

International Conference On

PLANT SCIENCE & MOLECULAR BIOLOGY

October 22-23, 2018 | Paris, France



Stephane Maury

University Orleans INRA, France

Role of epigenetic in tree phenotypic plasticity in a context of climate changes

Global climate changes in progress will impact forest productivity notably through reduced water availability and heat periods. One possibility to adapt is phenotypic plasticity for which epigenetic mechanisms are proposed to be a main source of flexibility. Our objective is to evaluate the potential of DNA methylation to significantly participate to phenotypic plasticity in trees, fixed and perennials organisms with major ecological roles. Over the 10 last years, using an integrative approach with ecophysiological, biochemical, transcriptomics, epigenomics (MeDIP, WGBS, Mobilome) and reverse genetics (RNAi lines) tools, we were able to dissect in the shoot apical meristem (center of the shoot morphogenesis) the response of trees to environmental variations. This work was assessed in distinct experimental set-ups from greenhouse to field plantations as well as during the stress or months post-stress. Our data (recently published and unpublished) showed that Differentially Methylated Regions (DMRs) are associated to active TE and differentially expressed genes with biological functions related to stress response and phytohormone

signaling. Altogether, our data proposed that DNA methylation is a source of flexibility associated to phenotypic plasticity in trees opening perspectives for tree breeding. The role of epigenetic mechanisms in tree adaptation and microevolution will be also presented through the results obtained in the frame of the national project EPITREE (ANR-17-CE32-0009-01). Quantitative and population genomics analyses carried out in WP2. *GEA: gene environment association ; epiGEA: epigenetics environment association ; QTL: quantitative trait locus ; epiQTL: epigenetic QTL ; eQTL: expression QTL ; QTEpi: quantitative trait epilocus ; eQTEpi: expression QTEpi ; QTT: quantitative trait transcript ; h2: heritability ; Fst: genetic differentiation between populations ; epiFst: epigenetic differentiation between populations ; Qst: quantitative differentiation between populations ; epiQst : epigenetic quantitative differentiation between populations ; SNP: single nucleotide polymorphism ; SMP: single methylation polymorphism ; DMR: differentially methylated region.*

Biography

Stephane Maury is the Professor at the University of Orleans (France) INRA, team leader (ARCHE) and has his expertise in plant physiology and epigenomics for teaching and research. He is working for 15 years in the development of epigenomics in crops and trees to better understand the physiology of plant response to abiotic stress and perspectives in plant breeding. He has a long expertise of working with academic and private partners in various projects concerning the role of epigenetic in plants. He is actually the coordinator of a national research project concerning the role of epigenetic in trees adaptation and microevolution (ANR EPITEE).

stephane.maury@univ-orleans.fr