

**Research Topic for the ParisTech/CSC PhD Program**  
(one page maximum)

**Subfield:** Evolutionary biology

**ParisTech School:** Agroparistech

**Title:** Insights into the secret life of plants' best friends and worst enemies

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**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 constraints and to succeed in genetic adaptation and innovation. 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 requested for their survival to adapt to their host biology and to the environment, for instance by convergence of TE 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

**A list of 5(max.) representative publications of the group:** (Related to the research topic)

1. 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.
2. Maumus F, Quesneville H: **Ancestral repeats have shaped epigenome and genome composition for millions of years in Arabidopsis thaliana.** *Nature communications* 2014, **5**.
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, Epert A, Nogu  F, Blanc G: **Plant genomes enclose footprints of past infections by giant virus relatives.** *Nature communications* 2014, **5**.