Epipredict

EXPLORATORY PROJECT

2022-2024

Integrative Epigenetics to predict the adaptive capacities of pests

Coordination

Nadia Ponts
UR MycSA
nadia.ponts@inrae.fr
Gael Le Trionnaire
UMR IGEPP
gael.le-trionnaire@inrae.fr
David Causeur
Institut Agro -Rennes Angers
david.causeur@agrocampus-ouest.fr

Key words

Environmental stress
Acclimation
Association models
High-throughput functional data
Stochastic de-pendence

INRAE units involved

MycSA
IGEPP

Partnerships

Institut Agro – Rennes Angers

Context and challenges

Today, agriculture faces many challenges, including to avoid the development of certain pathogens resulting from the reduction in the use of inputs with a view to sustainable agriculture as well as the effects of climate change.

In this context, many questions arise in the short term about the adaptive capacities of these bio-aggressors. Will an insect pest resist the next heat wave? Or will it instead be greatly affected by rising temperatures and cease to be a threat ?

The EPIPREDICT project proposes to answer these questions for two examples of pests with clonal reproduction and remarkable resilience :

- the pea aphid Acyrthosiphon pisum, which causes a wide range of damage on various leguminous plants and has remarkable phenotypic plasticity in response to its biotic and abiotic environment;
- the mycotoxin-producing filamentous fungus Fusarium graminearum, which is responsible for disastrous episodes of Fusarium head blight in wheat throughout the world, and which also displays a formidable capacity for adaptation.

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Métaprogramme
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digitbio@inrae.fr
www.inrae.fr/digitbio/

Goals

Epigenetic variations are heritable modifications of the expression of a genome that do not affect its sequence. Under environmental constraints, on short-time scales, the implementation of epigenetic modifications appears to be an efficient way for organisms to express new heritable phenotypes in order to ensure their survival and continue to develop. This epigenetic code is studied using high-throughput sequencing approaches, generating large volumes of data of a heterogeneous nature for which current analysis methods provide a limited understanding.

The EPIPREDICT project proposes to develop innovative statistical and mathematical approaches in order to identify in these data the elements that allow the description of variations in the expression of genes (in particular those responsible for the virulence and aggressiveness of pathogens and pests), taking into account the spatial characteristics of genomes.

Ultimately, decoding how genes are expressed in response to the environment could provide a decision support model for developing resilient and economically viable agro-ecosystems.

Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
Plant health and environment	MycSA	Fungal functional genomics and epigenomics, bioinformatics
	IGEPP	Functional genomics and epigenomics of insect pests
External partners		**Expertises**
Institut Agro – Rennes Angers	Irmar	Functional data, high dimensional dependence, co-expression networks, computational statistics, software tool development