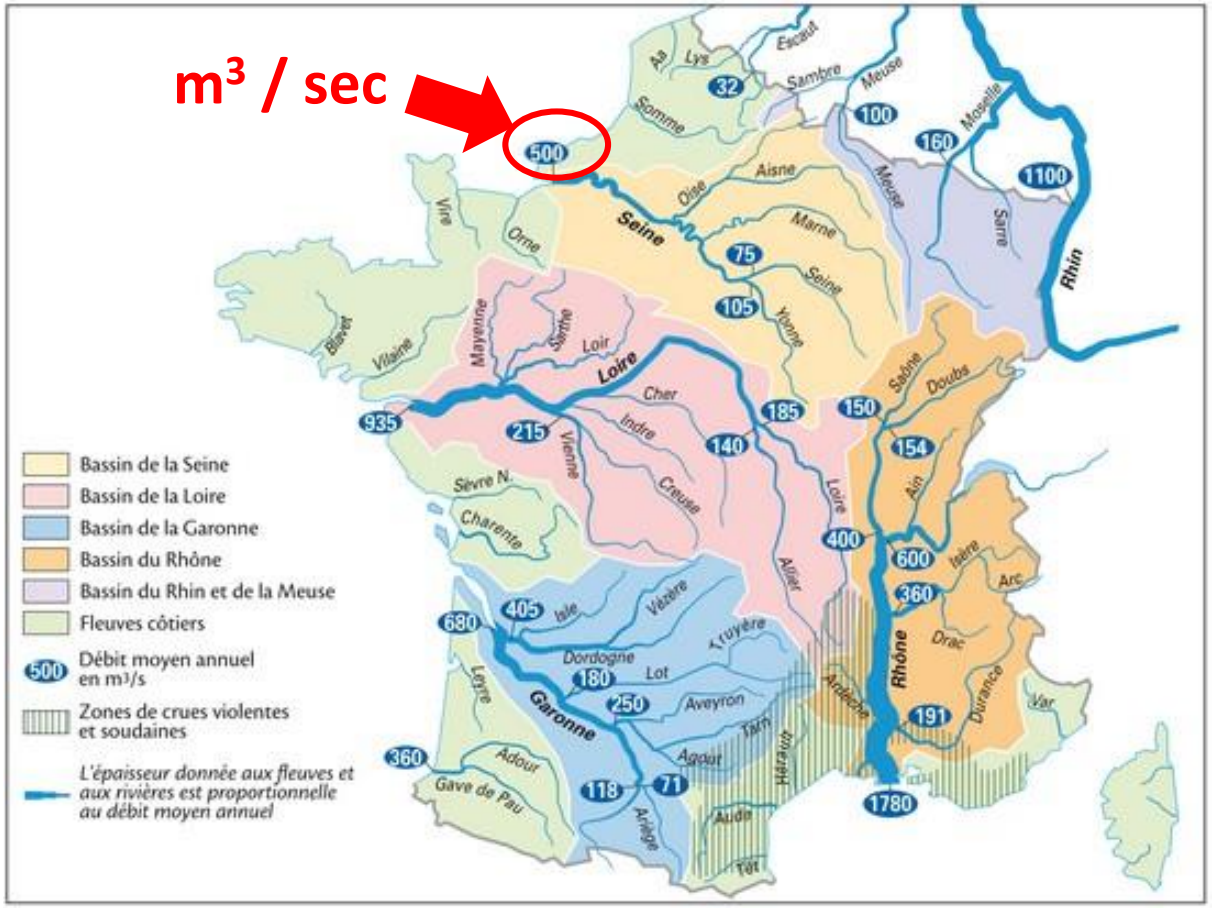
## Long distance dissemination via water and air



# Assessing long distance dissemination of *P. syringae* via water and air

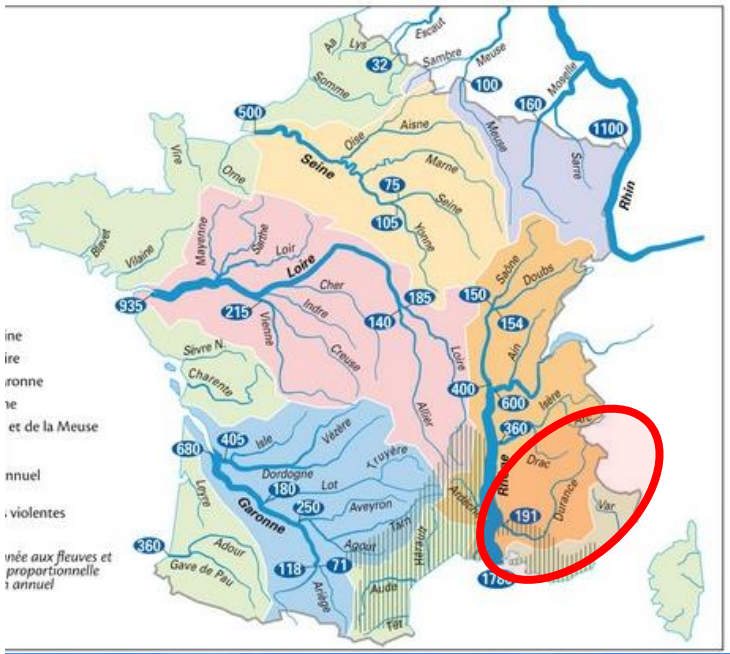
**SPREE: Strategic preemptive pathogen surveillance of air and water to anticipate plant disease emergence in scenarios of changing land use.**

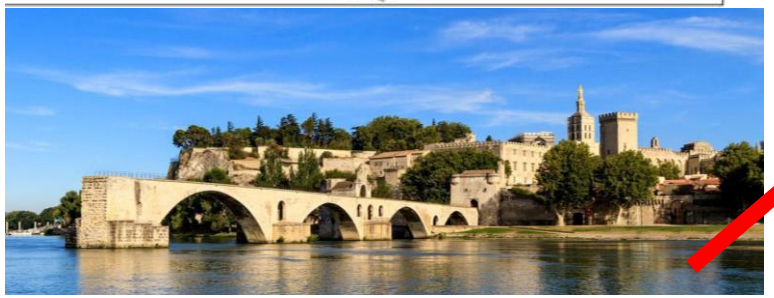
Project in progress (2017 – 2020): French National Research Agency




# Assessing long distance dissemination of *P. syringae* via water and air

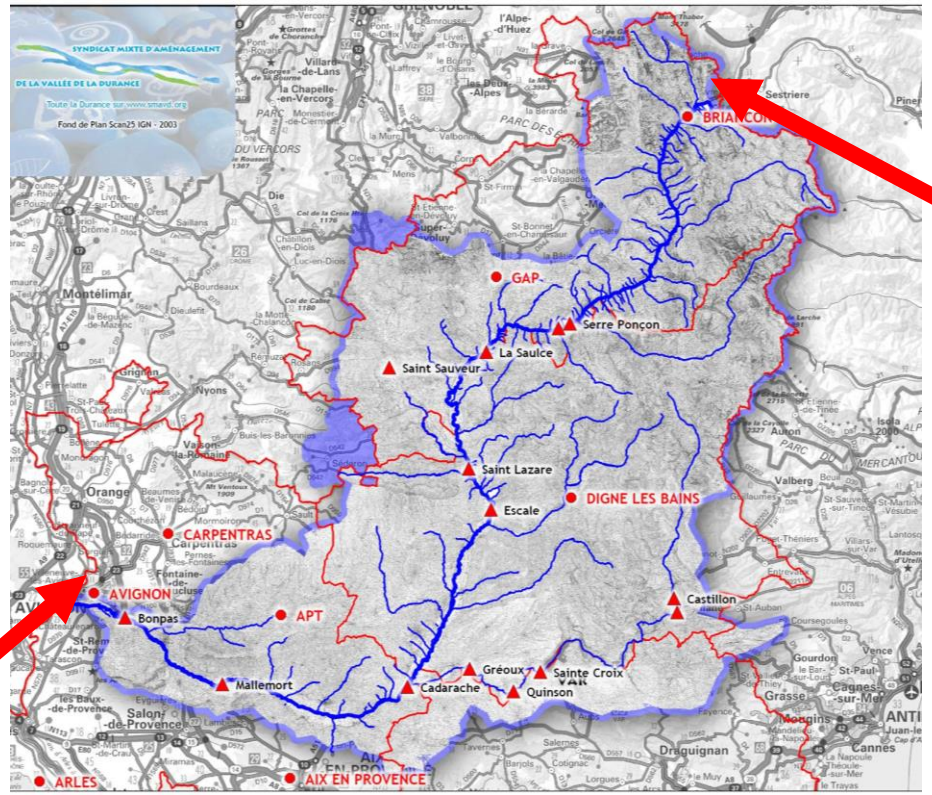
Characterize the flow of *P. syringae* within the Durance river basin catchment



