*Type of paper: Oral presentation*

**Combining landscape ecology, isotope chemistry and -omics to assess air pollution and climate change effects on circum-Mediterranean mountain conifer forests**

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Assessing the impact of air pollution and climate change on ecosystems is a challenging task. Field studies are typically confused by the concurrence of multiple stressors that show complex patterns of spatio-temporal variation. As a result, disentangling their partial contributions is obscure since the observed ecosystem response is the outcome of many interactive mechanisms operating across hierarchical levels, from the landscape to the molecular level. Moreover, current responses to those global change components are frequently constrained by legacy effects of past land-use changes. Fortunately, to cope with this challenge, new sensors, computational capacity and methodological approaches from the fields of environmental monitoring, advanced chemistry and molecular biology are now available and ready to be used in ecosystem studies under an integrative and collaborative frame. In this communication, we present the overall design and main observed trends from a research programme in which landscape analysis, forest and soil ecology, isotopic chemistry, dendrological, physiological, metabolomic, genomic and transcriptomic techniques are being integrated, to assess N deposition and climate change effects on western Mediterranean mountain conifer forests. At the landscape level, assessment of back trayectories of air masses, rainfall chemistry, 13C-15N in tree-rings and climatic trends allow to characterize temporal and geographic gradients of stressors. Additionally, natural abundance of 13C-15N in soil profiles further allow for inferences about differential past land-uses among regions (contribution of C3 or C4 plant inputs to the soil organic matter, overall openness of the N cycle). At the plot level, 15-N labelling manipulative experiments and vector analysis of soil eco-enzyme stoichiometric shifts reveals changes in biogeochemical fluxes and nutrient limitations. At the tree level, continuous monitoring of sap-flow and secondary growth, and metabolic profiles of plat tissues allow to draw a picture on the tree physiological responses. Finally, at the molecular level, genomic analysis of soil samples and transcriptomic analysis of plant tissues inform on shifts in soil microbial communities and in the capacity of the trees to cope with stress through differential gene expression.

Acknowledgements to MINECO-Spain, projects CGL2010-18976 and CGL2013-48843-C2-R