

Nitrogen metabolism and gene expression landscape in maritime pine.

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Maritime pine (*Pinus pinaster* Aiton) is one the most important conifer species in the southwestern Mediterranean region because of its economic and environmental potential. For this reason, a work program in functional genomics has been developed in the frame of the ProCoGen project. One objective was to complete the knowledge about *P. pinaster* transcriptome with the tissue-specific localization of the gene expression of the low accumulated transcripts in sharper regions (Cañas et al. 2017).

In order to reach these objectives total RNA was obtained from isolated tissues through laser capture microdissection (LCM). Due to the limiting amount from these extracts, the RNA samples were reverse-transcribed and the resultant cDNA amplified using our CRA+ protocol (Cañas et al. 2014). The obtained reads were assembled to improve the previous reference transcriptome. Reads were mapped against this transcriptome and the read accounts analyzed in order to found gene co-expression networks using the WGCNA software.

These results have allowed us the characterization of nitrogen metabolism in maritime pine during the seedling stage stablishing relationships between the different components. This include the identification of new genes with low or very localized expression as occurred for the *PpGS1c* gene encoding a new cytosolic glutamine synthetase. From this starting point, we are developing a new project, MicroNUPE, to identify and study the genes involved in ammonium uptake and regulation in different root tissues that will be isolated through LCM.

Cañas et al. (2017). Plant J, doi:10.1111/tbj.13617.

Cañas et al. (2014). Tree Physiol, 34:1278-1288.

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