Avignon

The Durance is used for irrigation in the major fruit and vegetable production region of France




Southern French Alps

# Assessing long distance dissemination of *P. syringae* via water and air

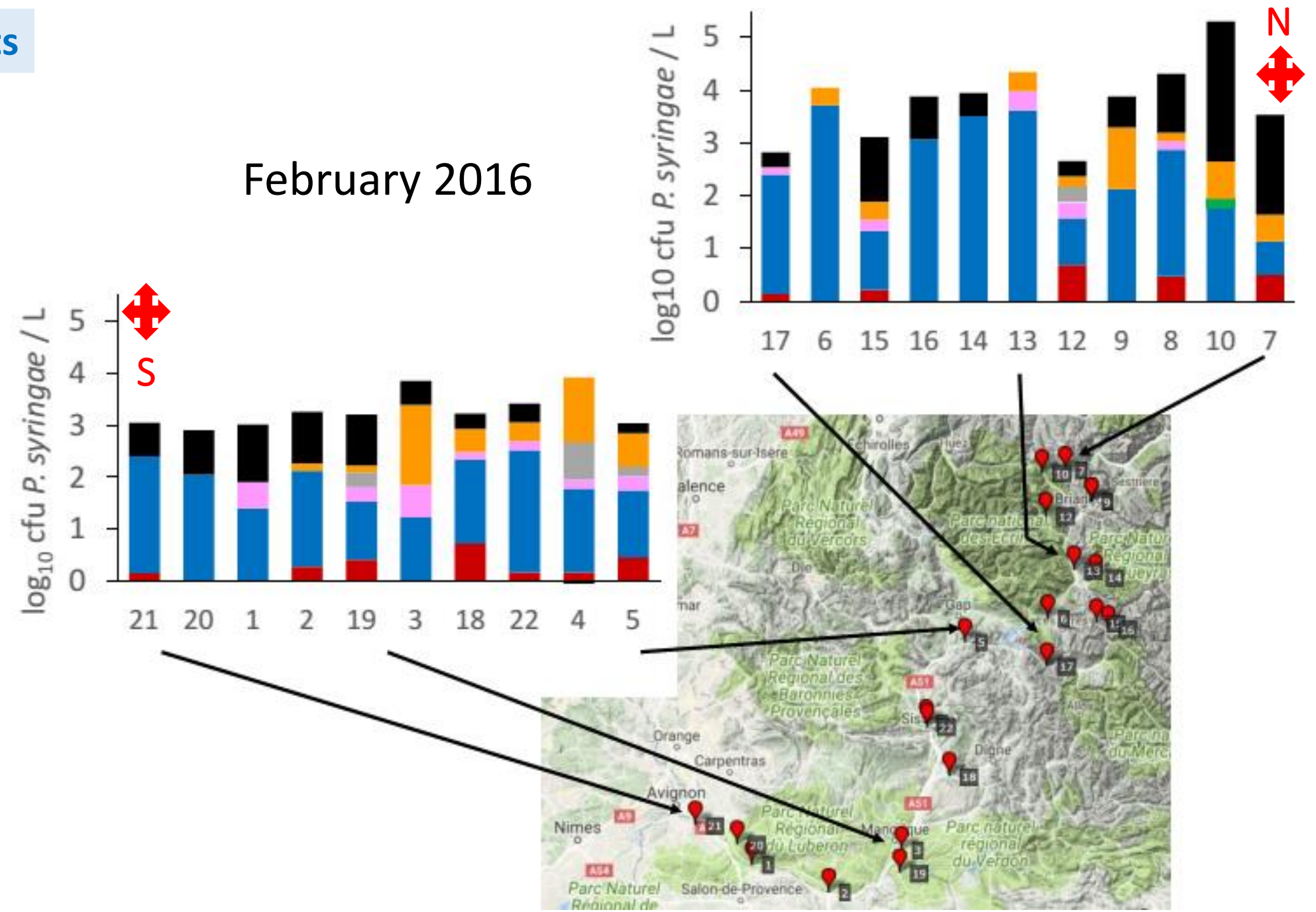

- 22 sampling sites
- 4 seasons / 2016 & 2017
- Quantify population densities in river water
- Isolate strains for further characterization (>**5000** from this study)

# Example results

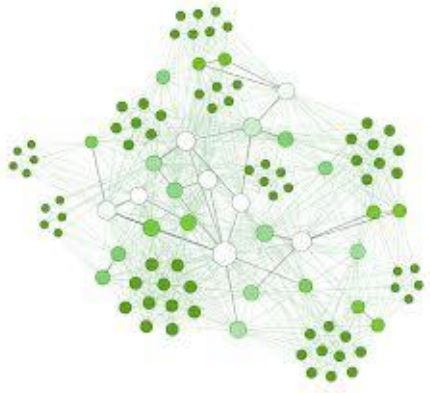
*Phylogroups*

- PG1
- PG2
- PG4
- PG7/8
- PG9
- PG13
- PG-other

February 2016



# Assessing long distance dissemination of *P. syringae* via water and air



Based on data for population size and genetic structure, network analyses will be used to assess

- the site-to-site relatedness of *P. syringae* populations along the river flow and
- the contribution of external inputs and influences to the flow (landscape, water chemistry, etc.)

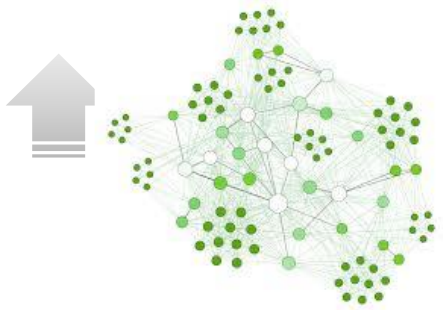
# Assessing long distance dissemination of *P. syringae* via water and air

Approximate the probable aerial trajectories of *P. syringae* based on historical data for air mass movement

**Example**

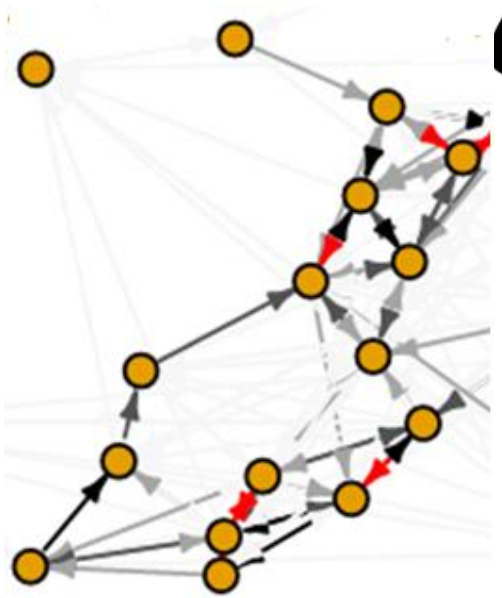
Trajectories of all of the air masses arriving at 500 m altitude in Pertuis, France in 2015

