

BIOLOGICAL CONTROL OF *ERWINIA AMYLOVORA*: WHAT ARE THE DRIVERS OF *MALUS DOMESTICA*'S MICROBIOME ASSEMBLY

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Introduction

FIRE BLIGHT

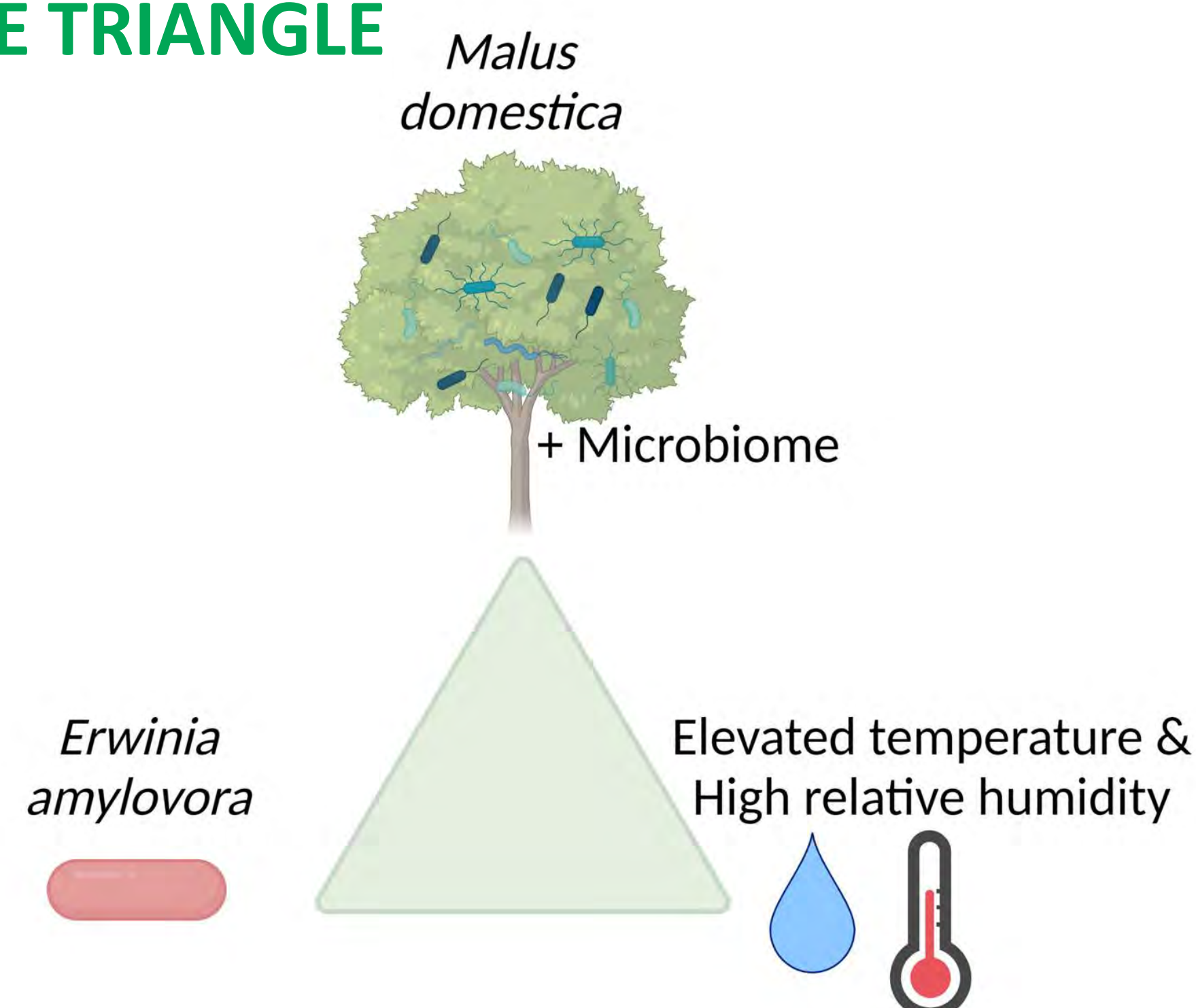
Erwinia amylovora is a Gram-negative bacterium that can cause fire blight in the *Rosaceae* plants.

Fruit trees such as the domesticated apple tree *Malus domestica* are particularly susceptible hosts.

E. amylovora enters its host through the nectaries ⁽¹⁾ or wounds and then forms a biofilm in the xylem ⁽²⁾.

The constriction of the vascular system as well as the secretion of virulence factors lead to the characteristic necrotic symptoms of fire blight ^(2,3).

DISEASE TRIANGLE



MICROBIOME

Before *E. amylovora* enters its host, it lives and interacts with other microbes at the surface of flowers and leaves.

Indeed, the phyllosphere of *M. domestica* is colonized by epiphytic microbial communities that can interfere with *E. amylovora*.

