TEMPLATE

EXPLORATORY PROJECT

2022-2024

Simulating plant-pathogen interactions to better understand plant immune responses

Coordination

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Key words

Modelling & simulation
DEVS
Multi-scale
Dynamic signalling
Plant pathology

INRAE units involved

MIAT
LIPME
IPSIM

Partnerships

Olivier Navaud (freelance consultant)

Context and challenges

Understanding how plants defend themselves against pathogens is a major challenge for moving towards an agriculture that uses fewer pesticides.

The immune response of plants differs from that of animals in that all plant cells are immunocompetent, i.e. they all have the same capacity to respond to the attack of a pathogen. This specificity has two im-portant consequences: (i) the regulation of immunity is an important determinant of the resistance phe-notype and (ii) the plant immune response is highly spatially structured, as the position of the cells is sta-ble.

Faced with attacks by necrotrophic fungi (including Sclerotinia sclerotiorum, which causes white rot), plants predominantly mount a form of immune response called Quantitative Disease Resistance (QDR). At present, QDR is mainly studied at the cellular level, without really taking into account the spatial and tem-poral dimensions of this resistance.

Recent work shows that plant-pathogen interactions are closely linked to the spatial and temporal charac-teristics of the entities and processes involved.

To better understand QDR, it is therefore necessary to integrate the dynamics of environmental percep-tion, signalling and transduction from the sub-cellular to the organ or whole-plant scale.

For this, we propose to use modelling and computer simulation techniques of plant tissues at the cellular and multi-cellular scales. Although the interest of this approach is widely recognised for studying complex systems, involving the interaction of a very large number of entities in a network, it is still innovative in plant biology.

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Goals

The TEMPLATE project aims to implement a dynamic model of plant-fungus interaction, in order to test several hypotheses on the establishment of the immune response in time and space by simulation. This model will attempt to represent the progression of a colony of mycelium of the pathogenic fungus Sclero-tinia sclerotiorum in a leaf of the model plant A. thaliana.

The biological question at the heart of this project will be that of the formation of patterns of immune response localised in time and space and associated with the modulation of the level of resistance linked to transcriptomic reprogramming.

We propose to use Discrete Event System Specification (DEVS), a formalism which is known for its repro-ducibility and modularity and allows a multi-formalism modelling approach.

In order to fully support biologists in their experiments, we will aim to develop a computational frame-work that allows interactive modelling and simulation bringing the experimenter, biological subject and digital model together.

This project therefore aims both for a better understanding of the immune response of plants and for the development of a new methodology for interactive simulation in the field of biology.

Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
Mathematics, computer and data sciences, digital technologies	MIAT	Computer science, modelling, simulation, bioinformatics
Plant health and environment	LIPME	Modelling, plant pathology, molecular biology
	IPSIM	Cellular signalling, plant physiology, imaging

External partners	Expertises
Olivier Navaud (freelance consultant)	Bibliographic synthesis, creation of a pathway signalling/plant immunity database

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