# Assessing long distance dissemination of *P. syringae* via air



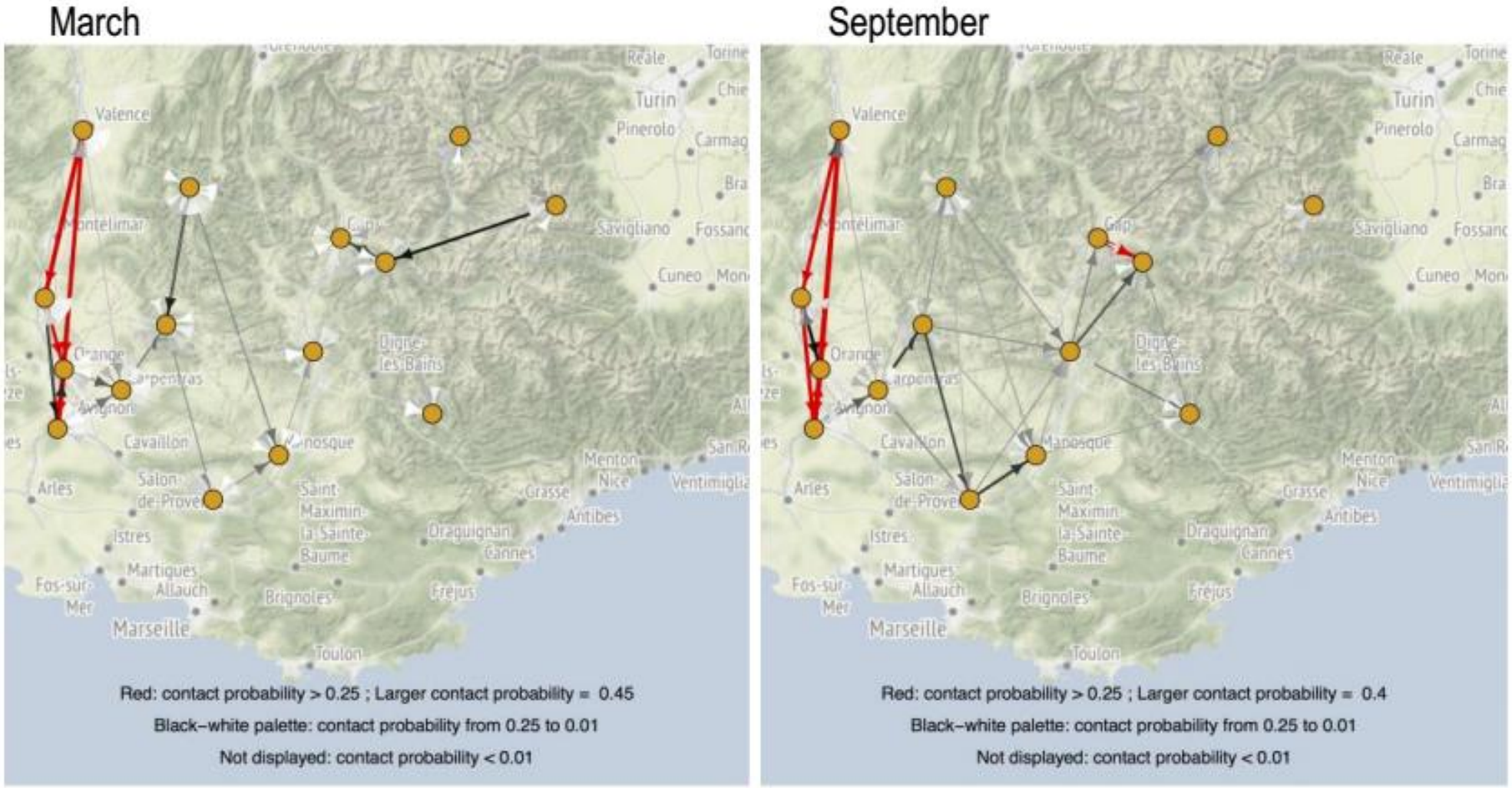
Based on a decade of historical data for air mass movement, network analyses will be used to

- assess the probable flow of air masses between sites in the Durance river basin

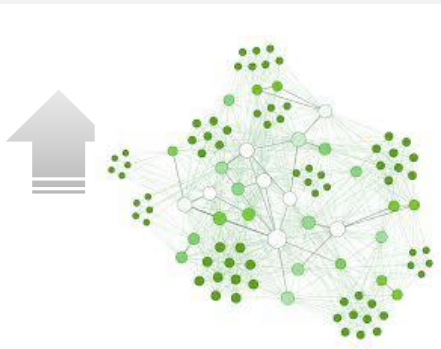


## Example results

# Difference in atmospheric connectivity, March vs. September (2013-2016)



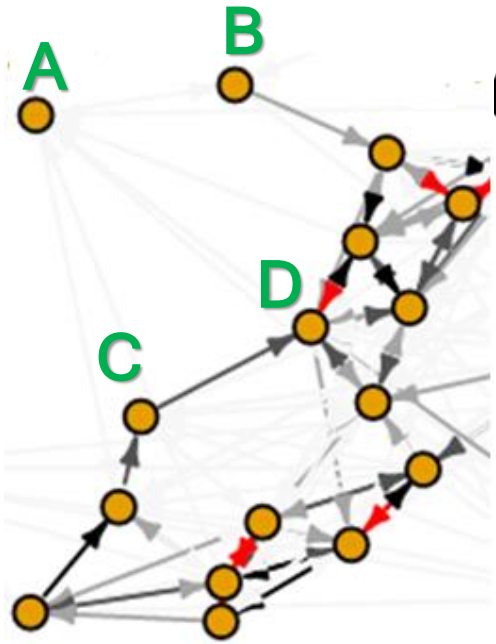
# Assessing long distance dissemination of *P. syringae* via air



Based on a decade of historical data for air mass movement, network analyses will be used to

- assess the probable flow of air masses between sites in the Durance river basin
- set up sampling campaigns to validate aerial movement of *P. syringae*

$H_0$: The similarity of populations of *P. syringae* washed out with rain at different sites depends on the aerial connectivity: $(C \approx D) \neq A \neq B$



# Parameters and variables

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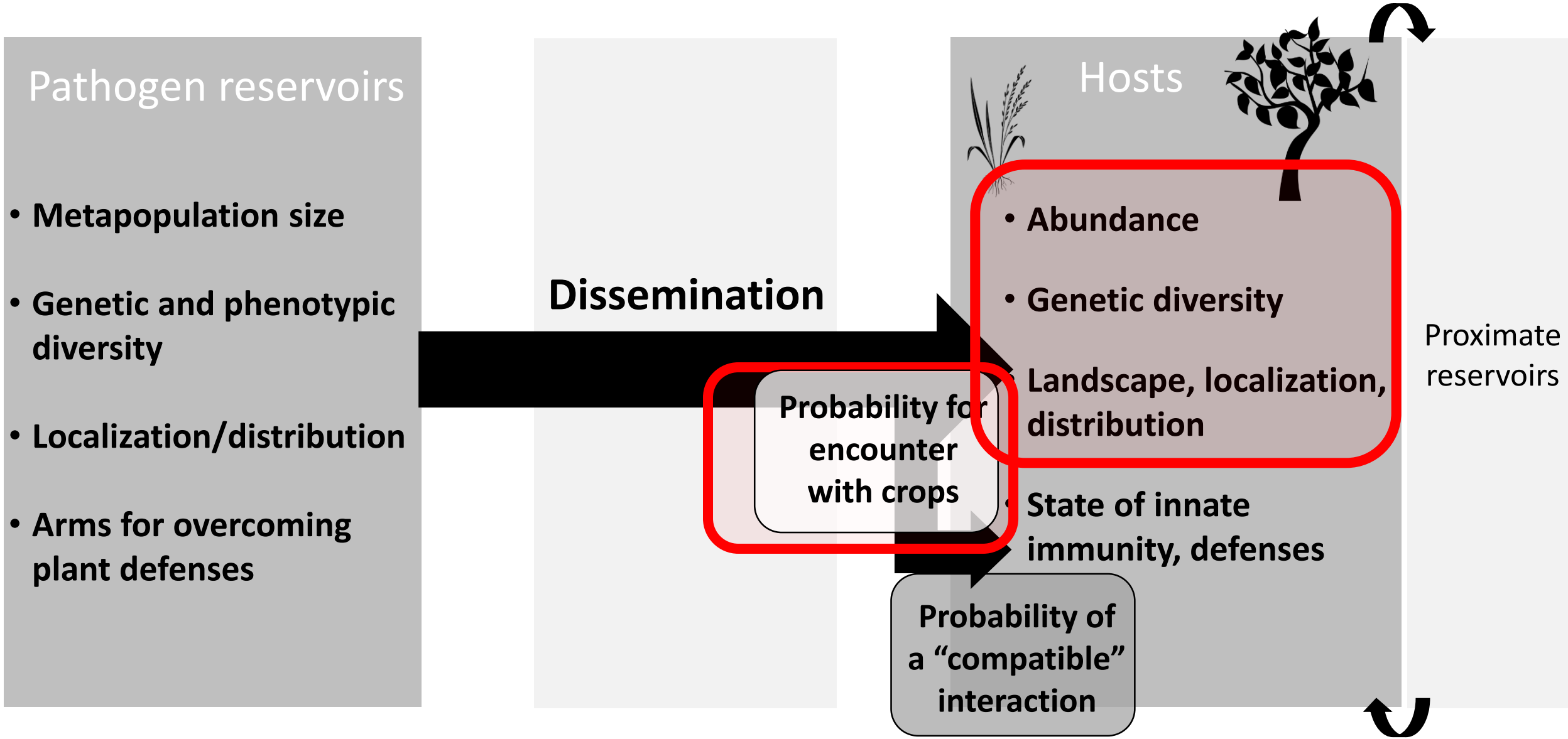
# Parameters and variables



