

Sujet de stage Semestre 4 - Master 2^{ème} année

IBMP | 2025-2026

Titre/Title

Functional Analysis and Protein Interactome Characterization of MET1, MET2a, and MET2b
DNA Methyltransferases in *Arabidopsis thaliana*

Contacts

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Project Description (20 lines max.)

English :

DNA methylation is a key epigenetic mechanism that regulates gene expression, transposon silencing, and genome stability. In plants, cytosine methylation occurs in three sequence contexts—CG, CHG, and CHH—with CG methylation maintained by a small family of MET DNA methyltransferases. Among these, MET1 is ubiquitously expressed and plays a central role in maintaining CG methylation patterns during vegetative development. Accordingly, *met1* mutants exhibit global hypomethylation, transcriptional misregulation, and developmental abnormalities.

While MET1 has been extensively characterized in sporophytic tissues, two homologues, MET2a and MET2b, are specifically expressed in reproductive tissues¹, where extensive epigenetic reprogramming occurs to ensure the faithful transmission of genetic and epigenetic information across generations². In wild *Arabidopsis* accessions, MET2a may also contribute to transposon silencing³. However, the biological functions of MET2a and MET2b remain poorly understood and are the focus of this project.

This project aims to:

- 1. Perform genetic complementation of the *met1-3* mutant** using MET1, MET2a, and MET2b expressed under the MET1 promoter, followed by phenotypic observation and DNA methylation level analysis.
- 2. Characterize the protein interaction networks of MET1, MET2a, and MET2b** through immunoprecipitation–mass spectrometry (IP–MS) to define their interactomes.

Together, these complementary approaches will tell us if MET2a and MET2b are functionally equivalent to MET1 and assess if they interact with the same protein in the cell. It will provide new insights into the evolutionary and functional divergence of MET1-like methyltransferases and contribute to a deeper understanding of epigenetic regulation during plant reproduction.



Méthodologies (mots clés):

Genotyping, Transgenic line characterization, Phenotypic analysis, DNA methylation analysis (*McrBC*, bisulfite sequencing), Western blot, Immunoprecipitation–mass spectrometry (IP–MS)

Références (maximum 3) :

- 1-Jullien PE, Susaki D, Yelagandula R, Higashiyama T, Berger F. DNA methylation dynamics during sexual reproduction in *Arabidopsis thaliana*. *Curr Biol*. 2012 Oct 9;22(19):1825-30. doi: 10.1016/j.cub.2012.07.061. Epub 2012 Aug 30. PMID: 22940470.
- 2-Tirot L, Jullien PE. Epigenetic dynamics during sexual reproduction: At the nexus of developmental control and genomic integrity. *Curr Opin Plant Biol*. 2022 Oct;69:102278. doi: 10.1016/j.pbi.2022.102278. Epub 2022 Aug 12. PMID: 35970063.
- 3- Quadrana L, Bortolini Silveira A, Mayhew GF, LeBlanc C, Martienssen RA, Jeddeloh JA, Colot V. The *Arabidopsis thaliana* mobilome and its impact at the species level. *Elife*. 2016 Jun 3;5:e15716. doi: 10.7554/eLife.15716. PMID: 27258693; PMCID: PMC4917339.

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

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- 2- Microbiologie :
- 3- Plantes, biologie moléculaire et biotechnologies : X
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- 7- Autres masters équivalents en France ou à l'étranger : X