Genomic maladaptation to climate change within-populations and adaptive potential of Scots pine (*Pinus sylvestris* L.)

M. Sammoudi, S.C. González Martínez, T. Francisco*

*National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux, BIOGECO, 69 Route d'Arcachon, 33612 Cestas Cedex, France, *mawsam.sammoudi@inrae.fr*

Keywords: climate change, climate (mal)adaptation, adaptive potential, *Pinus sylvestris*

Forests are vital to ecological balance and society, holding up to 80% of terrestrial biodiversity. However, they are increasingly showing signs of stress and decline. Long generation times and low dispersal abilities of forest trees could exacerbate climate change impacts through limited niche tracking and slow genetic adaptation, raising the risk of population maladaptation. Nevertheless, key determinants in forest trees, such as within-population variation in traits related to climate adaptation and the potential for rapid evolution, have often been overlooked, despite their potential to help mitigate the adverse effects of climate change. Understanding responses and quantifying the adaptive potential of forest trees to climate change is thus a critical challenge for conservation of terrestrial ecosystems.

In this study, we investigated population climatic (mal)adaptation across the Scots pine (*Pinus sylvestris* L.) range, extending work at shorter spatial scales, and assessed the within-population climate maladaptation and genetic adaptive potential of two contrasting populations using two cohorts (i.e., adults and juveniles).

More specifically, we used genotype–environment association (GEA) based on 34,848 SNPs across 1,670 trees from 79 populations covering the species' range to identify climate-associated loci and forecast future climate maladaptation using the genomic offset approach. Then, focusing on two natural populations located in Finland and Scotland, with 500 adults and 250 juveniles genotyped per population, we quantified individual deviations from the predicted optimal genomic compositions to estimate within-population (mal)adaptation variability. We compared adults' and juveniles' climatic maladaptation to assess intergenerational adaptive genetic responses to climate change.

We hypothesized that (1) individual climate (mal)adaptation greatly varies within-population, and (2) juveniles exhibit lower levels of climate maladaptation than adults due to adaptive genetic responses. This study, in addition to shedding light on the adaptive mechanisms of Scots pine, could guide forest management strategies in the face of climate change.