# Assessing the probability of encounter with crops via air and water

- Access digitalized data on land use (>25 yr of data, >125 land use categories for southern FR)

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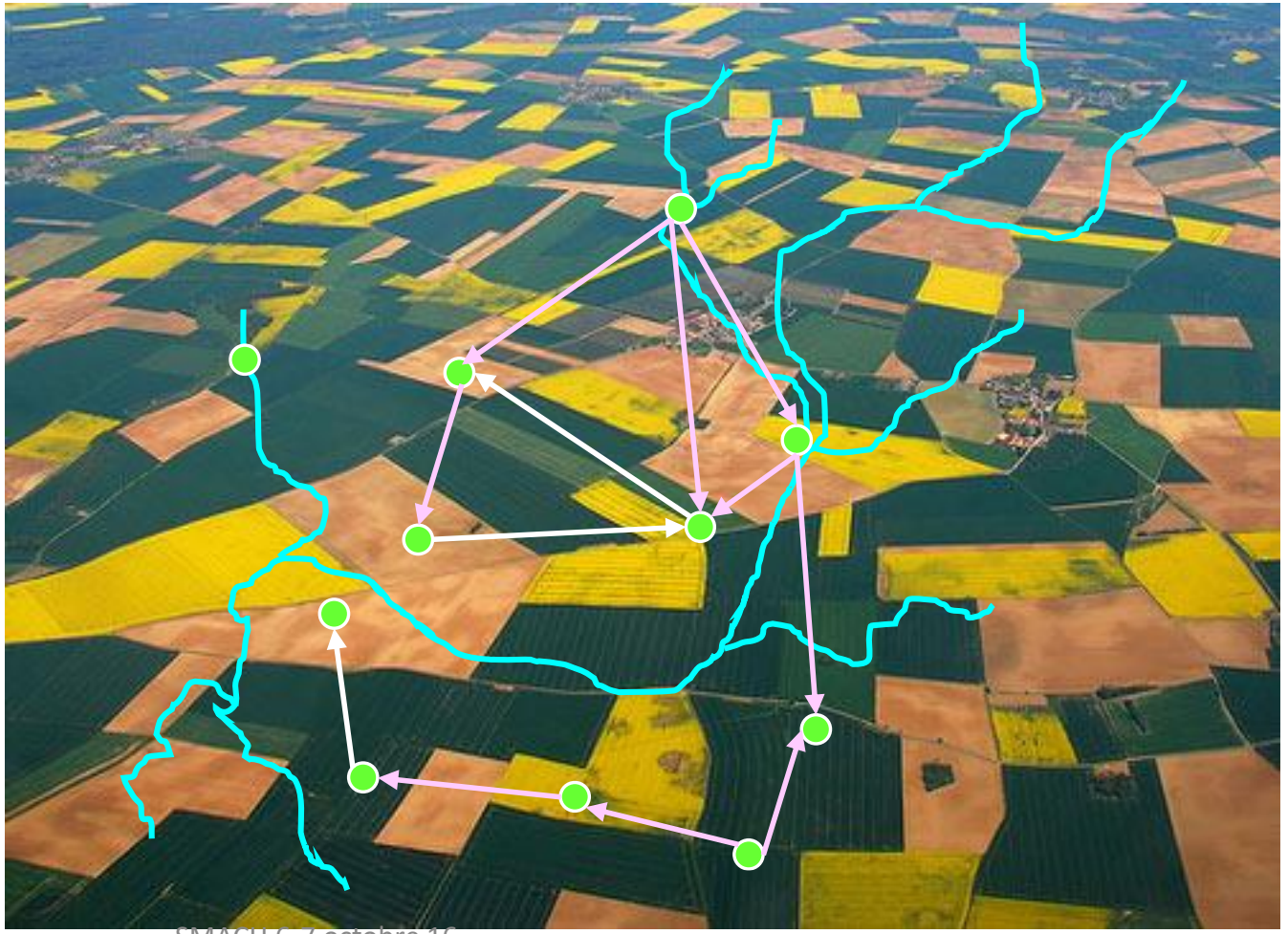

# Assessing the probability of encounter with crops via air and water

- Access digitalized data on land use (>25 yr of data, >125 land use categories for southern FR)
- Overlay **water** dissemination network
- Overlay **aerial** dissemination network
- Identify and characterize **hubs** where dissemination converges

# Parameters and variables

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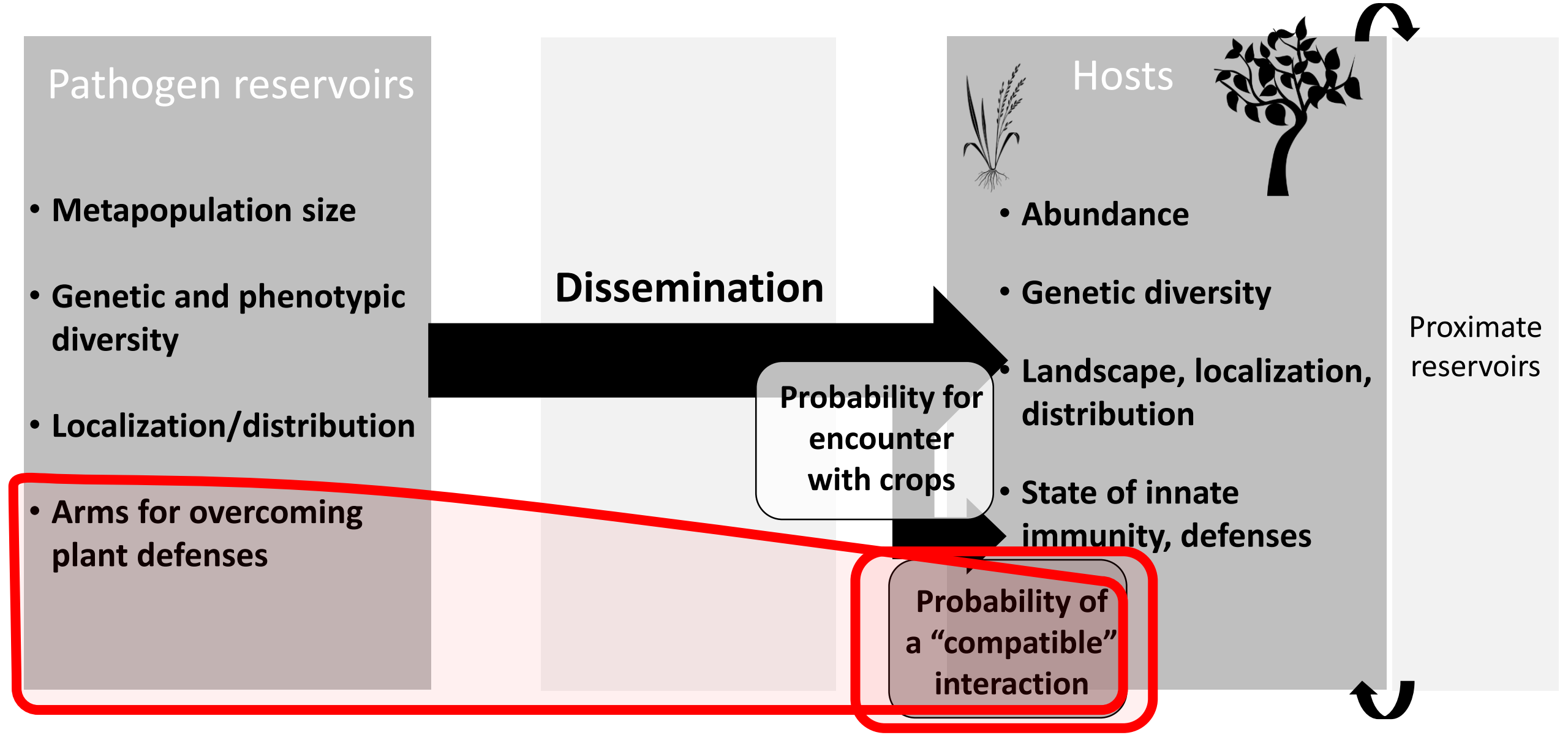

