

## ADAPTIVE GENETIC DIVERSITY OF CONIFEROUS FOREST TREES OF THE ITALIAN ALPS

Elena Mosca<sup>1</sup>, Nicola La Porta<sup>2</sup>, Giovanni G. Vendramin<sup>3</sup>, David B. Neale<sup>1</sup>

<sup>1</sup>*University of California at Davis, Department of Plant Sciences, Davis, United States*

<sup>2</sup>*Fondazione Edmund Mach Natural Resources, S. Michele, Italy*

<sup>3</sup>*Consiglio Nazionale delle Ricerche Plant Genetics Institute, Florence division, Sesto Fiorentino, Italy*

emosca@ucdavis.edu

Alpine environments are changing rapidly due to climate change and other anthropogenic factors. Coniferous trees are key components of the alpine landscape and are acutely impacted by changing environment. Our goal is quantify and understand the standing adaptive genetic diversity in Alpine conifers so that we can have a baseline reference to monitor genetic change in populations and to have diagnostic tools for assisted migration if that becomes a desired forest management option. We have begun by resequencing candidate genes for adaptive traits in four species: *Abies alba* Mill., *Larix decidua* Mill., *Pinus cembra* L. and *Pinus mugo* Turra. For each species 12 individuals were included in the sequencing panel. Trees were sampled from several diverse Alpine locations, such as Pyrenees, Massif Central, Alps, Apennines and Carpathian. Seeds from sampled trees were germinated and the DNA isolated from the megagametophyte tissue. Almost 800 amplicons were resequenced to identify the single nucleotide polymorphisms (SNP) in the four species. As expected, the two pines showed higher percentage of polymorphic amplicons, and higher number of "good" SNP than the others. After validating the called SNP by visual checking of chromatograms, population genetics will be described by estimating its diversity, divergence and tests of neutrality. A second aim is to determine the complex pattern of the adaptation to changing environment by calculating the population genetic analysis in the four species. Genotyping chips for the four species will be designed and genotyping will be conducted for 1000 trees per species in Italian Alps.