

# Using integrative *omics* to disentangle plant gene regulatory networks involved in plant-endophyte interactions

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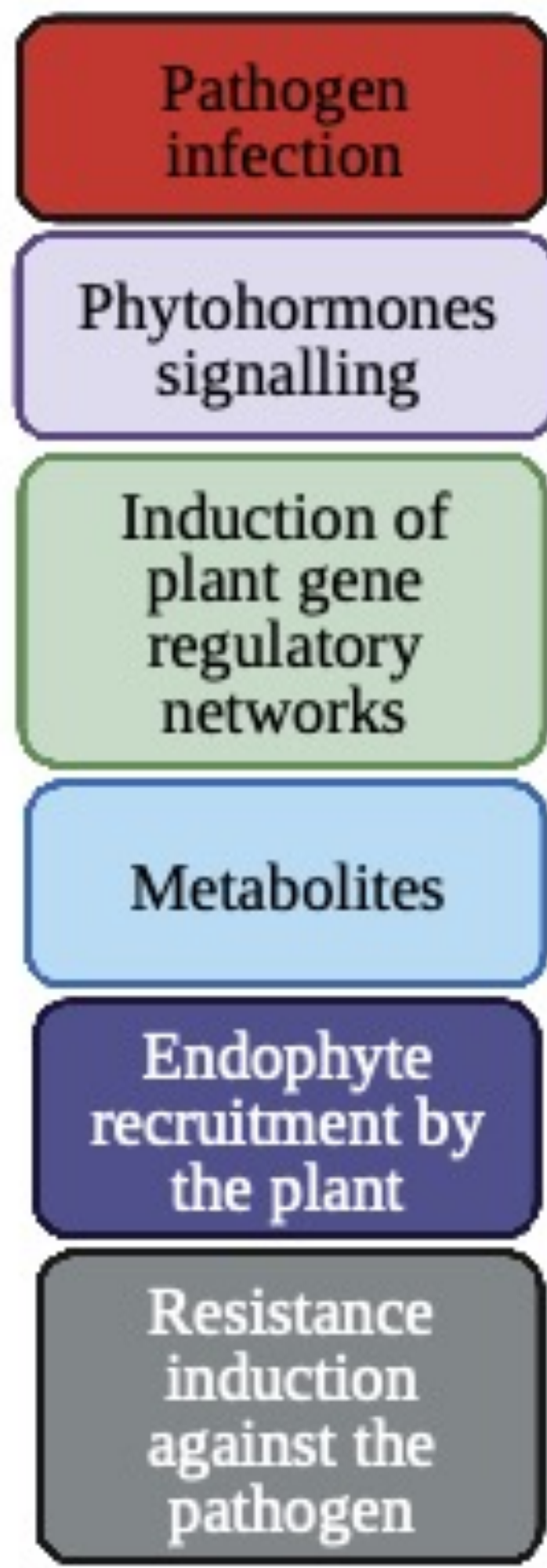
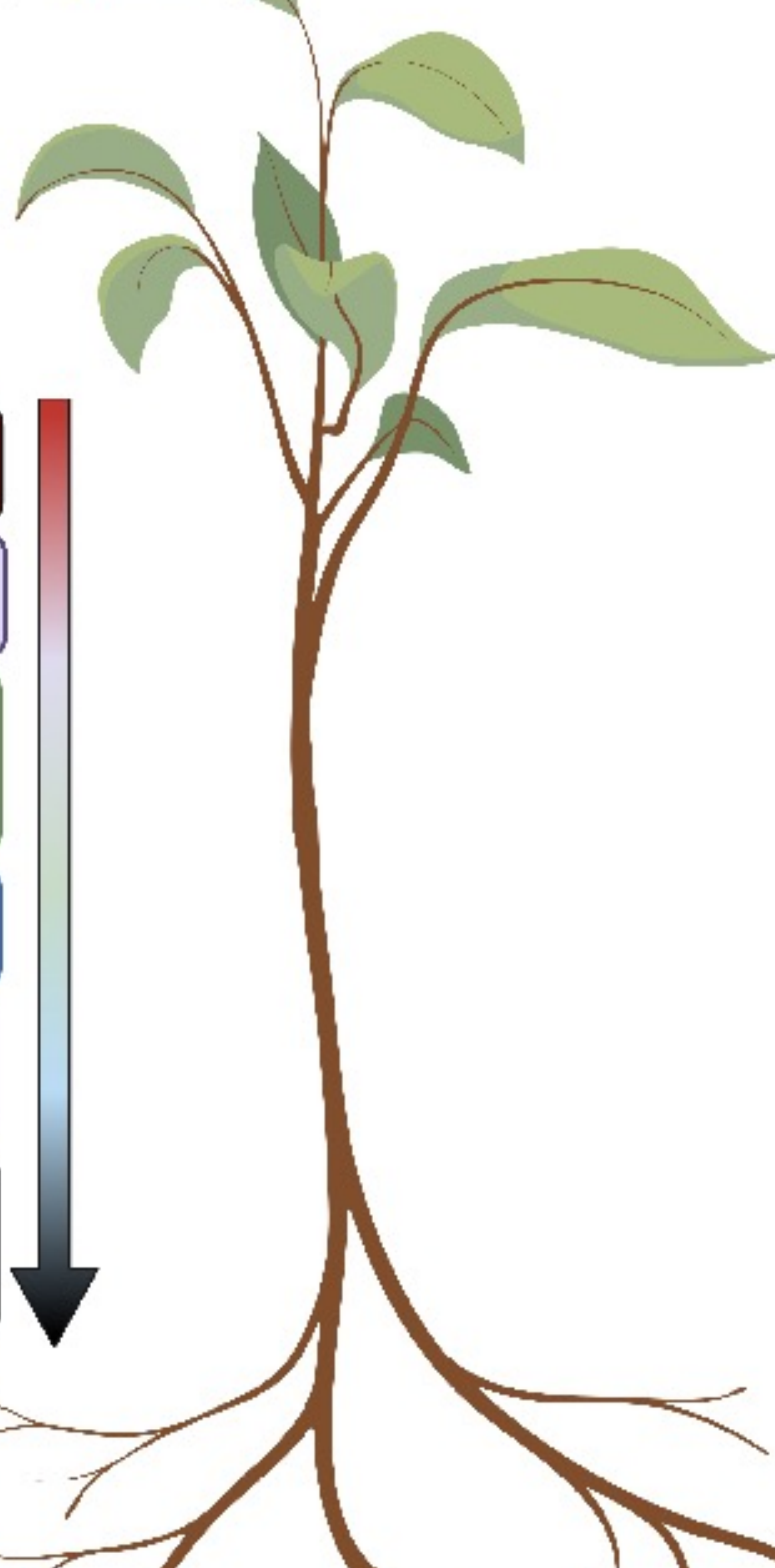
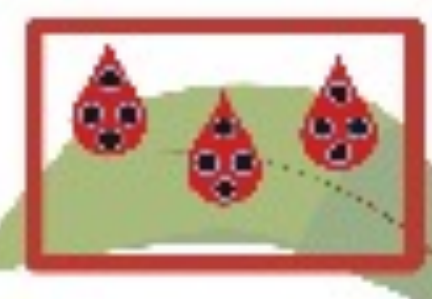
## Abstract