State of the art

- Reduced microbial diversity on the leaves of unhealthy trees. ⁽⁴⁾
- *Enterobacteriaceae* and *Pseudomonadaceae* dominance leads to a loss of diversity in the flower microbiome no matter if the tree is challenged with *E. amylovora* or not. ⁽⁵⁾
- Specific *Bacillus amyloliquefaciens*, *Pseudomonas poae*, and *Pantoea agglomerans* strains have biocontrol effect against *E. amylovora* strains. ⁽⁶⁾

Objectives

1. To study the temporal variation of the microbial community of *Malus domestica*'s phyllosphere
2. To determine if there is a host (cultivar) effect on the leaf and flower microbial community structure
3. To improve the detection method of *Erwinia amylovora*

Relevance of the study

- Fire blight causes important economic loss
- Fire blight onset and incidence is expected to change as global temperature rises
- The use of antibiotics is not a sustainable practice as we observe the development of antibiotic resistance

The project is in accordance with the following



2 - Zero Hunger

8 - Decent Work and Economic Growth

12 - Responsible Consumption and Production

13 - Climate Action

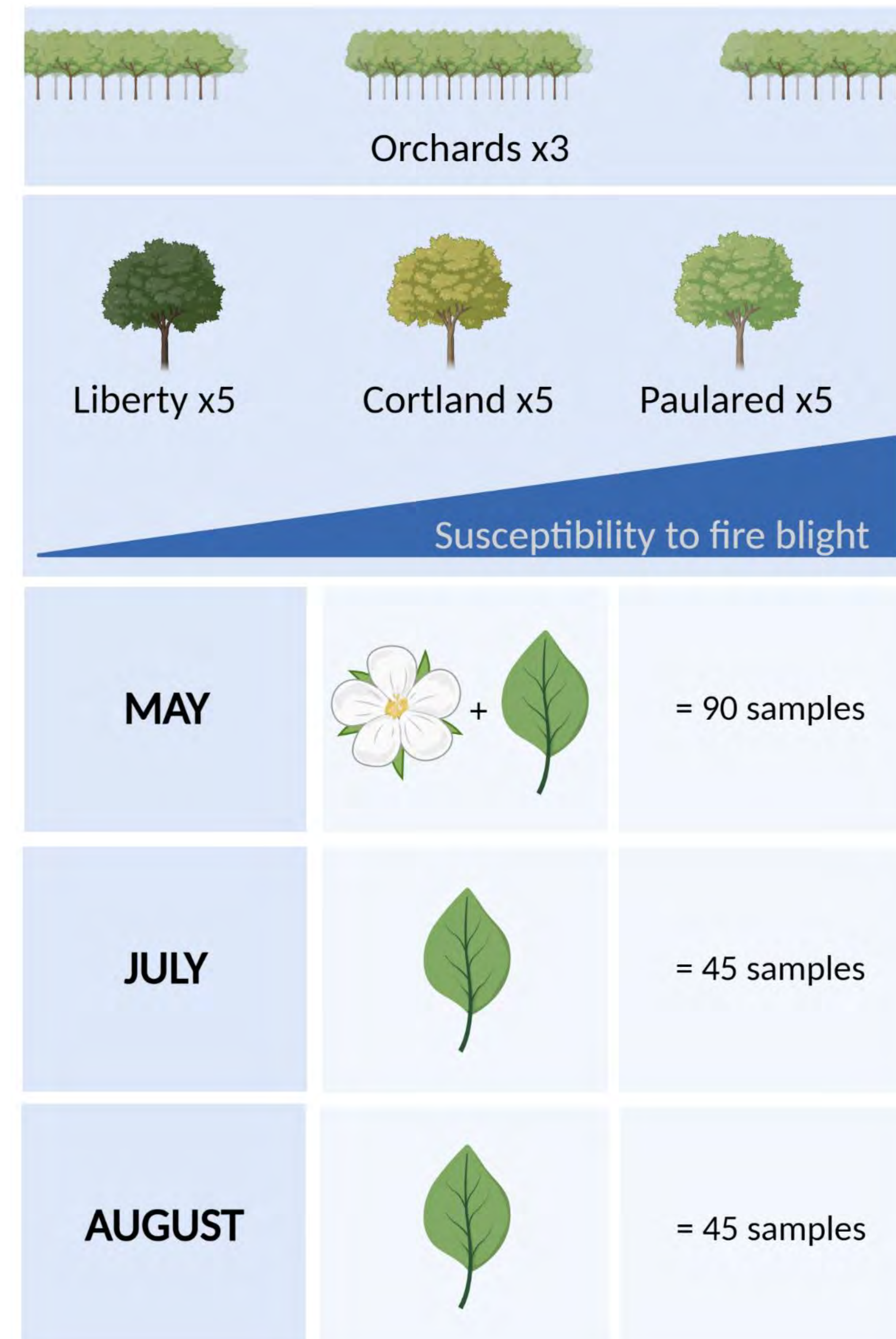
15 - Life on Land



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Methods

SAMPLING 2022



Hypothesis

Microbial diversity will shift during the season as some microbial taxa will become dominant

