

## **BioISI Research Seminar**

### **The cork oak EST project - Uncovering the molecular basis of mycorrhizal symbiosis using next generation sequencing**



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**BioISI / FCUL**

**When: May 28, Monday - 11h00**  
**Where: Building C1, Room 1.3.15**

Ectomycorrhizal symbiosis is essential for the life and health of trees in temperate and boreal forests where it plays a major role in nutrient cycling and in functioning of the forest ecosystem. Trees with ectomycorrhizal root tips are more tolerant to environmental stresses, such as drought, and biotic stresses such as root pathogens. Detailed information on these molecular processes is essential for the understanding of symbiotic tissue development in order to optimize the benefits of this natural phenomenon. The current project is integrated in the effort for covering the transcriptome of *Quercus suber* and is focused on ECM symbiotic interaction. Next generation sequencing tools allow the analysis of non model ectomycorrhizal plant-fungal interactions that can contribute to find the “symbiosis toolkits” and better define the role of each partner in the mutualistic interaction. By using 454 pyrosequencing we compared ectomycorrhizal cork oak roots with non-symbiotic roots. From the two cDNA libraries sequenced, over 2 million reads were obtained that generated 19552 cork oak root unique transcripts. A total of 2238 transcripts were found to be differentially expressed when ECM roots were compared with non-symbiotic roots. These up- and down-regulated genes lead to the identification of a number of insights into the molecular mechanisms governing this important symbiosis. In cork oak roots, ectomycorrhizal colonization resulted cell wall remodelling, activation of the secretory pathway, alterations in flavonoid biosynthesis, and expression of genes involved in the recognition of fungal effectors, like those implicated in pathogenic interactions. In addition, we identified genes involved in specific ectomycorrhizal functions such as nutrient exchange with the fungal partner, increased lateral root formation or root hair decay. These findings provide a global overview of the transcriptome of an ectomycorrhizal host root, and constitute a foundation for future studies on the molecular events controlling this important symbiosis.