Recently, interest in sustainably produced bio-energy and bio-based products has skyrocketed due to efforts to reduce reliance on nonrenewable fossil fuels, decrease environmental degradation, mitigate climate change, and develop robust knowledge-based bio-economies. Concomittantly, there has been an increased interest in the utilization of lignocellulosic biomass from forest plantations for second-generation renewable bio-energy feedstocks as they are non-food crops and offer the potential for generating a lower carbon footprint than annually produced crops. Fast-growing tree species such as poplar and eucalypts grown as short-rotation coppice (SRC) represent one of the most appealing sources of renewable biomass feedstock for Northern/Western and Southern Europe as they are easy to establish, produce high yields of lignocellulosic biomass, and offer secondary benefits such low nutrient input. Since the chemical and structural composition of lignified secondary cell walls render woody feedstocks particularly recalcitrant to degradation, improved genetic material is needed to use these SRC as energy crops in an efficient manner. The first step to accomplishing this is to identify genes regulating relevant cell wall properties before moving on to identify the specific desirable allelic variants for breeding. This is the overall goal of TREEFORJOULES with a focus on transcription factors (FT) and miRNAs essential in the regulation of wood formation. The project is organized in 4 workpackages:

• WP1 will investigate transcriptional and post-transcriptional regulation of wood formation in eucalypts and poplar, through in silico integration of global transcriptomics to select Candidate Genes (CG) i.e. TF transcription factors and miRNAs differentially expressed in contrasted wood samples. These GCs will be mapped in WP3 and up to 25 will be functionally validated in transgenic wood sectors. The effects of nutrition and biotic stresses on biomass production and wood properties in different eucalyptus and poplar genotypes will also be assessed.

• WP2 will develop high-throughput NIR spectroscopic methods for wood property measurements including all key cell wall constituants with impact on the saccharification potential of biomass polysaccharides for bio-ethanol production and bio-oil production from lignin.

• WP3 will compare the structural and functional architecture of wood quality in Eucalyptus and Populus by (i) improving the resolution of available genetic maps using high-throughput genotyping methods and common makers (ii) locating precisely and assessing QTLs for wood properties relevant to bioenergy, and (iii) dissecting a major lignin QTL.

• WP4 is devoted to project management, coordination through a website and common

**Background**

bioinformatic network to store, mine, and integrate the high-throughput genomic, genetic, and phenotypic data, as well as transfer of tools and technologies to industry and dissemination of results.