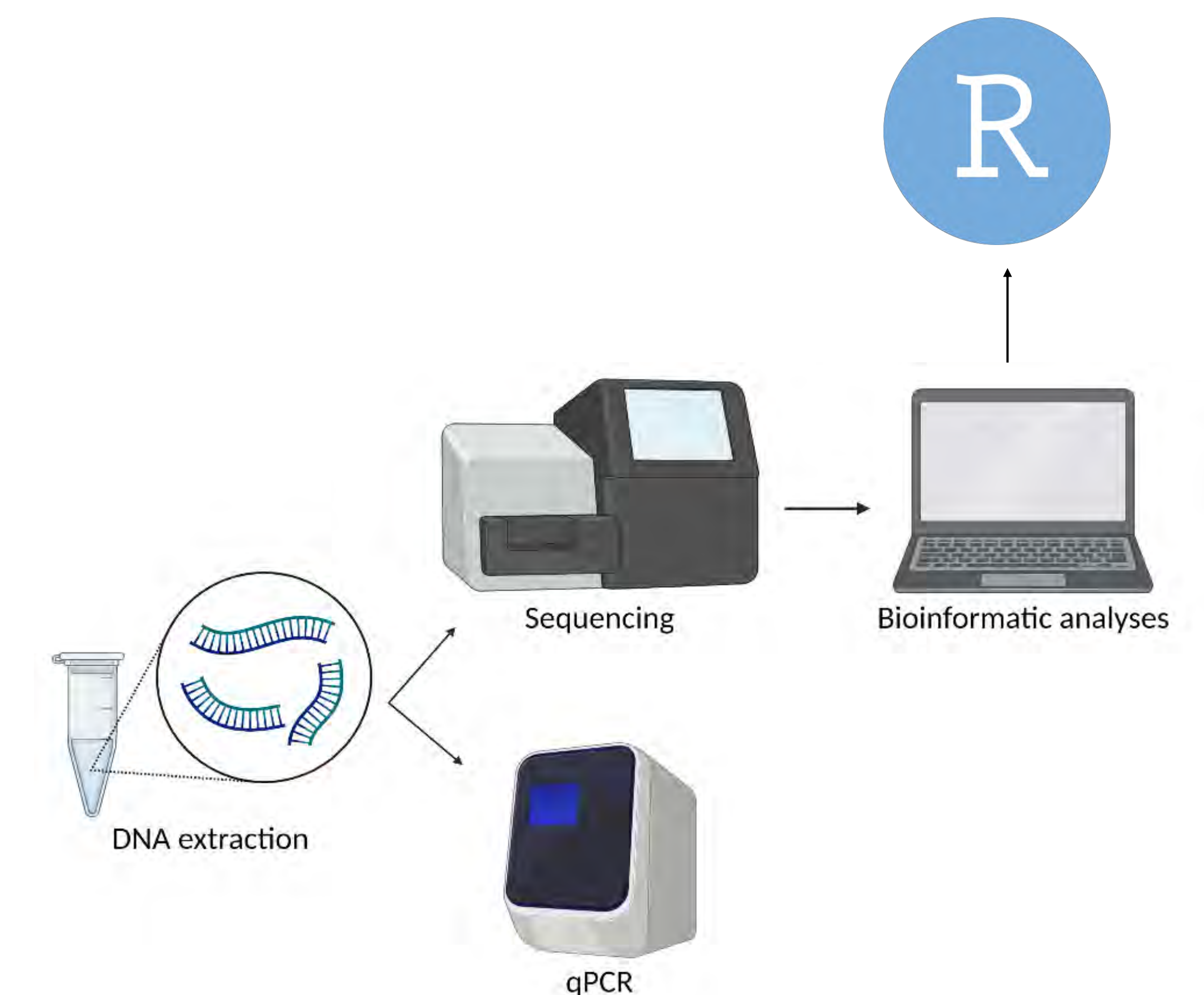


Host cultivar influences microbial community structure, but sampling site and agricultural practices are also important drivers of microbiome assembly



SAMPLES TREATMENT

Study of the microbiome community structure based on **bacterial 16S rRNA gene** and **fungal ITS region**



Detection and quantification of *Erwinia amylovora* bacterial load by **qPCR** targeting the **amsC** gene (involved in the production of exopolysaccharide amyovorran and known to be unique to *E. amylovora* ⁽⁷⁾)

Conclusion and perspectives

The results of this study will allow us to determine if specific microbial taxa dominate apple tree cultivars that are less susceptible to fire blight. If that is the case, we also aim to assemble a synthetic microbial community in a perspective of improving biological control of *Erwinia amylovora*.

Acknowledgments:

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