



## Biological impact of Transposable Elements

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One of the major discoveries of these last decades of genomic research is that genes (*i.e.* DNA sequences that contain the information necessary for the development and reproduction of individuals within species) are outnumbered by Transposable Elements (TEs) in most eukaryotic genomes. TEs are very diverse both in terms of structure and modes of transposition, but they all have in common that they can be mobilized and amplified (in various extents) within the genomes. TEs have long been considered as “useless” (junk DNA) or even “deleterious” (parasitic DNA), but these views have recently been challenged by experimental evidences showing that they could on the contrary be beneficial to organisms and thus have, through a process referred to as “domestication”, been repeatedly recruited by their host genome in various eukaryotic lineages to create biological novelty. With the advent of new sequencing technologies and the availability of genomic resources for many organisms (and even populations), the molecular mechanisms involved in this process start to be unravelled and show that both the regulatory sequences and the proteins encoded by TEs can be exaptated. Several aspects of TE dynamics in species and populations remain unclear : on one hand, comparative genomic studies in various organisms show that TEs significantly contribute to their genomic diversity, showing that transposition occurs frequently *in natura*. On the other, recent advances in epigenetics clearly show that transposition is strictly controlled *in planta* by several pathways at both transcriptional and post-transcriptional levels. This paradox needs to be resolved in order to understand how could TEs generate biological diversity at population level and be involved in adaptative processes *in natura*.

The Panaud lab has been involved in the study of the impact of TEs on plant genomes at structural and functional levels for two decades, using the genus *Oryza* (to which cultivated rice belongs) as a model through comparative genomic approaches at the genus level. We are now engaged in studying TE dynamics at population level in rice (exploiting the genomic resources made recently available for 3000 rice accessions), as well as in a natural ecosystem, the Massanne natural reservation, where we study TE dynamics in the beech forest and in various species with well characterized biological relationships, such as white rot fungi and xylophagous insects (with an emphasis on horizontal transfers -HTs).

The Gourbiere lab has a fifteen years experience in the modelling of host-parasite interactions and life-history evolution, and has recently joined LGDP to develop innovative theories that aim at integrating explicit descriptions of the molecular mechanisms involved in the regulation of gene expression and its interactions with TE dynamics into the current theories of plant adaptation to environmental changes and adaptive speciation. We are starting to develop such ‘Eco-genomic’ theories and to tackle the conceptual and technical challenges that are to be addressed to integrate molecular, demographic and evolutionary processes and data into multi-scale models. We anticipate that those models will provide key insights into the paradox described above by helping to understand the “arms race” between epigenetic control and transposition activation and its implications for plant adaptive evolution and diversification.

### **Link to Major Themes of Research of TULIP:**

The study of the role of TEs in adaptation in plants (both rice's and Massanne's projects) clearly fits with MTR1. The study of HTs in Massanne and the adaptation of ecological models to understand TEs/host genome interactions both fit with MTR2. The ecosystem-genomics approach of our Massanne project also fit with MTR4. Finally, to some extent, the development

of a new « genomic theory of evolution » that endeavours to consiliate structure/function genomic relationships and population biology may fit with MTR5.

**People:**

Panaud's team: 1PR UPVD, 2MCF UPVD, 1CR IRD, 1 IE CNRS, 1 AI CNRS, 2 PhDs.

Gourbiere's team: 1 MCF, 1 PhD.