POST-DOCTORAL POSITION
IMPACT OF ENVIRONMENTAL CHANGES ON METHYLOME IN AMPHIBIAN

Location	**Muséum national d'Histoire naturelle,** Site du jardin des plantes : 7, rue Cuvier, 75231 Paris Cedex 05
Position	**Academic environment** The laboratory UMR 7221, Molecular Physiology and Adaptation (PhyMA), co-affiliated with Centre National de la Recherche Scientifique (CNRS) and Muséum National d'Histoire Naturelle (MNHN) is one of the 16 research units of the MNHN. It is a major contributor to knowledge production and sharing on geological and biological diversity, cultural and societal diversity and on planet history. Its mission is to develop between applied and core research, expertise, valorisation, collections and educational training for all publics. The aim of the PhyMA laboratory is to characterize the biological processes in play in normal and altered environment. Of the three groups, the applicant will join the RoDEo (Cellular and Molecular Responses to Environmental Challenges) group, on understanding the control of tissular development and homeostasis in normal and altered conditions. Special attention will be drawn on endocrine disruptors and stress. The applicant will work under the direct supervision of the laboratory's director Dr L. Sachs, and will address the impact of stress and endocrine disruptors on the methylome of an anuran amphibian. **Scientific context** Nowadays, the ongoing anthropization of ecosystems results in natural species being increasingly exposed to chemical compounds and physical agents never seen before, with potential impact on human health and natural species. Homeostasis, i.e. the set of regulations safeguarding functional integrity, has been shaped during the course of evolution to respond to environmental challenges, but artificial compounds may pose novel threats. This can be monitored by precisely documenting the set of alterations of the control of genome expression. The long-term objective is to develop sensitive and specific biomarkers, together with providing prediction and mitigation strategies. The key point is that environmental changes often coincide with durable changes of DNA methylation profiles. In this context, the applicant will document methylome variations of an Anuran amphibian after environmental challenges. Anuran developed remarkable adaptation strategies to colonize very diverse (and sometimes extreme) niches. Nonetheless, over the last decades, environmental changes (climate, anthropization) have had a strong impact on natural populations, showing a steep and continuous decline. Given this sensitivity, they can be thought of as sentient species of ecosystems health. We specifically focus on a life cycle transition controlled by thyroid hormones (TH) and glucocorticoids (GC), both acting as a functional interface integrating internal and external cues and regulate a large set of cellular processes (mitosis, apoptosis, growth, metabolism and development …). This role is highly conserved among vertebrates. It is noteworthy that both GC, who are also stress mediator, and TH display target genes involved in DNA methylation dynamic. The applicant will process and analyse raw NGS data in order to map changes of DNA methylation, identify regions of dynamic DNA methylation in response to treatments with TH and or GC, or with endocrine disruptors. Experimentally, sample preparation is under way by DNA methylation capture coupled to deep sequencing (MethylCap-Seq). The bioinformatic tools are available in house or from the scientific community. Additional tools might be developed if needed. Initial results show clear DNA methylation dynamic in response to treatment and co-treatments. The functional connection with other genome components has to be addressed.
Training	NA
Professional network	**Internal** Small group, with connections to other working on TH and thyroid disruption, as well as users of bioinformatic tools (bioinformaticians, researchers). **External** Integrate in our partnership with ENS – Paris deep sequencing platform.

Competences, Knowledge and know-how	**Diploma / training** • PhD • Fluent English (spoken, written). This is an absolute requirement. • Fully operational with the following bio-informatic tools: bowtie/bowtie-2, the BEDTOOLS suite and/or bam/SAM tools • python3, R and advanced bash scripting, in Unix-like environment. This is an absolute requirement. **Knowledge and know-how** • Deep understanding and technical skills on functional genomics and epigenomics. • Robust operational bio-informatic skills for the processing of high throughput data in UNIX/Linux environment. • Theoretical and practical training on the repetitive fraction of the genome is welcomed. • Be critical and fully involved ion problem resolution, actively propose alternatives. • Oral and written presentation skills for internal or external communication. • Integrate in a work environment and respect the group dynamic and organization. • Follow instructions and established work plans. • Know how to communicate
Time table and work environment	Week days: 35h35 work hours per week, no work on weekends. Vacations: 44 days per year Location: UMR 7221 PhYMA, 7 rue Cuvier 75005 Paris Start date: October/November 2024 Contract type: Two years contract