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Genetic imprints and environment effects in a common garden of 500 Picea abies families from 160 sites throughout the Alps

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Norway spruce is one of the economically and ecologically most important tree species in the Alps as well as in Europe. Given current climate change scenarios, a full understanding of the function of complex traits and their genetic base appears to be the only way to cope with effects that may be a menace to the performance and the survival of this species. In 2013 we established a common garden nearby Trento, Italy, using seeds from a mapping population constituted by the half-sib progeny of 518 families from 160 sites in the Alps. The phenotypic traits assessed were: germination time, bud-set, bud-burst, height and biomass parameters. Preliminary results show significant differences in germination and bud-set, and Northern families generally grew more in the common garden conditions than Southern ones. Parallel to the phenotypic assessment, genotyping was carried out on needle samples from the mother trees, and a candidate gene-based approach was used to search for association between single-nucleotide polymorphisms (SNP) detected in genes putatively involved in the control of the measured adaptive traits and the observed phenotypic variation. The discovery of polymorphisms underlying adaptive phenotypic traits is a fundamental goal of molecular genetics. Elucidation of the genetic components for ecologically relevant traits through association mapping at markers in candidate genes has been achieved for a variety of adaptive phenotypes in other tree species, and it has important applications ranging from marker assisted breeding to gene conservation in the face of climate change.

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Adaptation of forest trees to climate change in the Alps: a study on ecologically different families of Pinus cembra and Picea abys

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This research project investigates the climate-change related adaptive potential of *Pinus cembra* L.and *Picea abies* L., two keyspecies of the subalpine and treeline ecotones in the Alps. The microclimate of these ecotones is known to be particularly sensitive to climate change, thus a full understanding of the function of given complex traits and their genetic base seems to be important to safeguard survival of the species. For both trees, there is some evidence that genetic variation may be associated to environment and in particular to precipitation, showing the importance of water availability. Another major cause of the species decline is the fungus *Phacidium infestans*, which attacks *P. cembra* at the juvenile stage.
For each species, four to six families from ecologically contrasting environments were chosen for an experiment on drought stress and phenology. The experiment was carried out in a growth chamber during spring 2014 and several phenotypic and physiological parameters were measured. Needle samples were collected to assess changes in gene expression among seedling provenances. For *P. cembra*, the potential differences in susceptibility to the pathogen infection was tested among seedling of different provenances. A gene expression study, intended as a first step towards landscape genomics and longer term adaptation studies, will allow the discovery of suites of genes involved in these adaptive responses. Moreover, a reciprocal trasplanting experiment across core-perypherical gradients will confirm the environmental effects on species survival and could provide important information for species genetic conservation and its forestry management.