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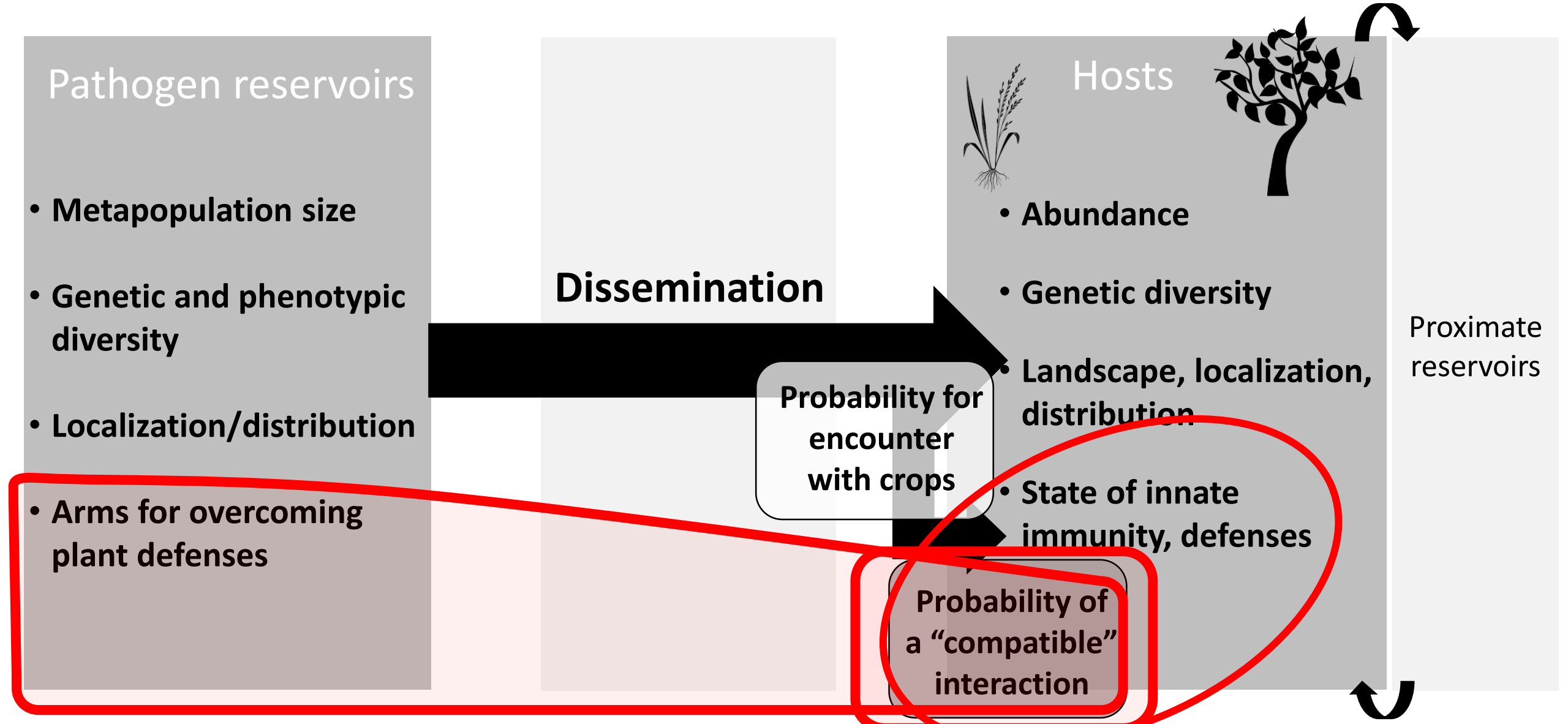


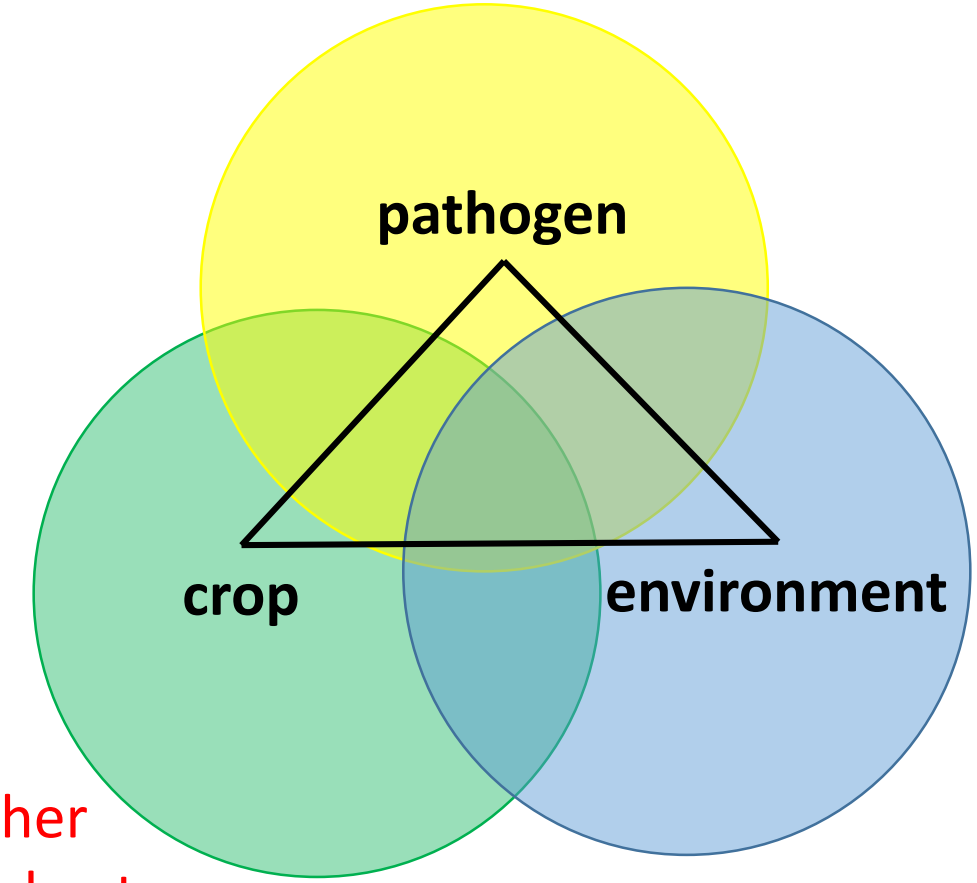
# Assessing the probability that a strain of *P. syringae* can cause disease on the crop it encounters

$P_{disease} = f$ (Extent of potential host range$_{Ps}$ X

Inherent sensitivity$_{Crop}$ X

Environment)

The wider the potential host range, the higher the probability for encountering a sensitive host.



# Assessing the probability that a strain of *P. syringae* can cause disease on the crop it encounters

What is the extent of host range of *P. syringae* ?

Can it be predicted from genetic traits or from other phenotypes?

