



Proposition d'un sujet de stage au M2 ADAM (2020) -

(1 page max photo comprise)

Titre	Emergence of transcription-factor binding sites from transposable element sequences and impact on gene expression
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Résumé	<p>SCIENTIFIC CONTEXT</p> <p>A large part of the spatiotemporal gene transcriptional regulation underlying plant development and response to the environment is controlled by distal cis-regulatory elements, among which enhancers. Their regulatory effect is mediated by the binding of transcription factors (TFs), which interact with target gene promoters through 3D-loops and drastically alter the rate and quantity of its mRNA biosynthesis. Transposable Elements (TEs) have been shown to participate in the rewiring of gene regulatory networks for some key tissue-specific biological functions in animals. In plants, examples of enhancer elements derived from a particular TE have been described. But how enhancers TF binding sites (TFBS) arise from TE sequences and how they rewire the gene regulatory network in plants remains unclear.</p> <p>RESEARCH PROPOSAL :</p> <p>In a recent study (Fagny et al., biorxiv), we found that enhancers specific to the development of maize husks (bracts protecting the ear) are enriched in miniature inverted-repeat transposable elements (MITEs, a group of non-autonomous DNA transposons). Closer analysis of these enhancer sequences revealed the presence of an unannotated putative TFBS in a particular MITE family. We now would like to investigate the molecular origin of the TFBS sequences within this MITE, and the impact of TE polymorphisms on gene expression regulation across different maize genotypes. For this, the student will first reconstruct the MITE amplification dynamics in the reference B73 maize genome (sequence extraction, dendrogram) and will analyze the presence/absence of the TFBS in the different copies of the tree. He/she will then analyze polymorphism of TFBS-carrying MITE copies among 8 maize genotypes for which we have full genome sequence assembly (comparative genomics). Finally, he/she will analyze the impact of TFBS polymorphisms on gene expression using mRNA-seq data already generated (transcriptomics). The student will acquire knowledge on biological features of transposable elements and enhancers, as well as know-how on the exploitation of genomic sequence and annotation, phylogeny and within-species comparative genomics. Most of the bioanalyses can be conducted using ready-to-use softwares, but if the student is interested, our team can train him/her to bioinformatic tools involving programming.</p>
Photo	<p>The diagram shows three scenarios for gene expression in maize:</p> <ul style="list-style-type: none"> Maize 1: A MITE with TFBS (represented by a blue box) is located upstream of a GENE (blue box). This configuration results in <i>Expression</i> of the gene, indicated by a wavy line above the gene. Maize 2: A MITE without TFBS (represented by an orange box) is located upstream of a GENE (blue box). This configuration results in <i>No expression</i>. Maize 3: No MITE is present upstream of the GENE (blue box). This configuration also results in <i>No expression</i>.