TEs as a major driver of genomic variation in trees ? Jumping MITEs in common beech revealed by TIPs and eccDNA

Abirami Soundiramourtty*[1], Lauren Clément[1], Christel Llauro[1], Olivier Panaud[1], Christophe Plomion[2], Marie-Christine Carpentier[1], Jean-Marc Aury[3], and Marie Mirouze[1,4]

[1]Laboratoire Génome et développement des plantes – Université de Perpignan Via Domitia, Centre National de la Recherche Scientifique – Bât. T 58, avenue Paul Alduy 66860 PERPIGNAN cedex, France

[2]Biodiversité, Gènes Communautés – Université de Bordeaux, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement – Site de recherche Forêt - Bois de Pierroton - 69, route d'Arcachon F-33612 Cestas Cedex FRANCE, France

[3]Genoscope - Centre national de séquençage [Evry] – Université Paris-Saclay, Direction de Recherche Fondamentale (CEA) – 2, rue Gaston Crémieux CP5706 91057 EVRY Cedex, France

[4]Diversité, adaptation, développement des plantes – Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Centre National de la Recherche Scientifique, Institut de Recherche pour le Développement, Université de Montpellier – Centre IRD de Montpellier 911 av Agropolis BP 604501 34394 Montpellier cedex 5, France

Abstract

Transposable elements (TEs) are predominant in most plant genomes but their ongoing activity and diversity in plant populations has been mostly characterized in annual species. Beech trees (*Fagus sylvatica*) make up most of European forests and are highly threatened by drought and climate change. We sought to investigate the genomic diversity caused by TEs and their adaptive potential in this long-living species. We characterized TE insertion polymorphism (TIPs) in a single population of 150 common beech trees from the preserved Massane forest, a UNESCO world heritage site located near Perpignan, France. Using 672 and 558 LTR (Long Terminal Repeats) retrotransposon and MITE (Miniature Inverted- repeat Transposable Element) families, respectively, we show that the majority of TIPs are highly polymorphic and mostly privately shared within the population. We conducted a Genome-Wide Association Study (GWAS) using these TIPs as markers and identified several candidate TIPs associated with bud burst date, implying their potential involvement in regulating this important phenotypic trait. TIPs distribution revealed several hotspots near stress responsive genes. Bud burst date being an adaptive trait, our results could open new perspectives for the selection of best adapted trees.

Furthermore, given this high level of recent TE activity in common beech, we investigated ongoing TE mobility using extrachromosomal circular DNA (eccDNA) sequencing or mobilome-seq. We detected several active TEs in different beech trees from the Massane and Verzy

---

*Speaker

French forests. Notably, we identified an highly active MITE family, responsible for somatic mutations. We further found several other active MITEs producing abundant eccDNA suggesting that MITEs could play a role in genome dynamics in this species. All together, our study sheds lights on how TEs impact genome evolution and adaptation in a non model perennial species. This could help us gain insights on TE dynamics and amplification *in natura*.

Keywords: Extrachromosomal circular DNA (eccDNA), Transposable Element insertion polymorphism (TIPs), Plants/Trees genomics and adaptations, Climate change, Active TEs, MITEs, LTRs