Postdoctoral position: Epigenetic programming of sperm for embryonic development

The possibility that sperm deliver to the egg epigenetic instruction for early embryonic development have far reaching implication for human health. Modified histones or DNA as well as small RNAs have all been implicated in this process, but a detailed mechanistic understanding of how sperm-derived epigenetic cues influence the developing embryos is still lacking. Here we aim at deciphering the mechanisms by which maternal factors process the paternal epigenome, focusing on modified histones. The project involves (i) Sperm epigenome profiling (ii) identification of egg factors involved in binding to the epigenetically programmed fraction of the sperm chromatin and (iii) Functional testing of candidate factors using targeted sperm epigenome interference and maternal factor depletion. The work will be primarily carried out using *Xenopus Laevis* as a model, with some experiment involving human samples.

The successful candidate will have a PhD or equivalent training, considerable experience in epigenetics, molecular biology, developmental biology or a similar field, and a proven track record in scientific publication. Prior experience in epigenetics and transcriptional regulation are essential, while experience with embryos work, and/or proteomic method, and/or genome-wide transcriptional analysis would be an advantage. Applicants must display an ability to undertake project management, work within a multi-disciplinary team environment, and have good presentation and communication skills.

The project is a collaborative effort between J.Jullien's group (Cell and Gene Engineering in Tolerance, Fertility and Regenerative Medicine Team, CR_2TI, Nantes, France. https://cr2ti.univ-nantes.fr/) and C.Pineau's group (Cellular and Molecular Actors of the Reproductive Function Group, IRSET, Rennes, France, https://www.irset.org/en and Protim proteomic facility, Rennes, France).

Please contact Dr. Jérôme Jullien (jerome.jullien@inserm.fr) with any informal enquiries.

Fixed-term: The funds for this post are available for 3 years in the first instance, with possibility of extension if further funding is secured.

Relevant papers from the host lab:

1. Oikawa, M. *et al.* Epigenetic homogeneity in histone methylation underlies sperm programming for embryonic transcription. ***Nat. Commun***. (2020) doi:10.1038/s41467-020-17238-w.
2. Teperek, M. *et al.* Sperm is epigenetically programmed to regulate gene transcription in embryos. ***Genome Res.*** **26**, (2016).
3. Teperek, M. *et al.* Sperm and spermatids contain different proteins and bind distinct egg factors. ***Int. J. Mol. Sci.*** **15**, (2014).
4. Jullien, J. *et al.* Gene Resistance to Transcriptional Reprogramming following Nuclear Transfer Is Directly Mediated by Multiple Chromatin-Repressive Pathways. ***Mol. Cell*** **65**, (2017).
5. Hörmanseder, E. *et al.* H3K4 Methylation-Dependent Memory of Somatic Cell Identity Inhibits Reprogramming and Development of Nuclear Transfer Embryos. ***Cell Stem Cell*** **21**, (2017).