

Track « Integrative Biology, Physiopathologies »

Proposal for a Master 2 internship – 2023-2024

Title: Role of TRBs proteins in epigenetic gene regulation

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Summary: **Chromatin** is a nucleoprotein structure that is a scaffold for many **epigenetic marks**, such as DNA methylation, the composition of nucleosomes in histone variants and post-translational modifications of histones. Its exceptional modularity and plasticity enable chromatin to respond and **adapt to environmental constraints** and to ensure proper growth and development of organisms. The **Polycomb/Trithorax complex** is one of the primary pathways that guarantee the organization plan of organisms by controlling the expression of **developmental genes** at the appropriate time and location.

In the laboratory, we are investigating the role of TRBs, a specific family of five chromatin-binding proteins, in gene expression control in relation to the Polycomb/Trithorax pathway. Preliminary data suggests both physical and genetic interactions between TRBs and Polycomb proteins, as well as a role in transcription linked to the deposition of **activating** (H3K4me3) and **repressive** (H3K27me3) **histone marks**. We also expect that these five members of the TRB protein family have either redundant or antagonist roles.

To understand the general and specific role of these proteins, we combine several complementary approaches: (i) **molecular analyses** of transcription (RNA-Seq and RT-qPCR) and chromatin immunoprecipitation (ChIP and ChIP-Seq), (ii) **cellular imaging** using confocal microscopy, in lines expressing proteins fused to fluorescent tags or by immunohistological labeling, and (iii) **genetic analyses** of loss-of-function lines and a genetic suppressor screen.

Combining these approaches will allow us to gain a better understanding of the contribution of TRBs proteins in chromatin organization and genome expression. Overall, our project aims to understand how an organism can rapidly and appropriately modify the expression of its genome during its development or in response to stress. Because of many practical and conceptual aspects, our study model *Arabidopsis thaliana* is an undeniable asset in understanding these fundamental mechanisms.

Methodologies (key words): Genetics, Molecular Biology, Immunocytology, Chromatin precipitation (ChIP, ChIP-seq), RNA-seq, Forward genetic screens, Confocal microscopy, ...

Publications of the research group on the proposed topic (3 max.)

“Histone H1 protects telomeric repeats from H3K27me3 invasion in *Arabidopsis* »

Teano et al. *bioRxiv* 2022, accepted in *Cell Reports* <https://doi.org/10.1101/2020.11.28.402172>

“The Linker Histone GH1-HMGA1 Is Involved in Telomere Stability and DNA Damage Repair.”

Charbonnel¹ et al. *Plant Physiol.* 2018 May;177(1):311-327.