# Sujet de stage Semestre 4 - Master 2ème année
# IBMP | 2025-2026

## Titre/Title

*English :* Epistatic Analysis of DNA Methylation Pathways in Plant Bacterial Defense

## Contacts

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## *Project Description* *(20 lines max.)*

*English :* This project will investigate genetic interactions between DNA methylation and demethylation pathways during bacterial defense by analyzing infection responses in various mutant combinations. The *ros1* mutants (DNA hypermethylation) are shown to be more susceptible to *Pseudomonas syringae*, while *met1* mutants (DNA hypomethylation) and RePat mutants (*ago3*, *ago9*, *drm1*) show increased resistance. This project will systematically test double mutants to understand epistatic relationships and determine whether different ecotype backgrounds influence infection outcomes. Standardized bacterial infiltration assays using *Pst DC3000* will be performed on 5 week old plants, with CFU quantification at 2-3 days post-infection to reveal whether resistance phenotypes are additive, epistatic, or background-dependent. Multiple *Col-0* lineages from different laboratory sources will be tested to account for spontaneous epigenetic variation that can confound genetic analysis, as different stocks may harbor distinct differentially methylated regions affecting baseline infection responses. Statistical analysis will determine epistatic interactions by comparing observed double mutant phenotypes to predicted additive effects. This systematic approach will clarify how opposing DNA methylation pathways interact during pathogen defense.

Méthodologies (mots clés) : Bacteria culture , Infection by infiltration, statistical genetics and epistatic analysis.

Références (maximum 3) :

1. Yu A, Lepère G, Jay F, Wang J, Bapaume L, Wang Y, Abraham AL, Penterman J, Fischer RL, Voinnet O, et al.: Dynamics and biological relevance of DNA demethylation in Arabidopsis antibacterial defense. Proc Natl Acad Sci U S A 2013, 110:2389–2394.
2. Dowen RH, Pelizzola M, Schmitz RJ, Lister R, Dowen JM, Nery JR, Dixon JE, Ecker JR: Widespread dynamic DNA methylation in response to biotic stress. Proceedings of the National Academy of Sciences 2012, 109:E2183–E2191.
3. Havecker ER, Wallbridge LM, Fedito P, Hardcastle TJ, Baulcombe DC: Metastable Differentially Methylated Regions within Arabidopsis Inbred Populations Are Associated with Modified Expression of Non-Coding Transcripts. PLoS ONE 2012, 7(9):e45242.

Illustration (1 photo ou 1 schéma, petit format)

## **Parcours de Master** (cochez le ou les parcours souhaités) **:**

Master « Sciences du Vivant », Faculté des Sciences de la Vie, Université de Strasbourg

1- Biologie et génétique moléculaire : X
2- Microbiologie : X
3- Plantes, biologie moléculaire et biotechnologies : X
4- Plantes, environnement et génie écologique :
5- Plantes, molécules bioactives et valorisation : X
6- Virologie :
7- Autres masters équivalents en France ou à l'étranger : X