Current data base of host range tests:

134 strains on 16 – 22 plant species

20 yrs of host range testing

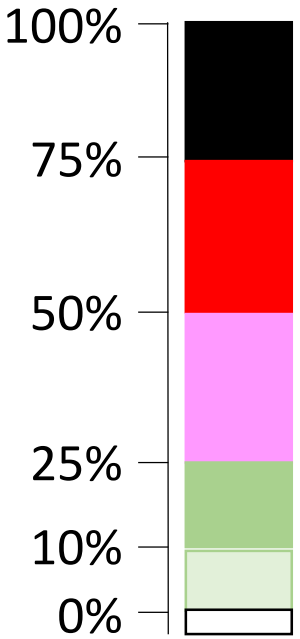
# Assessing the probability that a strain of *P. syringae* can cause disease on the crop it encounters

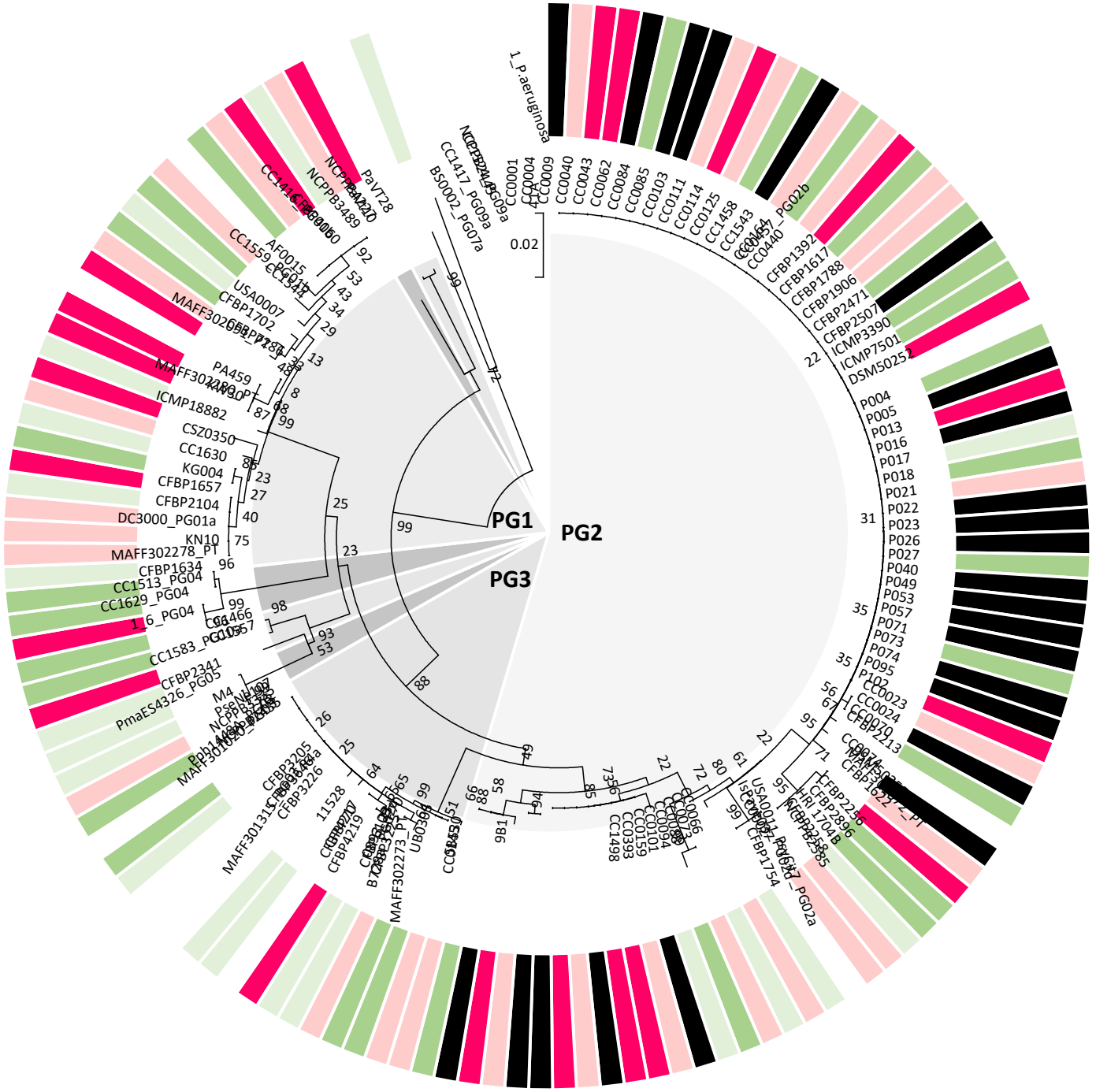
***In the next slide***

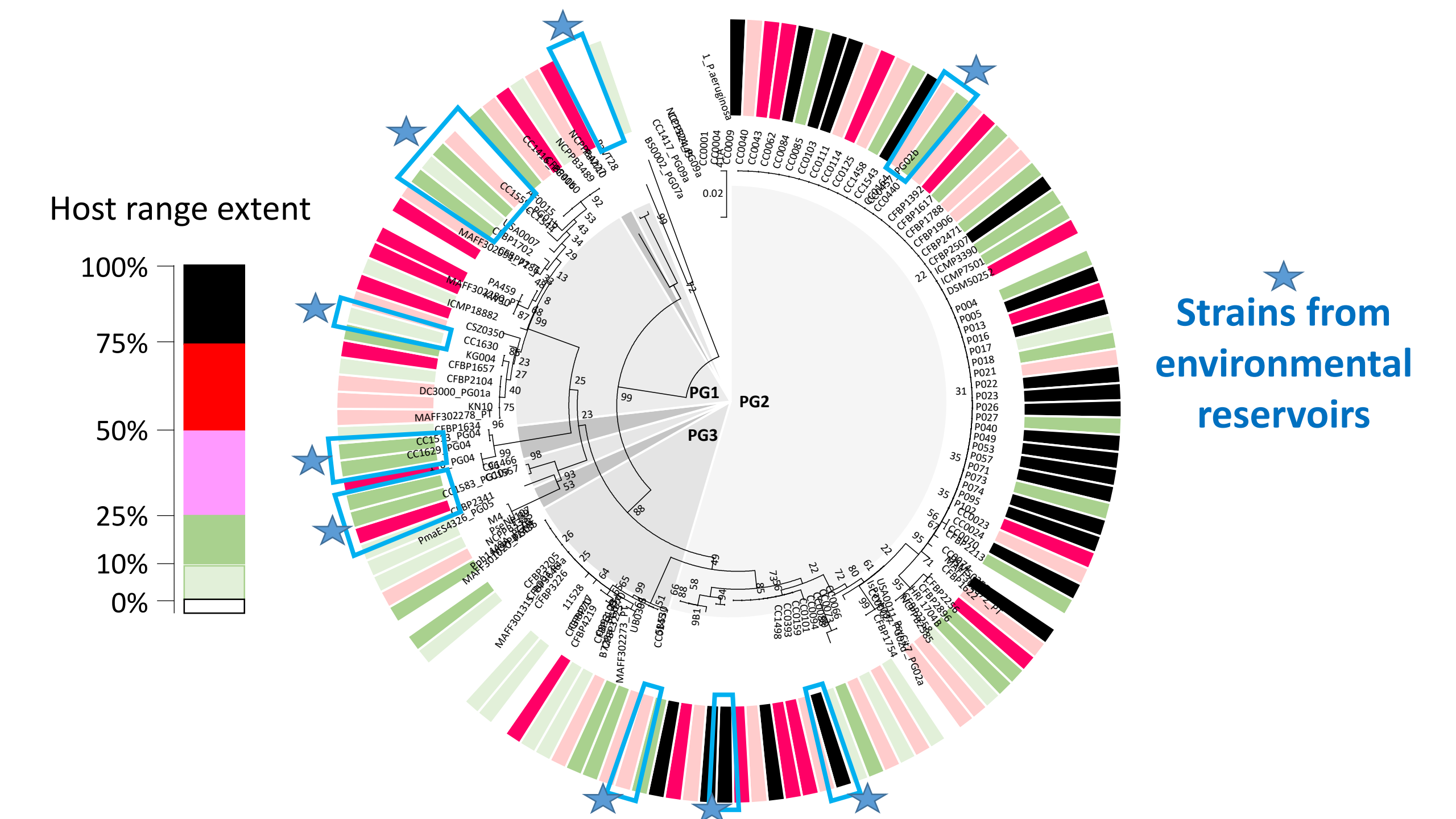
- 134 strains in their phylogenetic context, tested over 20 years in blocks of about 20 – 30 strains on 16 to 22 plant species

- Extent of host range expressed as % of the species of plants that repeatedly showed disease symptoms

Host range extent




Host range extent
100%
75%
50%
25%
10%
0%
PG1
PG2
PG3
0.02
Strains from environmental reservoirs

# Assessing the probability that a strain of *P. syringae* can cause disease on the crop it encounters

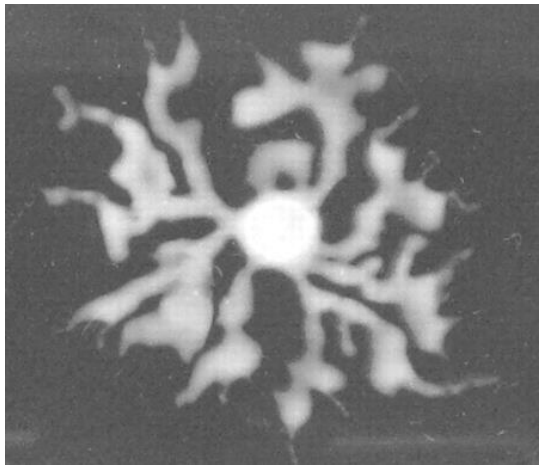
Are there any genomic traits that reflect broad or narrow host range?

