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**PROGRAM,  
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## Phenomics of *Picea abies*. Characterization of phenotypic traits involved in long-term adaptation to climate change and their genetic base

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Norway spruce (*Picea abies* (L.) Karst) is one of the ecologically and economically (timber, tourism) most important tree species in the Trentino-Alto Adige region as well as in the whole of Europe. Considered the current climate change scenarios, a full understanding of the functioning of given complex traits and their genetic base appears to be the only effective way to cope with effects that may be a menace to the performance and the survival of this species. Adaptation to drought stress is among the greatest challenges to forest trees in the current climate change scenario.

In spring 2013, a Norway spruce common garden was established at the Casteller (Trento) nursery run by the Forest service of the Provincia Autonoma di Trento. In early May seeds from 520 certified families covering the entire Alpine range (in cooperation with WSL Switzerland, BFW Vienna, INRA Avignon) seeds were planted as to obtain a half-sib population of 7750 individuals, 15 individuals per family. Mother trees were selected so as to best capture the ecological and specific diversity of Alpine *P. abies* ecosystems. Growth and phenology traits assessed were: germination time, bud burst and bud set, height at the end of the vegetation period. Parallel to the establishment of the common garden, DNA was extracted from needles and from mega gametophytes (IGV- CNR, Sesto Fiorentino) so as to perform the genotyping of a chip of 384 single-nucleotide polymorphisms (SNP) designed from previous work on *Picea* spp. (Chen *et al.* 2011; Canadian Arborea Project (<http://www.arborea.ulaval.ca>); Scalfi *et al.* submitted). A candidate gene-based approach will be then used to search for genetic association between single-nucleotide polymorphisms (SNP) markers detected in candidate genes putatively involved in the control of the measured adaptive traits and the observed phenotypic variation. The discovery of polymorphisms that underlie 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 putative applications ranging from marker assisted breeding to gene conservation in the face of climate change.

## Evidence for past and present hybridization in three Antarctic icefish species provides new perspectives in the study of an evolutionary radiation

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Determining the timing, extent, and underlying causes of inter-specific gene exchange during or following speciation is central to understanding species' evolution. Antarctic notothenioid fish, thanks to the acquisition of antifreeze glycoproteins during Oligocene transition to polar conditions, experienced a spectacular radiation to >100 species during Late Miocene cooling events. The impact of recent glacial cycles on this group is poorly known, but alternating warming and cooling periods may have affected species' distributions, promoted ecological divergence into recurrently opening niches, and/or possibly brought allopatric species into contact. Using microsatellite markers and statistical methods including Approximate Bayesian Computation, we investigated genetic differentiation, hybridization and the possible influence of the last glaciation/deglaciation events in three icefish species of the genus *Chionodraco*. Our results provide strong evidence of contemporary and past introgression by showing that: i) a substantial fraction of contemporary individuals in each species has mixed ancestry; ii) evolutionary scenarios excluding hybridization or including it only in ancient times have small or zero posterior probabilities; iii) the data support a scenario of interspecific gene flow associated with the two most recent interglacial periods. Glacial cycles might therefore have had a profound impact on the genetic composition of Antarctic fauna, as newly available shelf areas during the warmer intervals might have favoured secondary contacts and hybridization between diversified groups. If our findings are confirmed in other notothenioids, they offer new perspectives for understanding evolutionary dynamics of Antarctic fish, and suggest a need for new predictions on the effects of global warming in this group.