PI profile

## Tatjana Sauka-Spengler

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| https://www.rdm.ox.ac.uk/people/tatjan-sauka-spengler/@@haiku.profiles.portrait/5500e2e557f941cc9b3f3a6512aa033b/@@images/image/w1140?c766ad66-f042-4d2a-8583-1dc29f28bec1 | Professor Tatjana Sauka-Spengler**Titles:** Professor of Developmental Genomics and Gene Regulation, Wellcome Trust Senior Research Fellow**Location:** Weatherall Institute of Molecular Medicine**Department:** Radcliffe Department of Medicine (RDM)**Group:** Sauka-Spengler**Webpage:** https://www.rdm.ox.ac.uk/people/tatjan-sauka-spengler**Email:** tatjana.sauka-spengler@imm.ox.ac.uk**PA:** Yuki Hale <yuki.hale@imm.ox.ac.uk> |

### GMS themes:

[Please retain any that describe your research, deleting others:]

* Genomic and –omic technologies
* Functional genomics
* Genome biology (genomes and genetic variation)
* Genomics of disease
* Genomic analysis (bioinformatics and statistical genetics)
* From genes to clinic (target discovery, structural biology, medicinal chemistry)
* Application of genomics in the clinic (diagnostics and therapeutics)

### Research Overview

Gene Regulatory Networks in Development and Disease

Embryonic development is driven by a large set of finely orchestrated regulatory programs that control cell fate decisions, differentiation and morphogenesis, leading to formation of a complex organism. Understanding how these programs, encoded at the genome level, are translated into intricate networks of interacting biological components (genes, proteins, RNA) is essential to our understanding of mechanisms underlying developmental processes and human diseases, triggered when biological circuits go awry.

Modern epigenomic techniques are powerful tools to dissect complex regulatory networks, providing the ability to systematically analyse chromatin landscape and on-going transcriptional programs. Epigenomic profiling of histone modifications allows genome-wide chromatin signature mapping and classification of sites of regulatory activity (e.g. distal elements/enhancers, promoters, repressed regions, etc.). Concomitantly, active transcriptome analysis provides information about upstream inputs and downstream outputs within the Gene Regulatory Networks (GRNs) that orchestrate diverse cellular processes.

In order to mechanistically dissect GRNs during development, we are adapting systems level approaches, such as epigenomic and transcriptional profiling, to defined cell populations in the developing embryo. The data sets obtained allow us to annotate the sites of regulatory activity, and consequently assemble and test gene regulatory circuitry that controls given developmental process at the cellular level. We use two developmental models, the chicken (1) and the zebrafish (2) embryo.

(1) One of the main efforts in our laboratory is building a systems level understanding of the gene regulatory network that orchestrates early steps of neural crest formation in vertebrate embryos. We use the chicken embryo, a classical model for studying neural crest, whose mode of early development closely resembles human. The neural crest is multipotent, embryonic stem cell-like population which gives rise to a plethora of derivative tissues and organs, such as sensory and autonomic ganglia, adrenal and thyroid glands, smooth muscle of major blood vessels, craniofacial skeleton and the vast majority of body’s pigmentation. Due to their unique multipotency, coupled with the developmental plasticity, there is broad interest in using the regenerative capacity of neural crest cells in stem cell-based treatments. By deciphering GRNs that orchestrate early steps of neural crest formation, we aim to understand the mechanistic basis of their multipotency and stem-cell like potential, as well as and the biochemical hierarchy that controls the maintenance of those properties.

(2) In addition to being a powerful organism for studying embryonic development, in recent years zebrafish has become an important system for biomedical research, as one of the keys to understanding human disease and addressing critical questions in regenerative medicine. Zebrafish not only have the same genes as humans but also most of the same cell types, tissues, organs and biological circuits, assuring that the lessons from this model can be directly applied to other vertebrate systems and to human health.

We have developed a versatile, genetically encoded, binary in vivo biotinylation approach in zebrafish, which allows for tissue-specific biotinylation of defined targets. This is achieved by co-expression of proteins tagged with biotin acceptor peptide (Avi-tag) and bacterial biotin ligase, BirA in the same cells, allowing to isolate specific proteins or cell populations, using single step affinity purification procedure. Isolated genetically defined cell populations can then be profiled using genome-wide assays, adapted to small cell numbers. We are using this technology to analyze cellular circuitry at as many levels as possible and to address transcriptional and epigenomic mechanisms at play in an array of developmental systems, such as neural crest and hematopoietic lineages, but also in processes activated during inflammatory response to injury and cancer, or during organ regeneration.

Project areas: functional genomics, model organisms. Research: gene regulatory networks, epigenetics

### Specific project proposals:

* [Gene Regulatory Networks in Development and Disease](https://www.rdm.ox.ac.uk/study-with-us/supervisor-profiles/gene-regulatory-networks-in-development-and-disease) (see website for details)

Please contact directly for further information.

*These pages were reviewed/updated:* ***10/06/2022***

Project proposal

# **Title**: **[Project title here]**

Supervisors: [name and title of relevant individuals]

Wet/dry lab mix (approx): X% wet lab, X% dry lab

### Description:

[Write a ~ half-page page description of the project here].

### Training Opportunities:

[Write a brief description of the training opportunities the project will provide].

### Background reading / references:

Please include references as desired. Suggested format:

* [Surname] [Firstname], [other authors]… **(year in bold)** . [Title]. [Journal name], [other details]. Available at: [link]

Insert any additional project description(s) on subsequent pages if applicable. Please use the same template and use separate pages for each project.