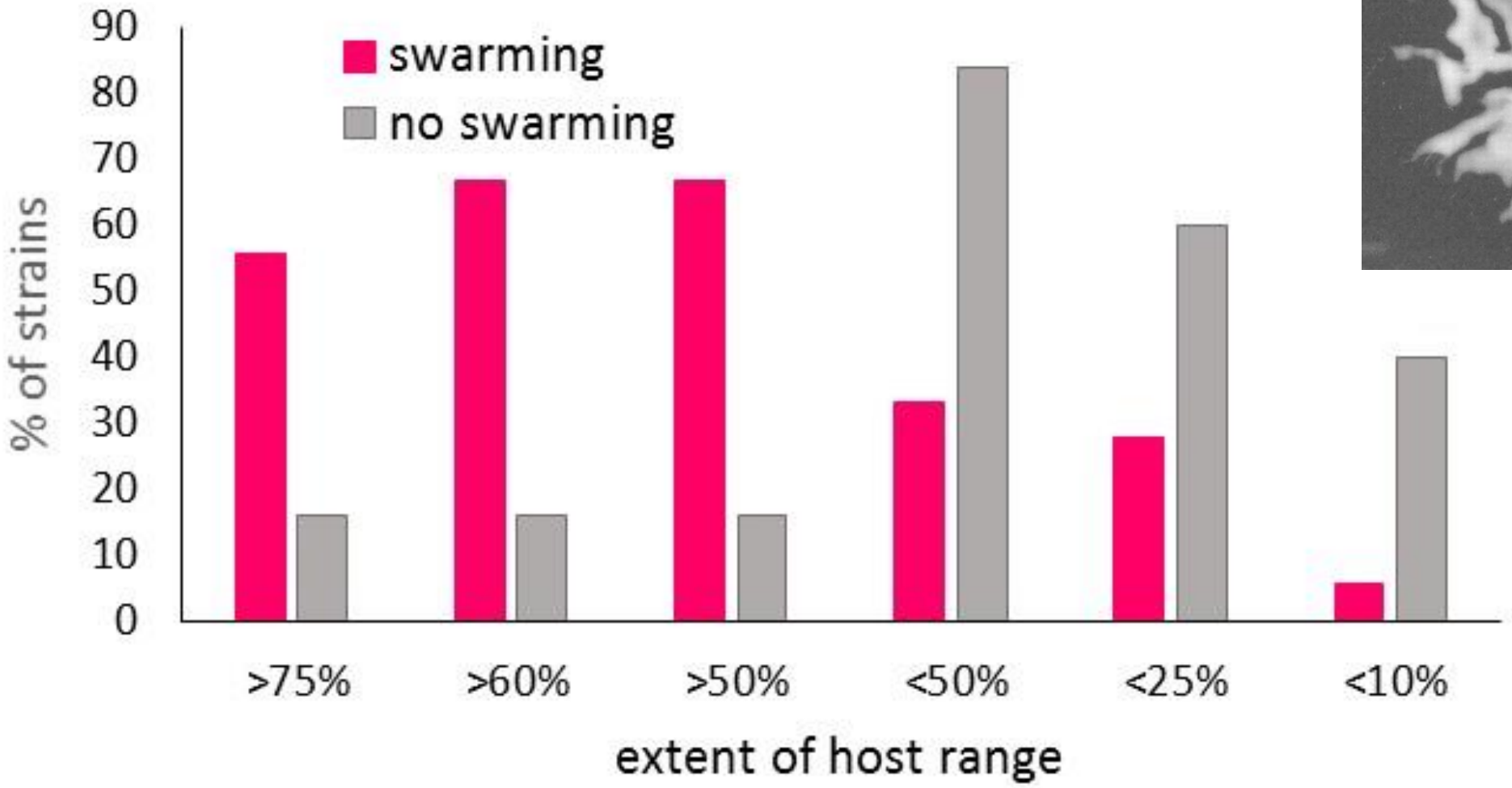
- The high genetic diversity across strains does not facilitate the search for such traits.

Are there phenotypes correlated with host range that could help to orient the search for genetic indicators of host range?

# Assessing the probability that a strain of *P. syringae* can cause disease on the crop it encounters

Example of a potential indicator of broad host range

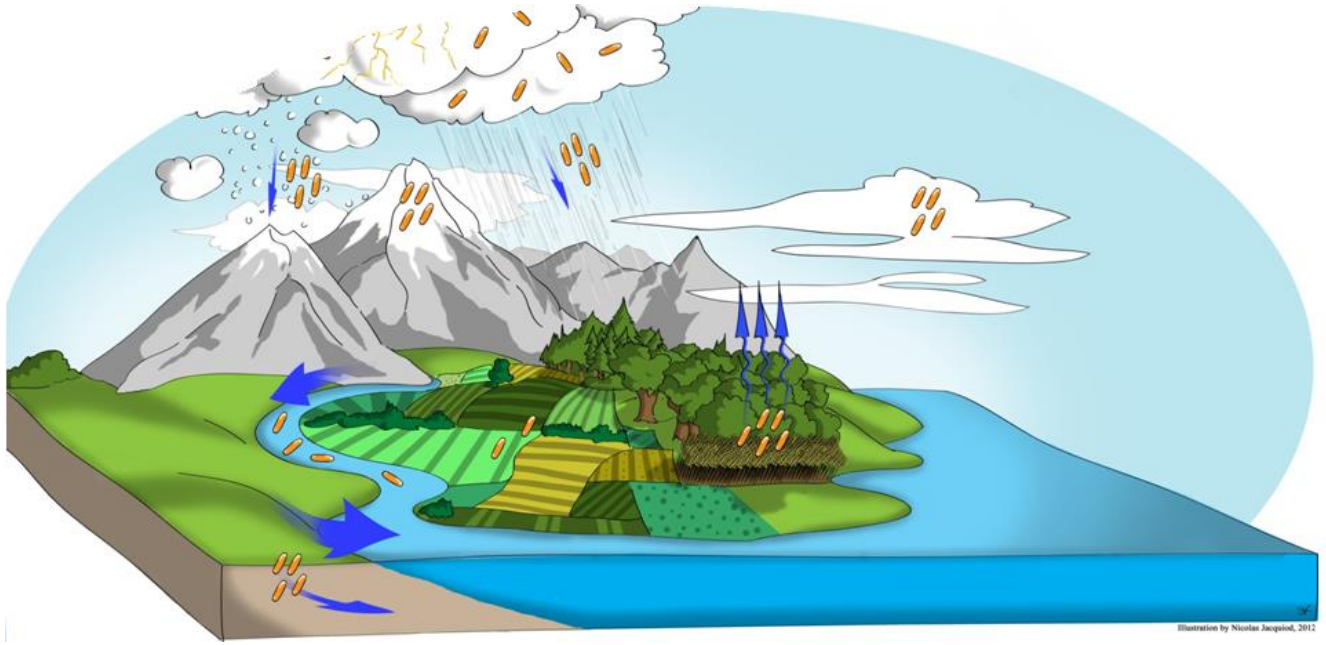




# Conclusions and perspectives

Build a paradigm for anticipating emergence of new plant pathogens that:

