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**NAC-MYB-BASED TRANSCRIPCIONAL NETWORK INVOLVED IN THE REGULATION OF PHENYLALANINE BIOSYNTHESIS IN P. PINASTER**

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Conifer trees divert large quantities of carbon into the biosynthesis of phenylpropanoids, particularly to generate lignin, an important constituent of wood. Since phenylalanine is the precursor for phenylpropanoid biosynthesis, the precise regulation of phenylalanine synthesis and use should occur simultaneously. This crucial pathway is finely regulated primarily at the transcriptional level. Transcriptome analyses indicate that the transcription factors (TFs) preferentially expressed during wood formation in plants belong to the MYB and NAC families. Craven-Bartle et al. (2013) have shown that Myb8 is a candidate regulator of key genes in phenylalanine biosynthesis involved in the supply of the phenylpropane carbon skeleton necessary for lignin biosynthesis. This TF is able to bind AC elements present in the promoter regions of these genes to activate transcription. In Arabidopsis, the transcriptional network controlling secondary cell wall involves NAC-domain regulators operating upstream Myb transcription factors. We have identified in the *P. pinaster* genome three NAC proteins as potential candidates to be involved in vascular development. One of them, PpNAC<sub>1</sub> is expressed both in xylem and compression wood from adult trees and has been thoroughly characterized. Its role upstream the transcriptional network involving Myb8 will be discussed. The understanding of the transcriptional regulatory network associated to phenylpropanoids and lignin biosynthesis in conifers is crucial for future applications in tree improvement and sustainable forest management.