

## Master project 2020-2021

### Personal Information

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| <b>Supervisor</b>  | Tanya Vavouri   |
| <b>Email</b>       | tvavouri@carrerasresearch.org   |
| <b>Institution</b> | Josep Carreras Leukaemia Research Institute (IJC)   |
| <b>Website</b>     | <a href="http://www.carrerasresearch.org/en/regulatory-genomics">http://www.carrerasresearch.org/en/regulatory-genomics</a> |
| <b>Group</b>       | Regulatory Genomics   |

### Project

## Computational genomics

### Project Title:

Evolution and biogenesis of mammalian PIWI-interacting RNAs (piRNAs).

### Keywords:

genomic repeats, small non-coding RNAs, gene regulation

### Summary:

Transposons and other repeats substantially contribute to genetic diversity in a species, to spontaneous mutations and regulatory innovations. PIWI-interacting RNAs (piRNAs) bound to PIWI proteins repress transposon activity in the germline. Repression of transposons is essential for normal progression of mammalian spermatogenesis. Transposons are highly enriched among piRNA producing loci and are transcriptionally and post-transcriptionally repressed by piRNAs. Nearly half of all piRNA-producing loci are protein-coding genes but, to date, it remains unknown why/how certain protein-coding genes are targeted for piRNA production during gametogenesis. The dynamic landscape of mammalian transposon insertions in genes and the strong association between piRNAs and transposons raise the question whether transposon insertions in genes have triggered piRNA production from these genes. The goal of this project is to use bioinformatics tools and available data (both from the lab and from other publications) to understand the effect of transposon insertions on gene function in the mammalian male germline. The specific objectives are to understand the extent and genetic causes of inter-individual variation in piRNA expression in mouse and to gain mechanistic insight into piRNA production from protein-coding genes.

### References:

Ozata, D.M., Gainetdinov, I., Zoch, A. et al. PIWI-interacting RNAs: small RNAs with big functions. Nat Rev Genet 20, 89-108 (2019). <https://doi.org/10.1038/s41576-018-0073-3>

### Expected skills::

R, scripting in bash, perl/python

### Possibility of funding::

To be discussed

**Possible continuity with PhD: :**

To be discussed

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