Impact of transposable elements on transcriptional diversity in stressed plants

Antoine Lagarde[1], Axelle Costa[1], Camilo Pesantez[1], Guillaume Moissiard[1], and Nathalie Picault*[1]

[1]LGDP-UMR5096, CNRS/University of Perpignan Via Domitia – CNRS, Laboratoire Génome et Développement des Plantes (LGDP), Université de Perpignan Via Domitia, Perpignan, France – Perpignan, France

Abstract

Alternative splicing (AS), alternative transcriptional start site (ATSS) using proximal or distal promoters, and alternative transcriptional termination site (ATTS) using alternative polyadenylation (APA) signals are fundamental processes allowing a swift genetic rearrangement of messenger RNA molecules into various RNA isoforms with potentiality for proteome diversity. In plants, modulations of ATSS, ATTS and AS can occur in response to environmental stimuli such as heat stresses, most likely to optimize plant thermotolerance. Accordingly, mutant plants impaired in splicing factors are more sensitive to heat, and AS might be an important component of heat-shock memory.

Transposable elements (TEs) are DNA elements representing significant proportions of plant genomes, usually transcriptionally repressed. Previously seen as invasive junk DNA, there is increasing evidence that TEs contribute to host genetic innovation throughout evolution. Particularly, TEs can colonize genes, and therefore they can be involved in AS, ATSS or ATTS events when those genes are transcribed. In this project, we propose to decipher the contribution of these intragenic TEs in host genetic diversity in two different plant species (*Arabidopsis thaliana* and *Solanum lycopersicum*) subjected to two temperature regimes (20ºC and 37ºC). To do so, we are using an integrated approach combining long read Oxford Nanopore Technologies (ONT) direct RNA sequencing (ONT-DRS) and Illumina short-read RNA sequencing (shR RNA-seq) that will allow to fully picture RNA isoforms and assess the impact of TEs on genetic innovation by AS, ATSS or ATTS events in response to heat stress.

Keywords: transposable elements, alternative splicing, Direct RNA sequencing

*Speaker