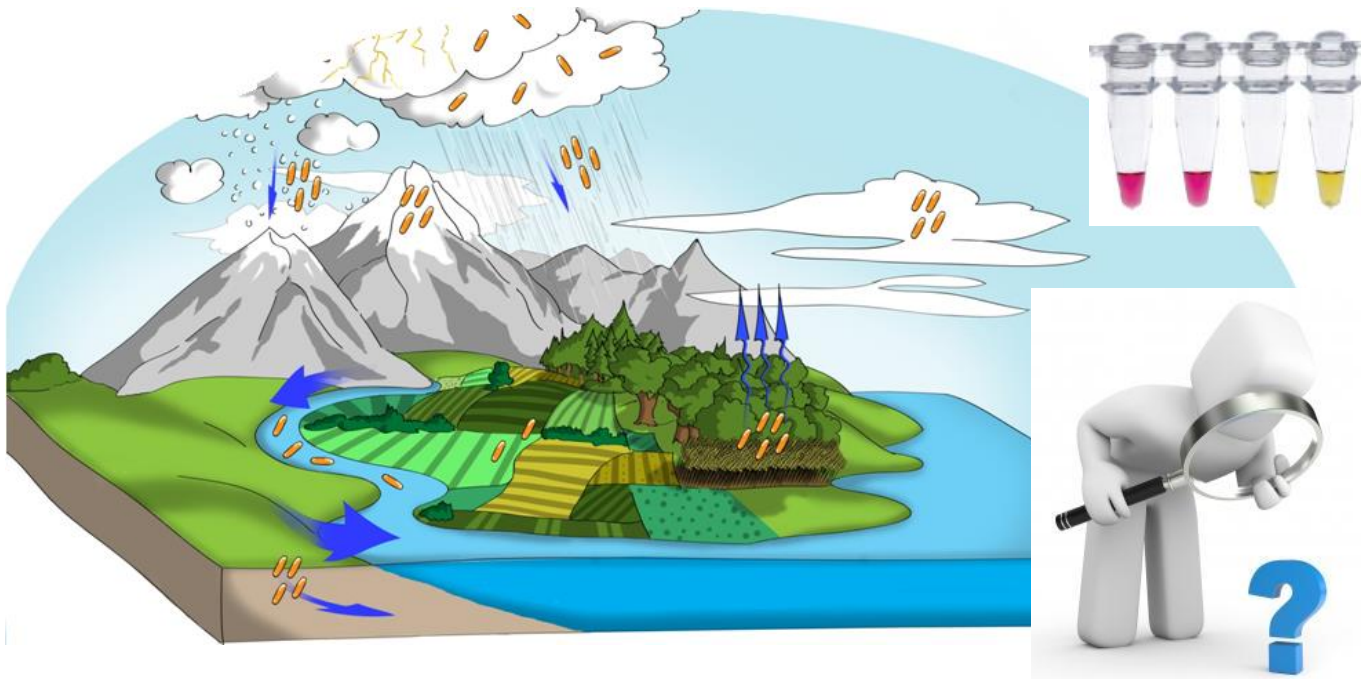
- accounts for environmental reservoirs, diverse substrates, long distance movement



# Conclusions and perspectives

Build a paradigm for anticipating emergence of new plant pathogens that:

- accounts for environmental reservoirs, diverse substrates, long distance movement
- is pertinent to realistic practices of surveillance







- Markers to target an ensemble of “risky” microbial lines
- Easy-to-use, inexpensive, reliable diagnostics
- A plan for strategic, cost-effective deployment

# Conclusions and perspectives

**What other pathogens are pertinent for this approach?**

- **Free-living pathogens with saprophytic phases**

  ***Fungi***

  *Fusarium* *Botrytis* *Alternaria* *Pythium*
  *Sclerotina* *Cladosporium* *Aspergillus* etc.

  ***Oomycetes***

  *Phytophthora*

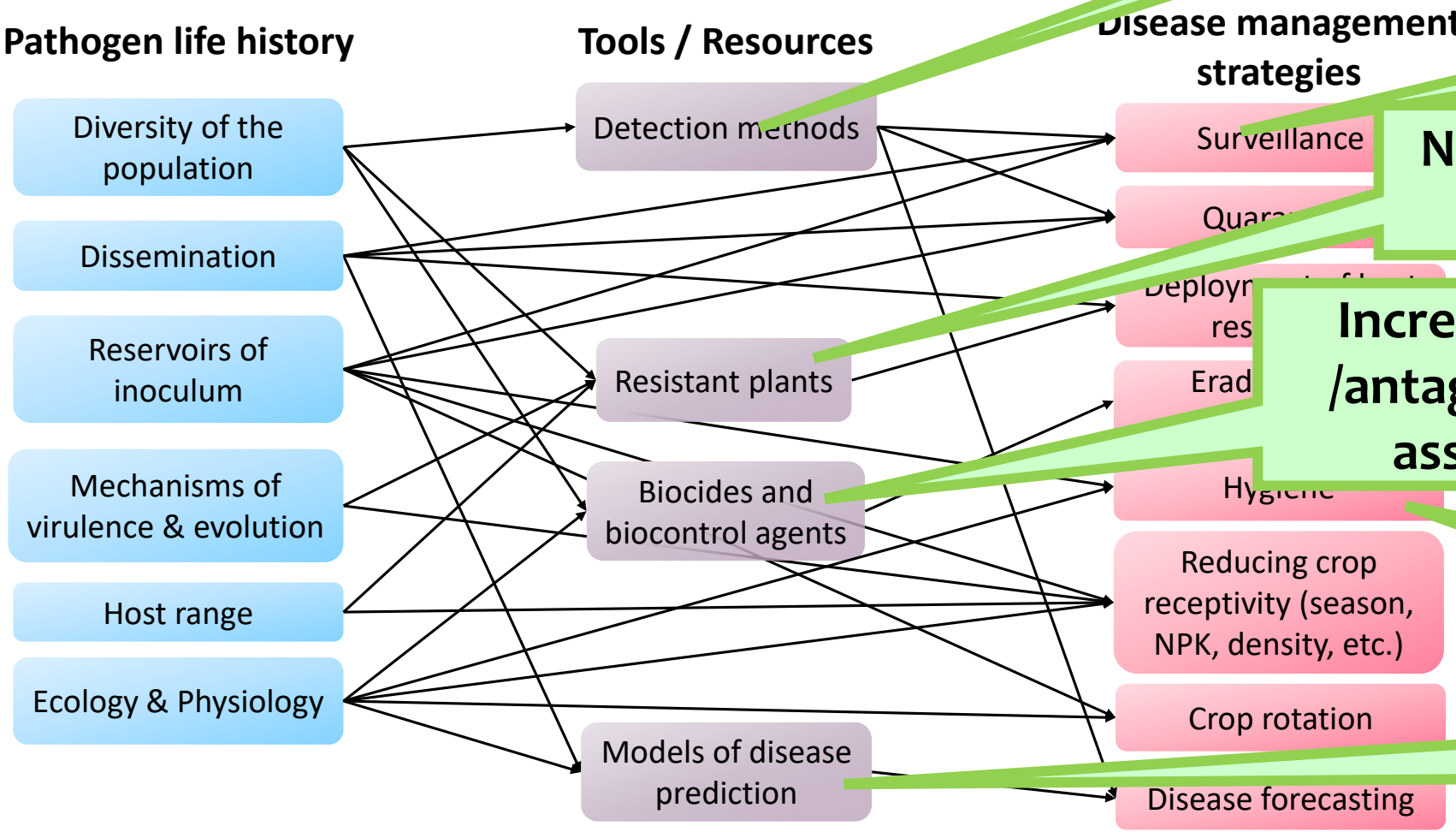
  ***Bacteria***

  *Pectobacterium* *Dickeya* *Ralstonia* etc.

- **Pathogens with living vectors** (insects, fungi, ……)

# Conclusions and perspectives

## New opportunities for disease management




New targets

New locations/habitats to survey.

New criteria for the scope of disease resistance

Increased scope for biocidal /antagonistic activity and for assessing sustainability

New scope for hygiene

New sources of inoculum

Morris et al. 2017. Frontiers for research on the ecology of plant pathogenic bacteria… *Molec. Plant Pathol*. 18 :308-319 doi: 10.1111/mpp.12508

# Acknowledgements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