POST_DOCTORAL POSITION in PLANT EPITRANSCRIPTOMICS

Location: Université de Perpignan-Plant Genome and Development Laboratory (http://lgdp.univ-perp.fr/)

Team: Stress induced post-transcriptional reprogrammings in plants

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How to apply: Please send by email your CV with publication list and a cover letter together with the names and contacts of two referees. Informal email inquiries are also welcome.

Qualification: PhD degree in biochemistry or molecular biology

Intended starting date: February 1st 2018
Duration: 1 year contract renewable 1 year, and up to three years.

Job description:
Our team is interested in understanding how plant acclimate and survive heat. We are particularly focused on deciphering the molecular mechanisms that govern the reprogrammings of mRNA stability and translation. Over the past three years, we started to investigate a putative link between the m^6^A epitranscriptomic mark and the heat stress response of the model plant Arabidopsis thaliana. The present position will be part of this research axis.

Chemical modifications added to RNA polymerase II transcripts, now called epitranscriptomic marks, emerged as a new crucial layer in the regulation of gene expression. The most widespread and abundant of these marks is the m^6^A (methylation at position N^6^ of internal adenosines). m^6^As are found in animals, yeasts and plants. They are detected on mRNAs but also on precursors to microRNAs and long non-coding RNAs. Their physiological functions are diverse but a common feature to all organisms is that they are crucial for reproduction, development and growth. At the cellular level, they regulate mRNA stability and translation and very recently they were found to play a direct role on chromatin where they contribute to DNA repair and to IncRNA-dependent gene silencing. At the molecular level, m^6^As act as anchors of specific RNA binding proteins, known as “readers” that will convey m^6^A impact on mRNA homeostasis or IncRNA function. One class of readers, consists in a superfamily of eukaryotic RNA Binding Proteins, that share a structured RNA binding domain known as the YTH domain. The YTH domain, through an evolutionarily conserved aromatic cage, directly binds the m^6^A mark and in turn recruits other proteins to the mRNP that will act to control mRNA homeostasis.
So far, the functional roles of the m^6^A mark and its YTH readers have been documented in mammalian cells and almost exclusively under constitutive conditions, i.e outside of the dynamic situation of stress exposure. In plants, the existence of the m^6^A mark has been recognized and its crucial role for embryogenesis and plant growth and development demonstrated. But beyond that, nothing is known about its cellular nor molecular roles. YTH reader proteins exist in higher plants, but here again, no data are so far available in the literature.
Several of our data support that the m^6^A mark and at least some of its YTH readers contributes to the heat stress response of the plant. The present project will consist in studying how two of the Arabidopsis YTH domain proteins are regulated by stress exposure to participate in the post-transcriptional reprogramming of gene expression to allow the plant to cope with heat.

Job profile: Candidates must be highly motivated and have a PhD degree in biological sciences. Strong knowledge of biochemistry and molecular biology, with hands-on experience is required. Prior experience with plant biochemistry would be an asset.
You must be able to work independently within a team environment, be hard working and have good communication skills. French speaking is NOT required but english speaking is compulsory.