

# XIII REUNIÓN DE BIOLOGÍA MOLECULAR DE PLANTAS

## FORMULARIO PARA EL ENVÍO DE COMUNICACIONES

### DATOS DE CONTACTO

**NOMBRE Y APELLIDOS:** M<sup>a</sup> BELÉN PASCUAL MORENO

**CENTRO:** UNIVERSIDAD DE MÁLAGA

**e-mail:** bpascual@uma.es

**TELÉFONO:** 625720181

**SESIÓN:** Metabolismo y aplicaciones biotecnológicas

**TIPO:** x Oral ( ) Póster

### TRANSCRIPTIONAL REGULATION OF PHENYLALANINE BIOSYNTHESIS AND UTILIZATION

**M<sup>a</sup> Belén Pascual**, Rafael A. Cañas, Blanca Craven-Bartle, Francisco M. Cánovas, Concepción Ávila

*Departamento de Biología Molecular y Bioquímica. Facultad de Ciencias. Universidad de Málaga.  
Campus de Teatinos s/n, Málaga, Spain.*

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 utilization 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 in conifers 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. Constitutive overexpression of Myb8 in white spruce increased secondary-wall thickening and led to ectopic lignin deposition (Bomal et al. 2008). In *Arabidopsis*, the transcriptional network controlling secondary cell wall involves NAC-domain regulators operating upstream Myb transcription factors. Functional orthologues of members of this network described have been identified in poplar and eucalyptus, but in conifers functional evidence had only been obtained for MYBs. We have identified in the *P. pinaster* genome 37 genes encoding NAC proteins, which 3 NAC proteins could be potential candidates to be involved in vascular development (Pascual et al. 2015). 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.

This work is supported by the projects BIO2012-33797, BIO2015-69285-R and BIO-474

#### *References:*

Bomal C, et al. (2008) Involvement of *Pinus taeda* MYB1 and MYB8 in phenylpropanoid metabolism and secondary cell wall biogenesis: a comparative in planta analysis. *J Exp Bot.* 59: 3925-3939.

Craven-Bartle B, et al. (2013) A Myb transcription factor regulates genes of the phenylalanine pathway in maritime pine. *Plant J*, 74: 755-766.

Pascual MB, et al. (2015) The NAC transcription factor family in maritime pine (*Pinus pinaster*): molecular regulation of two genes involved in stress responses. *BMC Plant Biol*, 15: 254.