

Research Topic for the ParisTech/CSC PhD Program

Field: Biology, Biophysics and Bio Chemistry

Subfield: Evolutionary biology

Title: Genomics-enabled evolutionary biology study of jumping genes

ParisTech School: Agroparistech

Advisor(s): Florian Maumus, florian.maumus@inra.fr

Host lab: URGI at French national institute for agricultural research, [website](#)

Short description of possible research topics for a PhD:

By integrating host genomes repeatedly in a stochastic manner, selfish genetic elements (SGEs - including viruses and transposable elements) can profoundly influence the biology of their hosts. They represent a predominant part of most eukaryotic genomes and constitute a major source of genetic and epigenetic changes. Friends or foes? The integration of SGEs in genomes causes deleterious mutations most of the time, but it occasionally mediates key evolutionary adaptations and transitions.

Plant genomes commonly comprise a significant proportion of transposable elements (TEs) (*e.g.* 80% in maize) and different superfamilies of TEs have been “populating” plant genomes under the form of repetitive genetic elements since the emergence of green plants, over one billion years ago. Although their impact on plant evolution is paramount, macro-evolutionary studies are lacking and the evolutionary secrets of their success largely remain to be unveiled.

The survival and success of TEs profoundly depends on their capacity to resist to the restraints applied by their host and to succeed in genetic adaptation and innovation. Indeed, TEs are the subject of substantial compositional constraints owing for instance to being targets of DNA methylation. In the other hand, continuous evolution of TEs is required for their survival to adapt to their host biology and to the environment, for instance by convergence of regulatory sequences towards proper host transcription factors binding sites.

In this context, the applicant is expected to perform a large-scale bioinformatics analysis to collect TE sequences from dozens of plant genomes. Making the most of this data, the applicant will address the coevolution of TEs with plants, and more specifically attempt to link TE regulatory elements to the evolution of cis-acting elements and of gene networks.

Required background of the student: Bioinformatics, Genomics

List of representative publications of the group:

1. Maumus F, Quesneville H: **Impact and insights from ancient repetitive elements in plant genomes.** *Curr Opin Plant Biol* 2016, **30**:41-46.
2. Jouffroy O, Saha S, Mueller L, Quesneville H, Maumus F: **Comprehensive repeatome annotation reveals strong potential impact of repetitive elements on tomato ripening.** *BMC Genomics* 2016, **17**(1):624.
3. Maumus F, Quesneville H: **Deep investigation of Arabidopsis thaliana junk DNA reveals a continuum between repetitive elements and genomic dark matter.** *PLoS One* 2014, **9**(4):e94101.
4. Maumus F, Quesneville H: **Ancestral repeats have shaped epigenome and genome composition for millions of years in Arabidopsis thaliana.** *Nat Commun* 2014, **5**:4104.