

Sonja Kujala: “Convergent adaptation in northern *Pinus sylvestris* and *Picea abies*? – Genotyping the Evoltree ISS Punkaharju”

I was granted 10,000 euros by Evoltree for genotyping the Evoltree ISS (Intensive Study Site) in Punkaharju, Finland. Within the site, roughly 500 Scots pine trees have been selected as the study population to represent natural variation found in Southern Finland, and several phenotypes have been measured for these trees over the years.

The genotyping of 470 of these trees took place during 2019-2020. This work was linked with the development of a new 50K SNP-chip for Scots pine, done in collaboration with University of Oulu, Finland, and UK Centre of Ecology and Hydrology, Scotland (Kastally et al, 2022; EU funded B4est programme).

A 400K Thermo Fisher chip was designed from a large number of candidate SNPs arising from various previous sequencing efforts. Punkaharju ISS was genotyped with this 400K chip (Kastally et al, 2022). Genotyping service was done by Thermo Fisher Scientific at Santa Clara, US. Total cost for this 400K genotyping was roughly 60,000 €, of which this Evoltree grant paid 10,000 €. The remaining costs were covered from other funding sources. Link to the published article: <https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.15628>

After quality filtering, roughly 60,000 – 150,000 SNPs remain for the Punkaharju ISS set of 470 trees, depending on the minor allele frequency and linkage disequilibrium cutoffs. The genotyping data is currently being used in various ways: The fine spatial genetic structure of the study site has been investigated by Niskanen et al. (in prep). With the various phenotypes that we have collected over the years from this site, association studies are in progress (Kujala et al., in prep). These projects are proceeding well.

Unfortunately the growth rhythm and cold tolerance data for Norway spruce that was planned to be available through another linked project to study the topics of convergent adaptation was not produced. We will however keep on looking for other opportunities to eventually do this kind of analyses that require careful production of matching phenotypes among the species in comparison. This genotype data, now available for Scots pine, is essential for those efforts.