

P0989**A Field Experiment to Identify the Molecular Mechanisms Involved in Drought Stress Adaptation in Maritime Pine (*Pinus pinaster* Ait.)***Date: Monday, January 12, 2015**Room:***Gregoire Le Provost** , INRA, BIOGECO, UMR 1202, CESTAS, France

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Maritime pine is a foreground species in South-Western Europe for which a breeding program started half a century ago. Early indirect selection criteria are now being investigated to develop varieties adapted to more limited water resource. In this context, genes in particular, offer diagnostic tools of choice, given that they are link to trait variation. With the main goal to identify key molecular players involved in drought stress adaption, we implemented a field experiment where two full sib families (Corses*Landes, Landes*Maroco) were analysed. For each family, the Maximum Daily Shrinkage (Maximum of Diameter (M) - minimum of diameter (m) per day, MDS) or MDS has been used to identify extreme phenotypes (Low vs. high MDS) over dried period. Two needles sampling (August and September) were performed in 2012 on 10 individuals for each phenotype and family. Two transcriptomics approaches were put in place to identify relevant genes for drought stress response. A targeted approach based on cuticle biosynthesis genes and a whole transcriptome characterization using a high through put sequencing approach. Our results revealed that high MDS phenotypes are characterized by a higher cuticular wax content. An ecophysiological characterization have also been implemented (predaw and midday leaf water potential). These analyses have shown that during water stress, high MDS phenotypes are (i) able to function in a greater range of water potential and (ii) have also a better recovery during the night suggesting different strategies in water metabolism in these contrasted phenotypes.

Handouts

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January 10 - 14, 2015

Where:

San Diego, CA

