Master's degree in Biology – Chemistry-Biology Department

Master 2 internship project
Year 2026-2027

Laboratory/Institute: BGE/IRIG
Director: Marie-Odile Fauvarque
Team: Metanucleomics
Head of the team: Delphine Pflieger

Name and status of the scientist in charge of the project: Christophe Masselon
HDR: yes ☒ no ☐

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Program of the Master's degree in Biology:

☐ Microbiology, Infectious Diseases and Immunology ☒ Biochemistry & Structure
☒ Physiology, Epigenetics, Differentiation, Cancer ☐ Neurosciences and Neurobiology

Title of the project: Structural impact of histone lactylation on nucleosome stability: a comparative approach using proteomics and native mass spectrometry.

Objectives (up to 3 lines):

Determine potential nucleosome structure alterations resulting from histone lysine hyper-lactylation. Produce and characterize modified versus unmodified nucleosomes to assess structure and stability. Establish a methodological foundation for future analysis of longer-range chromatin compaction effects.

Abstract (up to 10 lines):

Histone lactylation is an emerging post-translational modification identified in key physiological processes and in pathological contexts including neurodegenerative diseases. Unlike acetylation, lactylation introduces a lactyl group bearing an additional hydroxyl moiety, potentially modifying electrostatic histone-DNA interactions and hydrogen bonding networks within the nucleosome. While genome-wide lactylation profiles are beginning to be mapped, its structural consequences on nucleosome assembly and stability remain unexplored. This structure-function dimension is essential to understand how lactylation regulates DNA accessibility and chromatin compaction. The intern will produce modified (lactylated and acetylated controls) recombinant nucleosomes using chemical *in-vitro* lactylation (resp. acetylation). Comparative analysis of modified and unmodified nucleosomes will shed light on the structural effects of lactylation compared to acetylation and pave the way for future analyses of polynucleosomes.

Methods (up to 3 lines):

LC-MS/MS-based proteomics of digested histones to determine modification sites; Native Mass Spectrometry and Thermal Shift Assay of intact nucleosomes to assess structural integrity and stability.

Up to 3 relevant publications of the team:

1. Manessier J., Hijazi H., Brugière S., Courçon M., Masselon C., de la Iglesia A., Cocquet J., Pflieger D. Both L-lactyl and D-lactyl enantiomers modify histones in mouse testis. Mol. Cell Proteomics 2026, 25, 7, 101601
2. El Kennani, S.; Crespo, M.; Govin, J.; Pflieger, D. Proteomic Analysis of Histone Variants and Their PTMs: Strategies and Pitfalls. Proteomes 2018, 6, 29.

Requested domains of expertise (up to 5 keywords):

Native mass spectrometry • Proteomics • Chromatin structure • Protein biochemistry • Post-translational modifications