

EGU2020-19733

<https://doi.org/10.5194/egusphere-egu2020-19733>

EGU General Assembly 2020

© Author(s) 2022. This work is distributed under the Creative Commons Attribution 4.0 License.



Hybridization capture of larch (*Larix* Mill.) chloroplast genomes from sedimentary ancient DNA reveals past changes of Siberian forest

Luise Schulte^{1,2}, Nadine Bernhardt¹, Kathleen Stoof-Leichsenring¹, Heike Zimmermann¹, Luidmila Pestryakova³, Laura Epp¹, and Ulrike Herzschuh^{1,2,4}

¹Alfred-Wegener-Institut Helmholtz-Zentrum für Polar- und Meeresforschung, Forschungsstelle Potsdam, Germany (luise.schulte@awi.de)

²Institut für Biochemie and Biologie, Universität Potsdam, Potsdam, Germany

³Institute of Natural Sciences, North-Eastern Federal University of Yakutsk, Yakutsk, Russia

⁴Institut für Geowissenschaften, Universität Potsdam, Potsdam, Germany

Siberian larch (*Larix* Mill.) forests dominate vast areas of northern Russia and contribute important ecosystem services to the earth. To be able to predict future responses of these forests to a changing climate, it is important to understand also past dynamics of larch populations. One well-preserved archive to study vegetation changes of the past is sedimentary ancient DNA (sedaDNA) extracted from lake sediment cores. We studied a lake sediment core covering 6700 calibrated years BP, from the Taymyr region in northern Siberia. To enrich the sedaDNA for DNA of our focal species *Larix*, we combine shotgun sequencing and hybridization capture with long-range PCR-generated baits covering the complete *Larix* chloroplast genome. In comparison to shotgun sequencing, hybridization capture results in an increase of taxonomically classified reads by several orders of magnitude and the recovery of near-complete chloroplast genomes of *Larix*. Variation in the chloroplast reads confirm an invasion of *Larix gmelinii* into the range of *Larix sibirica* before 6700 years ago. In this time span, both species can be detected at the site, although larch populations have decreased from a forested area to a single-tree tundra at present. This study demonstrates for the first time that hybridization capture applied to ancient DNA from lake sediments can provide genome-scale information and is a viable tool for studying past changes of a specific taxon.