Plant endophytes that are known to enhance plant's tolerance against (a)biotic stress have a largely unexplored functional potential. Unravelling the dynamics of interaction between the plant and endophytes provides enormous opportunities to address key societal problems of the 21st century, in particular the increased global demands for crops that are more resilient to (a)biotic stress and less dependent on fertilizers and pesticides. Hence, a critical step in developing new microbiome-assisted approaches to improve plant growth and health is to unravel the regulatory networks in plant-endophyte interactions. To this end, our project investigates the dynamics and architecture of plant gene regulatory networks and aims to decipher plant biosynthetic pathways by integrative omics strategies. Whole transcriptome and metabolomes from plant roots and root exudates will be investigated to connect genes and their expression patterns to metabolites that play a crucial role in the plant-endophyte interactions. With the proposed work, we aim to deepen the mechanistic understanding of plant-microbe interactions.

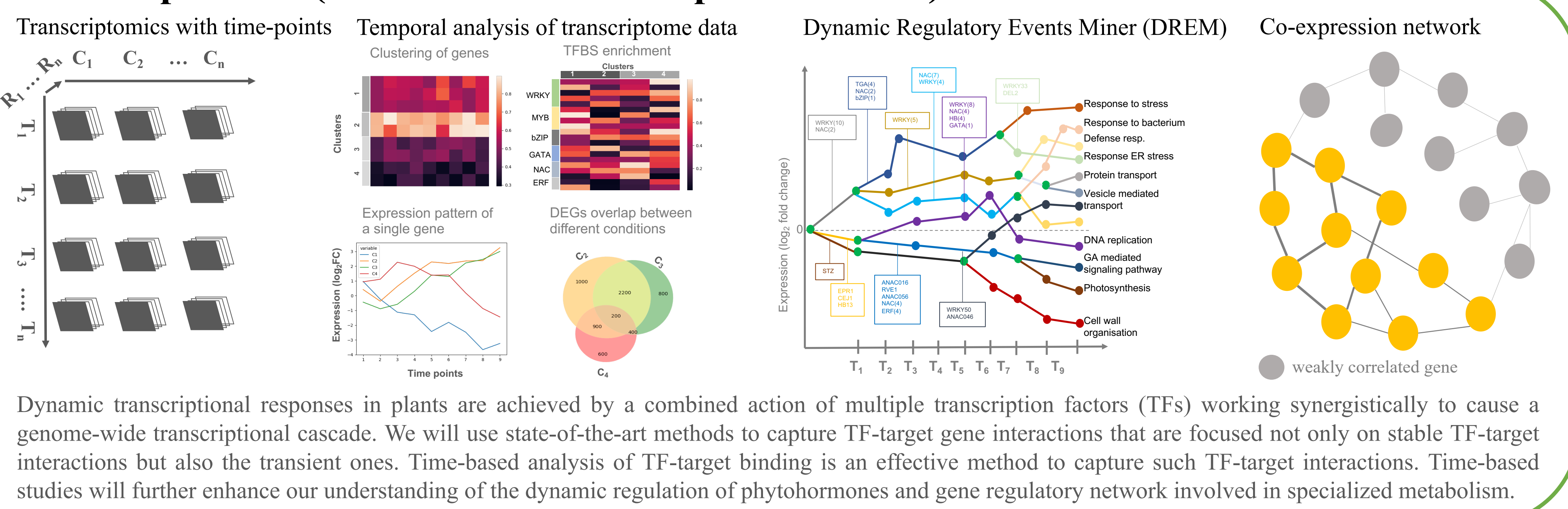
## Objectives

1. Investigate transcriptional and metabolic changes that are induced in the roots upon pathogen infection.
2. Explore components of plant immune gene regulatory network (GRN) involved in pathogen-induced recruitment of protective endophytes and activation of beneficial microbial biosynthetic gene clusters (BGCs).
3. Discover plant biosynthetic pathways and metabolites that are responsible for the underlying interactions with the root microbiome.

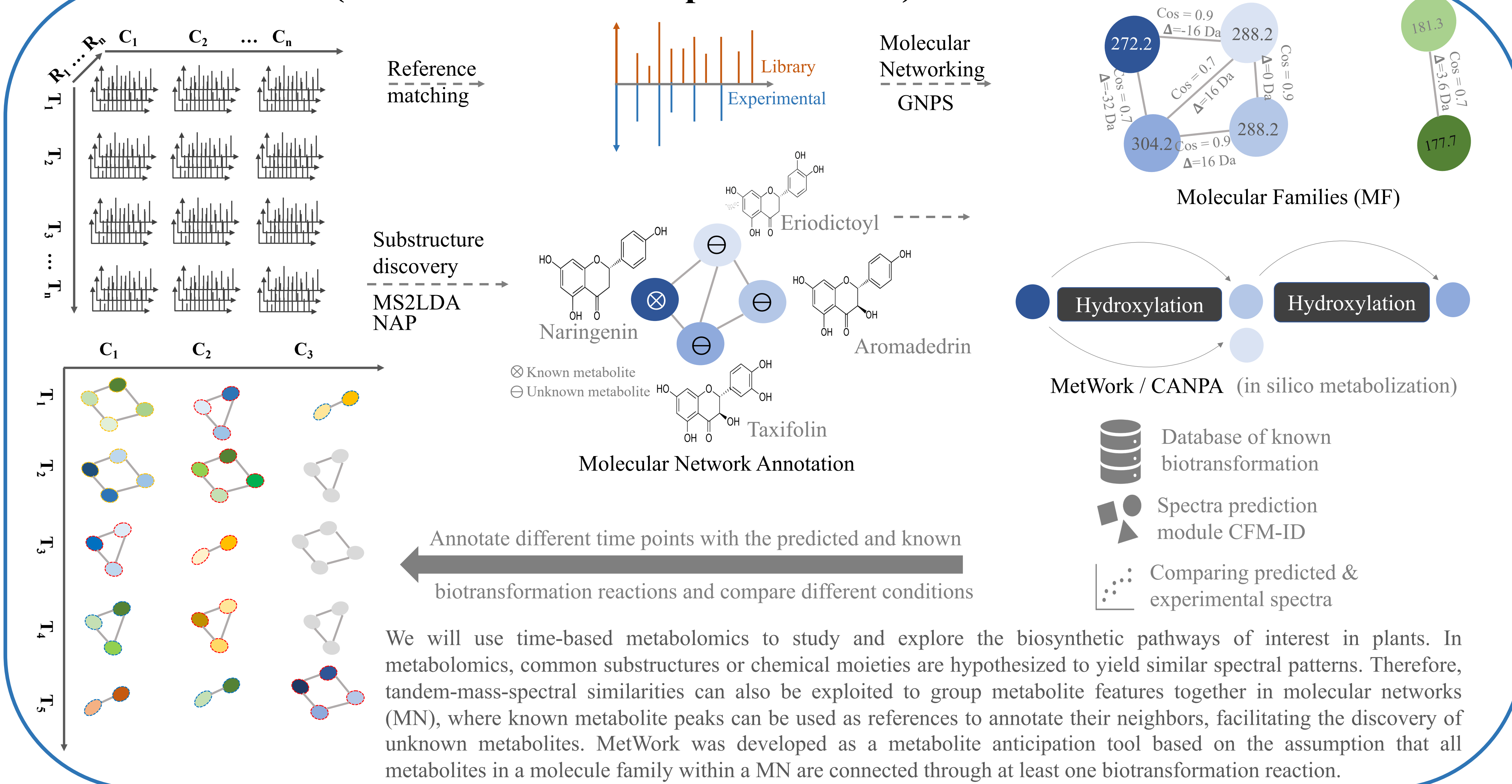
Infection by *Hyaloperonospora arabidopsidis* (Hpa)



## Transcriptomics (time-series with multiple conditions)



## Metabolomics (time-series with multiple conditions)



## MEtabolite ANticipation tools (MEANtools)

