

EGU2020-21385

<https://doi.org/10.5194/egusphere-egu2020-21385>

EGU General Assembly 2020

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Early Holocene presences of Norway spruce (*Picea abies* L. Karst.) at high latitudes in Norway and Sweden: the genetic story of up to 9550 year old spruce clones in the Scandinavian mountains

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The survival of boreal trees in ice-free cryptic refugia's at high latitudes during the Last Glacial Maximum has been subjected to a long-standing debate. Norway spruce (*Picea abies* L. Karst) is generally believed to have recolonised Scandinavia from the east. Spruce appears for the first time in the pollen assemblages in central Sweden around 3000 years before present (yr BP), however, a growing body of macrofossil and genetic evidence suggested that spruce might have survived in ice-free areas around the Norwegian shore or closer to the Weichselian ice sheet than previously thought. These satellite populations may have contributed to the recolonisation of Scandinavia from the west and may be ancestors to the ancient (up to 9550-year-old) but still living clonal spruce trees occurring today in the Scandinavian mountains (e. g. Old Tjikko and Old Rasmus). Genetic research has shown that modern *P. abies* contain two sequence variants for the maternal inherited mitochondrial mh05 fragment across its Eurasian distribution, of which one is unique to Scandinavia. The Scandinavian variant shows the highest frequency in western Scandinavia and its modern distribution suggests that it was already present before the last glacial period. The Scandinavian variant was also detected in lake sediment dating back to 10300 yr BP at Trøndelag in Central Norway (63°N).

We are using sensitive melting curve qPCR assay and high-throughput sequencing to detect the presence of the Scandinavian variant in several sediment cores covering Scandinavia and north-east & southern Russia. So far, the qPCR melting curve assay detected the Scandinavian variant in peat sediment from northern Finland (~52,000 – 42,000 yr BP), in lake sediments in central Sweden and central Norway (~10,000 – 900 yr BP) and in southern Sweden (~12000 – 11000 yr BP), which is far earlier than currently believed. Additional lakes are being processed and samples positive for the Scandinavian variant will be sequenced to confirm sequence identity. We are also conducting population genetic analysis of the ancient clonal spruce stands to see how these trees are related to the modern spruce forest and weather they have contributed to the recolonization of Scandinavia. The results of this study will increase our understanding of the post glacial colonisation of *P. abies* in Scandinavia after the Last Glacial Maximum.