

Genomic data provides new insights on the demographic history, local adaptation pattern and genetic basis of quantitative traits in Norway spruce.

Pascal Milesi^{1,2}, Jun Chen¹, Lili Li¹, Marion Orsucci¹, GG Vendramin⁵, Jelena Aleksic⁶, Gunnar Jansson³, Bo Karlsson⁴, Mats Berlin³ and Martin Lascoux¹

¹Department of Ecology and Genetics, Evolutionary Biology Center, Uppsala University, Sweden.

²Science for Life Laboratory, Uppsala University, Sweden.

³Forestry Research Institute of Sweden (Skogforsk), Uppsala, Sweden.

⁴Forestry Research Institute of Sweden (Skogforsk), Ekebo, Sweden.

⁵Institute of Biosciences and BioResources, CNR, Sesto Fiorentino, Italy

⁶Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia

Norway spruce (*Picea abies*) is a dominant conifer species of major economic importance in northern Europe. Extensive breeding programs were established to improve phenotypic traits of economic interest. In a first study, based on the exome-sequencing of > 1500 trees, we showed that the origin of the breeding material in southern Sweden was highly heterogeneous: some were of local origin but many were recent introductions from the rest of the natural range. The mixed origin of the trees together with phenotypic data retrieved from the Swedish breeding program offered a unique opportunity to i) investigate the evolutionary and demographic history of Norway spruce (Chen*, Li*, Milesi* et al. 2019), and ii) dissect the genetic basis of local adaptation of three quantitative traits: height, diameter and bud-burst (Milesi et al. 2019). First, we reasoned that high pairwise correlations between genotype, phenotype and climatic variables at origin would not be obtained if the current genetic structure among populations were only the result of past demographic events and isolation by distance, reflecting a strong pattern of adaptation to ancestral environment. Through genome-wide association studies (GWAS), we then investigated both the genetic basis of local adaptation to climate and the genetic control of the three afore-mentioned phenotypic traits in Norway spruce. In particular, we showed that the genetic control of growth traits is much more polygenic than that of bud-burst. Our data also highlighted how traits with different patterns of geographical variation can be used to assess the impact of correction for population structure in GWAS. From an applied perspective, we argue that while data from breeding programs might sometimes be incomplete or suboptimal, they are readily available and contain a lot of valuable information for evolutionary biologists.

Keywords: *Demography history inferences, Local adaptation, quantitative traits, polygenic adaptation, Picea abies.*

Chen, J.*, L. Li*, P. Milesi*, G. Jansson, M. Berlin, B. Karlsson, J. Aleksic, G. G. Vendramin, and M. Lascoux. 2019. Genomic data provide new insights on the demographic history and the extent of recent material transfers in Norway spruce. *Evol. Appl.* 12:1539–1551.

Milesi, P., M. Berlin, J. Chen, M. Orsucci, L. Li, G. Jansson, B. Karlsson, and M. Lascoux. 2019. Assessing the potential for assisted gene flow using past introduction of Norway spruce in southern Sweden: Local adaptation and genetic basis of quantitative traits in trees. *Evol. Appl.* 1–14.